

Protein Sequence Searches - February 2005

All of the sequence databases on ARSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 22, 2005, 09:08:09 ; Search time 11.1333 Seconds
(without alignments)
129.633 Million cell updates/sec

Title: US-08-991-628-1

Perfect score: 74

Sequence: 1 ATQKITYRISGVGID 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 2523

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 79:*

2: pirl:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	37.8	10	2 A60589	sperm-activating p
2	27	36.5	10	2 E60787	sperm-activating p
3	25	33.8	15	2 A27504	histone H2A - mous
4	24	32.4	10	2 E60589	sperm-activating p
5	23	31.1	10	2 PC2044	beta-Kirilowin - M
6	22	29.7	10	2 PT0230	Ig heavy chain CDR
7	22	29.7	15	2 PA0075	fructose-bisphosph
8	22	29.7	15	2 PA0102	fructose-bisphosph
9	22	29.7	15	2 B45115	peptidylprolyl iso
10	21	28.4	10	2 PH0946	T-cell receptor be
11	21	28.4	10	2 G60787	sperm-activating p
12	21	28.4	10	2 F60589	sperm-activating p
13	21	28.4	10	2 G60589	sperm-activating p
14	21	28.4	14	2 PT0259	Ig heavy chain CDR
15	21	28.4	15	2 I65478	C-Ki-ras - hamster
16	21	28.4	15	2 A35417	28K serine protein
17	20	27.0	8	2 F60588	sperm-activating p
18	20	27.0	8	2 G60588	sperm-activating p
19	20	27.0	10	2 C45474	thrombospondin 2 -
20	20	27.0	10	2 A60588	sperm-activating p
21	20	27.0	10	2 E39572	sperm-activating p
22	20	27.0	10	2 D60589	sperm-activating p
23	20	27.0	10	2 B60589	sperm-activating p
24	20	27.0	12	2 A33099	163K exoantigen -
25	20	27.0	12	2 S29830	dimethylalanine mo
26	20	27.0	14	2 C35141	T-cell receptor de
27	20	27.0	15	2 PA0097	starch phosphoryla
28	20	27.0	15	2 S70719	H+-transporting tw
29	19.5	26.4	12	2 S21163	NAD ADP-ribosyltra

30 19 25.7 8 2 S63493
31 19 25.7 8 2 S65647
32 19 25.7 9 2 I49406
33 19 25.7 10 2 A47364
34 19 25.7 10 2 F60787
35 19 25.7 10 2 I60588
36 19 25.7 12 2 D28551
37 19 25.7 12 2 S32473
38 19 25.7 14 2 S59495
39 19 25.7 15 2 PH1320
40 19 25.7 15 2 S71396
41 18.5 25.0 15 2 PT0095
42 18 24.3 6 2 A41946
43 18 24.3 10 2 PT0322
44 18 24.3 10 2 C60527
45 18 24.3 10 2 G60527

ALIGNMENTS

RESULT 1

A60589 sperm-activating peptide (Tyr-2, Asn-3, Gly-5, Ile-9, Asp-10 SAP-I) - slate-pencil urchi
C:Species: Heterocentrotus mamillatus
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C:Accession: A60589

R.Yoshino, K.I.; Kajiwara, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamagu
Comp. Biochem. Physiol. B 94, 739-751, 1989
A:Title: A halogenated amino acid-containing sperm activating peptide and its related p
otus nudus, Echinometra mathaei and Heterocentrotus mamillatus.
A:Reference number: A60527

A:Accession: A60589

A:Molecule type: protein

A:Residues: 1-10 <YOS>

A:Cross-references: UNIPROT:Q7M4B7

C:Superfamily: unassigned animal peptides

Query Match 37.8%; Score 28; DB 2; Length 10;
Best Local Similarity 55.6%; Pred. No. 76;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 YRISGVGID 15

Db 2 YNLGGGGID 10

RESULT 2

E60787 sperm-activating peptide (Ser-3,5,7, Asp-10 speract) - sea urchin (Hemicentrotus pulche
C:Species: Hemicentrotus pulcherimus
C:Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 16-Aug-2004

R.Suzuki, N.; Kajiwara, H.; Nomura, K.; Garbers, D.L.; Yoshino, K.; Kurita, M.; Tanaka, I
Comp. Biochem. Physiol. B 89, 687-693, 1988
A:Title: Some more speract derivatives associated with eggs of sea urchins, Pseudocent

A:Reference number: A60787; MUID:88242184; PMID:3378407

A:Accession: E60787

A:Molecule type: protein

A:Residues: 1-10 <SUZ>

A:Cross-references: UNIPROT:Q7M4C9

C:Comment: This oligopeptide from egg jelly is one of several from this species, all of
at shows some, but not absolute, species restriction.

Query Match 36.5%; Score 27; DB 2; Length 10;

Best Local Similarity 44.4%; Pred. No. 1.2e+02;

Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 7 YRISGVGID 15

Db 2 FSLSGSGVD 10

```
RESULT 3
A27504
Histone H2A - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 17-Feb-1994
C:Accession: A27504
R:Liou, T.J.; Liu, L.; Marzluff, W.F.
Nucleic Acids Res. 15, 3023-3039, 1987
A:Title: Mouse histone H2A and H2B genes: four functional genes and a pseudogene undergo
A:Reference number: A93660; MUID:87174824; PMID:3562244
A:Accession: A27504
A:Molecule type: DNA
A:Residues: 1-15 <IU>

Query Match 33.8%; Score 25; DB 2; Length 15;
Best Local Similarity 62.5%; Pred. No. 4.1e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 TYRISGVG 13
|||:|
Db 4 TYMMSGRG 11

RESULT 4
E60589
sperm-activating peptide (Tyr-2, Ser-3,5, Ala-8, Asp-10 SAP-I) - Echinomatra mathaei
C:Species: Echinomatra mathaei
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-2004
C:Accession: E60589
R:Yoshino, K.I.; Kajitara, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamaguchi,
Comp. Biochem. Physiol. B 94, 739-751, 1989
A:Title: A halogenated amino acid-containing sperm activating peptide and its related pe
ocus nudus, Echinomatra mathaei and Heterocentrotus mamillatus.
A:Reference number: A60527
A:Accession: E60589
A:Molecule type: protein
A:Residues: 1-10 <YOS>
A:Cross-references: UNIPROT:Q7M4C1
A:Note: An identical peptide was isolated from Echinomatra mathaei type A and type B

Query Match 32.4%; Score 24; DB 2; Length 10;
Best Local Similarity 44.4%; Pred. No. 4e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 7 YRISGVGID 15
|||:|
Db 2 YSLSGGAVD 10

RESULT 5
PC2044
beta-Kirilowin - Mongolian snake-gourd (fragment)
C:Species: Trichosanthes kirilowii (Mongolian snake-gourd)
C:Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
C:Accession: PC2044
R:Dong, T.X.; Ng, T.B.; Yeung, H.W.; Wong, R.N.S.
Biochem. Biophys. Res. Commun. 199, 387-393, 1994
A:Title: Isolation and characterization of a novel ribosome-inactivating protein, beta-k
A:Reference number: PC2044; MUID:94168605; PMID:8123040
A:Accession: PC2044
A:Molecule type: protein
A:Residues: 1-10 <DON>
A:Cross-references: UNIPROT:Q7MI16
A:Experimental source: seed
C:Comment: This protein exhibited strong abortifacient activity, and is a ribosome inact
C:Keywords: seed

Query Match 31.1%; Score 23; DB 2; Length 10;
Best Local Similarity 57.1%; Pred. No. 6.1e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 IYRISG 11
|||:|
```

```
Db 3 IIFRLSG 9

RESULT 6
PT0230
lg heavy chain CDR3 region (clone 1-118A) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0230
R:Yanada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Roversa, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0230
A:Molecule type: DNA
A:Residues: 1-10 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match 29.7%; Score 22; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 9.3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 ISGVGI 14
|||
Db 5 IFGVGI 10

RESULT 7
PA0075
fructose-bisphosphate aldolase (EC 4.1.2.13) I - fungus (Fusarium sporotrichioides) (fra
N:Alternate names: aldolase; fructose-1,6,-bisphosphate triosephosphate-lase
C:Species: Fusarium sporotrichioides
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: PA0075; PA0077
R:Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JIPID, October 1994
A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich
A:Reference number: PA0051
A:Accession: PA0075
A:Molecule type: protein
A:Residues: 1-15 <CHO>
A:Cross-references: UNIPROT:Q7M4Z5
A:Note: This form (I) had a molecular weight of 30.6K and an isoelectric point of 5.3
A:Accession: PA0077
A:Molecule type: protein
A:Residues: 1-15 <CH2>
A:Note: this form (II) had a molecular weight of 31.6K and an isoelectric point of 5.4
C:Keywords: aldehyde-lyase; carbon-carbon lyase

Query Match 29.7%; Score 22; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 QKITVRIISGV 12
|::|
Db 3 QEVLSRDSGV 12

RESULT 8
PA0102
fructose-bisphosphate aldolase (EC 4.1.2.13) III - fungus (Fusarium sporotrichioides) (f
C:Species: Fusarium sporotrichioides
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: PA0102
R:Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JIPID, October 1994
A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich
A:Reference number: PA0051
A:Accession: PA0102
A:Molecule type: protein
A:Residues: 1-15 <CHO>
A:Cross-references: UNIPROT:Q7M4Z4
```


C:Keywords: aldehyde-lyase; carbon-carbon lyase

Query Match 29.7%; Score 22; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 QKIVTRISGV 12
: : : : :
DB 3 QEVLGRKSGV 12

RESULT 9

B45115
peptidylprolyl isomerase (EC 5.2.1.8) FKBP51 - human (fragment)
N/Alternative names: FK506-binding protein FKBP51; peptidylprolyl cis-trans isomerase FKBP51
C:Species: Homo sapiens (man)
C>Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: B45115
R:Wiederrecht, G.; Hung, S.; Chan, H.K.; Marcy, A.; Martin, M.; Calaycay, J.; Boulton, D.
J. Biol. Chem. 267, 21753-21760, 1992
A:Title: Characterization of high molecular weight FK-506 binding activities reveals a novel protein
A:Reference number: A45115; MUID:93016131; PMID:1383226
A:Accession: B45115
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <WIE>
A:Cross-references: UNIPROT:O9UDK1
A:Experimental source: JURKAT cells
A:Note: sequence extracted from NCBI backbone (NCBIP:116748)
C:Keywords: cis-trans-isomerase; cyclosporin A binding

Query Match 29.7%; Score 22; DB 2; Length 15;
Best Local Similarity 57.1%; Pred. No. 1.4e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATQKITY 7
: : : : :
DB 1 ATESIAY 7

RESULT 10

PH0946
T-cell receptor beta chain V-D-J region (clone BB12) - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C:Accession: PH0946
R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic encephalomyelitis
A:Reference number: PH0891; MUID:92078857; PMID:1836012
A:Accession: PH0946
A:Molecule type: mRNA
A:Residues: 1-10 <GL>
A:Experimental source: myelin basic protein fragment-reactive T-cell, recovered from experimental allergic encephalomyelitis
C:Keywords: T-cell receptor

Query Match 28.4%; Score 21; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 SGVGID 15
: : : : :
DB 4 SGTGTD 9

RESULT 11

G60787
sperm-activating peptide (Ser-3,5,7 speract) - sea urchin (Anthocidaris crassispina)
C:Species: Anthocidaris crassispina
C>Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 16-Aug-2004
C:Accession: G60787
R:Suzuki, N.; Kajiyura, H.; Nomura, K.; Garbers, D.L.; Yoshino, K.; Kurita, M.; Tanaka, H.
Comp. Biochem. Physiol. B 89, 687-693, 1988

A:Title: Some more speract derivatives associated with eggs of sea urchins, Pseudocentrotus
A:Reference number: A60787; MUID:88242184; PMID:3378407
A:Accession: G60787
A:Molecule type: protein
A:Residues: 1-10 <SUZ>
A:Cross-references: UNIPROT:Q7M4D8
C:Comment: This oligopeptide from egg jelly is one of several from this species, all of which show some, but not absolute, species restriction.

Query Match 28.4%; Score 21; DB 2; Length 10;
Best Local Similarity 37.5%; Pred. No. 1.4e+03;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 7 YRISGVGI 14
: : : : :
DB 2 FSLSGSGV 9

RESULT 12

F60589
sperm-activating peptide (Asn-3, Ser-5 SAP-I) - Echinometa mathaei (type A)
C:Species: Echinometa mathaei
C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-2004
C:Accession: F60589
R:Yoshino, K.I.; Kajiyura, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamaguchi, K.
Comp. Biochem. Physiol. B 94, 739-751, 1989
A:Title: A halogenated amino acid-containing sperm activating peptide and its related peptides from the sea urchin, Echinometa mathaei and Heterocentrotus mamillatus.
A:Reference number: A60527
A:Accession: F60589
A:Molecule type: protein
A:Residues: 1-10 <YOS>
A:Cross-references: UNIPROT:Q7M4C5

Query Match 28.4%; Score 21; DB 2; Length 10;
Best Local Similarity 37.5%; Pred. No. 1.4e+03;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 7 YRISGVGI 14
: : : : :
DB 2 FNLGGGV 9

RESULT 13

G60589
sperm-activating peptide (Tyr-2, Asn-3, Asp-7,10, Arg-8, Ile-9 SAP-I) - Echinometa mathaei
C:Species: Echinometa mathaei
C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-2004
C:Accession: G60589
R:Yoshino, K.I.; Kajiyura, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamaguchi, K.
Comp. Biochem. Physiol. B 94, 739-751, 1989
A:Title: A halogenated amino acid-containing sperm activating peptide and its related peptides from the sea urchin, Echinometa mathaei and Heterocentrotus mamillatus.
A:Reference number: A60527
A:Accession: G60589
A:Molecule type: protein
A:Residues: 1-10 <YOS>
A:Cross-references: UNIPROT:Q7M4C2

Query Match 28.4%; Score 21; DB 2; Length 10;
Best Local Similarity 44.4%; Pred. No. 1.4e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 7 YRISGVGI 15
: : : : :
DB 2 YNLGDRID 10

RESULT 14

PF0259
Ig heavy chain CRD3 region (clone 2-118C) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C;Accession: PT0259
R;Yanada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0259
A;Molecule type: DNA
A;Residues: 1-14 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 28.4%; Score 21; DB 2; Length 14;
Best Local Similarity 57.1%; Pred. No. 2e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 ISGVGID 15
|: |||
Db 6 IAAAGID 12

RESULT 15
I65478
C-Ki-ras - hamster (fragment)
C;Species: Cricetinae gen. sp. (hamster)
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 28-Feb-1997
C;Accession: I65478
R;Takahashi, T.; Moyer, M.P.; Cano, M.; Wang, Q.J.; Mountjoy, C.P.; Sanger, W.; Adrian,
Carcinogenesis 16, 931-939, 1995
A;Title: Differences in molecular biological, biological and growth characteristics betw
A;Reference number: I52734; MUID:95246257; PMID:7728976
A;Accession: I65478
A;Status: Preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-15 <RES>
A;Cross-references: GB:S77069; NID:g914177
C;Genetics:
A;Gene: c-Ki-ras

Query Match 28.4%; Score 21; DB 2; Length 15;
Best Local Similarity 44.4%; Pred. No. 2.2e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 7 YRISGVGID 15
|: |||
Db 4 YKLIVVGAD 12

Search completed: February 22, 2005, 09:46:22
Job time : 12.1333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 22, 2005, 08:53:13 ; Search time 52.6 Seconds
(without alignments)
146.030 Million cell updates/sec

Title: US-08-991-628-1

Perfect score: 74

Sequence: 1 ARQKITYRISGVGID 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 6622

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	37.8	10	2 Q7M4B7	Q7M4B7 heterocentrotus
2	27	36.5	10	2 Q7M4C9	Q7M4C9 hemicentrotus
3	27	36.5	15	2 Q9QVN0	Q9QVN0 rattus sp.
4	26	35.1	12	1 OP83 DROVI	P17645 drosophila
5	24	32.4	10	2 Q7M4C1	Q7M4C1 echinometra
6	24	32.4	11	2 Q7M4G1	Q7M4G1 echinometra
7	24	32.4	11	2 Q77899	Q77899 oreochromis
8	24	32.4	11	2 Q77900	Q77900 oreochromis
9	24	32.4	11	2 Q77901	Q77901 oreochromis
10	24	32.4	11	2 Q77902	Q77902 oreochromis
11	24	32.4	11	2 Q77903	Q77903 oreochromis
12	24	32.4	11	2 Q77904	Q77904 oreochromis
13	24	32.4	11	2 Q77905	Q77905 oreochromis
14	24	32.4	11	2 Q77916	Q77916 oreochromis
15	24	32.4	11	2 Q77917	Q77917 oreochromis
16	24	32.4	13	1 FLET LIMFT	P82064 limnodystat
17	23	31.1	10	1 VES6_BACSU	P80699 bacillus su
18	23	31.1	10	2 Q7M1I6	Q7M1I6 trichosanthe
19	23	31.1	15	1 D1DH PSBSP	P80701 pseudomonas
20	23	31.1	15	2 Q9UCC0	Q9UCC0 homo sapien
21	22	29.7	15	2 Q7M4Z4	Q7M4Z4 fusarium sp
22	22	29.7	15	2 Q7M4Z5	Q7M4Z5 fusarium sp
23	21	28.4	8	1 DY51 LIMIN	P82079 limnodystat
24	21	28.4	8	2 O52062	O52062 bacillus me
25	21	28.4	10	2 Q7M4C2	Q7M4C2 echinometra
26	21	28.4	10	2 Q7M4C5	Q7M4C5 echinometra
27	21	28.4	10	2 Q7M4D8	Q7M4D8 anthocidari
28	21	28.4	15	1 R13A SPIOL	P82454 spinacia ol
29	21	28.4	15	2 Q6JDJ7	Q6JDJ7 canis famli
30	21	28.4	15	2 Q7M3G3	Q7M3G3 bos taurus
31	21	28.4	15	2 Q9WTA3	Q9WTA3 amorphophal

32 21 28.4 15 2 Q80X04 mesocricetu
33 20 27.0 8 2 Q7M4C6 pseudobolat
34 20 27.0 10 2 Q7M3T4 tripneustes
35 20 27.0 10 2 Q7M4B3 strongyloce
36 20 27.0 10 2 Q7M4B9 heterocentr
37 20 27.0 10 2 Q7M4C4 echinometra
38 20 27.0 10 2 Q95H99 papio anubi
39 20 27.0 10 2 Q95HF4 papio anubi
40 20 27.0 10 2 Q95HF5 papio anubi
41 20 27.0 10 2 Q95HF6 papio anubi
42 20 27.0 10 2 Q95HF7 papio anubi
43 20 27.0 10 2 Q95HF8 papio anubi
44 20 27.0 10 2 Q95HF9 papio anubi
45 20 27.0 10 2 Q95H90 papio anubi

ALIGNMENTS

RESULT 1

Q7M4B7 PRELIMINARY; PRT; 10 AA.
AC Q7M4B7;
DT 01-MAR-2004 (TRENBLrel. 26, Created)
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Sperm-activating peptide (Tyr-2, Asn-3, Gly-5, Ile-9, Asp-10 SAP-I).
DS I.
OS Heterocentrotus mammillatus (Slate-pencil urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinometridae;
OC Heterocentrotus.
OX NCBI_TaxID=31180;
RN [1]_SEQUENCE.
RP Yoshino K.I., Kajiyura H., Nomura K., Takao T., Shimonishi Y.,
RA Kurita M., Yamaguchi M., Suzuki N.;
RT "A halogenated amino acid-containing sperm activating peptide and its
RT related peptides isolated from the egg jelly of sea urchins,
RT Tripneustes gratilla, Pseudoboletia maculata, Strongylocentrotus
RT nudus, Echinometra mathaei and Heterocentrotus mammillatus.";
RL Comp. Biochem. Physiol. 94:739-751(1989).
DR PIR; A60589; A60589.
SQ SEQUENCE 10 AA; 922 MW; 128AC37878787724 CRC64;

Query Match 37.8%; Score 28; DB 2; Length 10;
Best Local Similarity 55.6%; Pred. No. 7.9e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 YRISGVGID 15
| | | | |
Db 2 YNLGGGGID 10

RESULT 2

Q7M4C9 PRELIMINARY; PRT; 10 AA.
AC Q7M4C9;
DT 01-MAR-2004 (TRENBLrel. 26, Created)
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Sperm-activating peptide (Ser-3,5,7, Asp-10 speract).
OS Hemicentrotus pulcherrimus (Sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
OC Hemicentrotus.
OX NCBI_TaxID=7650;
RN [1]_SEQUENCE.
RP Suzuki N., Kajiyura H., Nomura K., Garbers D.L., Yoshino K., Kurita M.,
RA Tanaka H., Yamaguchi M.;
RT "Some more speract derivatives associated with eggs of sea urchins,
RT Pseudocentrotus depressus, Strongylocentrotus purpuratus,

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RT Hemientrotus pulcherrimus and Anthocidaris crassispina.";
RL Comp. Biochem. Physiol. 89:687-693(1988).
DR PIR; E60787; E60787.
SQ SEQUENCE 10 AA; 925 MW; 933B53658865B735 CRC64;

Query Match          36.5%; Score 27; DB 2; Length 10;
Best Local Similarity 44.4%; Pred. No. 1.2e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 7 YRISGVGID 15
   :|||:|
Db 2 FSLSGSGVD 10

RESULT 3
Q9QVNO
ID Q9QVNO PRELIMINARY; PRT; 15 AA.
AC Q9QVNO;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Rattus sp.
OS G12a-derived nexin, GDN, protease nexin-1 (Fragment).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=92207980; PubMed=1554734;
RA Rovelli G., Stone S.R., Guidolin A., Sommer J., Monard D.;
RT "Characterization of the heparin-binding site of glia-derived
RL nexin/protease nexin-1.";
RL Biochemistry 31:3542-3549(1992).
FT NON_TER 1 1
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1702 MW; 3D999487E58AF9A2 CRC64;

Query Match          36.5%; Score 27; DB 2; Length 15;
Best Local Similarity 57.1%; Pred. No. 1.7e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 7 YRISGVG 13
   :|||:|
Db 2 YNNGVG 8

RESULT 4
OPS3 DROVI
ID OPS3 DROVI STANDARD; PRT; 12 AA.
AC P17645;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Opsin Rh3 (Inner R7 photoreceptor cells opsin) (Fragment).
GN Name=Rh3;
OS Drosophila virilis (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7244;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90249748; PubMed=2140105;
RA Fortini M.E., Rubin G.M.;
RT "Analysis of cis-acting requirements of the Rh3 and Rh4 genes reveals
RT a bipartite organization to rhodopsin promoters in Drosophila
RL melanogaster.";
RL Genes Dev. 4:444-463(1990).
CC -!- FUNCTION: Visual pigments are the light-absorbing molecules that
CC mediate vision. They consist of an apoprotein, opsin, covalently
CC linked to cis-retinal.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- MISCELLANEOUS: Each Drosophila eye is composed of 800 facets or

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ommatidia. Each ommatidium contains 8 photoreceptor cells (R1-R8),
the R1 to R6 cells are outer cells, while R7 and R8 are inner
cells.
CC -!- MISCELLANEOUS: Opsin Rh3 is sensitive to UV light.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC Opsin subfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X51350; CAA35742.1; -
CC FlyBase; FBgn0013091; Dvir\Rh3.
CC InterPro; IPR000276; GPCR_Rhodopsn.
CC InterPro; IPR001760; Opsin.
CC PROSITE; PS00237; G-PROTEIN RECEPTOR FL_1; PARTIAL.
CC PROSITE; PS00238; OPSIN; PARTIAL.
KW G-protein coupled receptor; Glycoprotein; Phosphorylation;
KW Photoreceptor; Retinal protein; Transmembrane; Vision.
FT CARBOHYD 10 10 N-linked (GlcNAc. .) (Probable).
FT NON_TER 12 12
FT NON_TER 15 15
SQ SEQUENCE 12 AA; 1253 MW; 04024E43495865B0 CRC64;

Query Match          35.1%; Score 26; DB 1; Length 12;
Best Local Similarity 57.1%; Pred. No. 2.1e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 7 YRISGVG 13
   :|||:|
Db 3 FNISGIG 9

RESULT 5
Q7M4C1
ID Q7M4C1 PRELIMINARY; PRT; 10 AA.
AC Q7M4C1;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Sperm-activating peptide (Tyr-2, Ser-3, 5, Ala-8, Asp-10 SAP-I).
OS Echinometra mathaei (Rock boring urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinoidea; Euechinoidea; Echinacea; Echinoidea; Echinometridae;
OC Echinometra.
OX NCBI_TaxID=31178;
RN [1]
RP SEQUENCE.
RA Yoshino K.I., Kajiwara H., Nomura K., Takao T., Shimonishi Y.,
RA Kurita M., Yamaguchi M., Suzuki N.;
RT "A halogenated amino acid-containing sperm activating peptide and its
RT related peptides isolated from the egg jelly of sea urchins,
RT Tripneustes gratilla, Pseudoboletia maculata, Strongylocentrotus
RT nudus, Echinometra mathaei and Heterocentrotus mammillatus.";
RL Comp. Biochem. Physiol. 94:739-751(1989).
DR PIR; E60589; E60589.
SQ SEQUENCE 10 AA; 925 MW; 8B9856D87865B735 CRC64;

Query Match          32.4%; Score 24; DB 2; Length 10;
Best Local Similarity 44.4%; Pred. No. 4e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 7 YRISGVGID 15
   :|||:|
Db 2 YSLSGGVD 10

RESULT 6
O77899
ID O77899 PRELIMINARY; PRT; 11 AA.

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AC O77899;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE MHC class II B locus 14 (Fragment)
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Labroidel;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98315113; PubMed=9649539;
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
RA Figueroa F., Sultmann H., Klein J.;
RT "Linkage relationships and haplotype polymorphism among cichlid MHC
RT class II B loci.";
RL Genetics 149:1527-1537(1998).
DR EMBL; AF050009; AAC41348.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 11 AA; 1349 MW; 81C12D8EB7341B41 CRC64;

Query Match 32.4%; Score 24; DB 2; Length 11;
Best Local Similarity 66.7%; Pred. NO. 4.3e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 IYTRIS 10
DB 3 MYRLS 8

RESULT 7
O77900 PRELIMINARY; PRT; 11 AA.
ID O77900
AC O77900;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE MHC class II B locus 14 (Fragment)
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Labroidel;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98315113; PubMed=9649539;
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
RA Figueroa F., Sultmann H., Klein J.;
RT "Linkage relationships and haplotype polymorphism among cichlid MHC
RT class II B loci.";
RL Genetics 149:1527-1537(1998).
DR EMBL; AF050010; AAC41349.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 11 AA; 1349 MW; 81C12D8EB7341B41 CRC64;

Query Match 32.4%; Score 24; DB 2; Length 11;
Best Local Similarity 66.7%; Pred. NO. 4.3e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 IYTRIS 10
DB 3 MYRLS 8

RESULT 8
O77901 PRELIMINARY; PRT; 11 AA.
ID O77901
AC O77901;
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DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE MHC class II B locus 14 (Fragment)
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Labroidel;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98315113; PubMed=9649539;
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
RA Figueroa F., Sultmann H., Klein J.;
RT "Linkage relationships and haplotype polymorphism among cichlid MHC
RT class II B loci.";
RL Genetics 149:1527-1537(1998).
DR EMBL; AF050011; AAC41350.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 11 AA; 1349 MW; 81C12D8EB7341B41 CRC64;

Query Match 32.4%; Score 24; DB 2; Length 11;
Best Local Similarity 66.7%; Pred. NO. 4.3e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 IYTRIS 10
DB 3 MYRLS 8

RESULT 9
O77902 PRELIMINARY; PRT; 11 AA.
ID O77902
AC O77902;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE MHC class II B locus 14 (Fragment)
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Labroidel;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98315113; PubMed=9649539;
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
RA Figueroa F., Sultmann H., Klein J.;
RT "Linkage relationships and haplotype polymorphism among cichlid MHC
RT class II B loci.";
RL Genetics 149:1527-1537(1998).
DR EMBL; AF050012; AAC41351.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 11 AA; 1349 MW; 81C12D8EB7341B41 CRC64;

Query Match 32.4%; Score 24; DB 2; Length 11;
Best Local Similarity 66.7%; Pred. NO. 4.3e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 IYTRIS 10
DB 3 MYRLS 8

RESULT 10
O77903 PRELIMINARY; PRT; 11 AA.
ID O77903
AC O77903;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
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DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DE MHC class II B locus 14 (Fragment).
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidel;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98315113; PubMed=9649539;
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
RA Figueroa F., Sultmann H., Klein J.;
RT "Linkage relationships and haplotype polymorphism among cichlid MHC
class II B loci.";
RL Genetics 149:1527-1537(1998).
DR EMBL; AF050013; AAC41352.1; -.
FT NON_TER 1
FT NON_TER 11
SQ SEQUENCE 11 AA; 1349 MW; 81C12D8EB7341B41 CRC64;

Query Match 32.4%; Score 24; DB 2; Length 11;
Best Local Similarity 66.7%; Pred. No. 4.3e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 IYTRIS 10
DB 3 MTYRLS 8

RESULT 11
O77904
ID O77904 PRELIMINARY; PRT; 11 AA.
AC O77904;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II B locus 14 (Fragment).
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidel;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98315113; PubMed=9649539;
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
RA Figueroa F., Sultmann H., Klein J.;
RT "Linkage relationships and haplotype polymorphism among cichlid MHC
class II B loci.";
RL Genetics 149:1527-1537(1998).
DR EMBL; AF050014; AAC41353.1; -.
FT NON_TER 1
FT NON_TER 11
SQ SEQUENCE 11 AA; 1349 MW; 81C12D8EB7341B41 CRC64;

Query Match 32.4%; Score 24; DB 2; Length 11;
Best Local Similarity 66.7%; Pred. No. 4.3e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 IYTRIS 10
DB 3 MTYRLS 8

RESULT 12
O77905
ID O77905 PRELIMINARY; PRT; 11 AA.
AC O77905;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)

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DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II B locus 14 (Fragment).
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidel;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98315113; PubMed=9649539;
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
RA Figueroa F., Sultmann H., Klein J.;
RT "Linkage relationships and haplotype polymorphism among cichlid MHC
class II B loci.";
RL Genetics 149:1527-1537(1998).
DR EMBL; AF050015; AAC41354.1; -.
FT NON_TER 1
FT NON_TER 11
SQ SEQUENCE 11 AA; 1349 MW; 81C12D8EB7341B41 CRC64;

Query Match 32.4%; Score 24; DB 2; Length 11;
Best Local Similarity 66.7%; Pred. No. 4.3e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 IYTRIS 10
DB 3 MTYRLS 8

RESULT 13
O77916
ID O77916 PRELIMINARY; PRT; 11 AA.
AC O77916;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II B locus 14 (Fragment).
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidel;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98315113; PubMed=9649539;
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
RA Figueroa F., Sultmann H., Klein J.;
RT "Linkage relationships and haplotype polymorphism among cichlid MHC
class II B loci.";
RL Genetics 149:1527-1537(1998).
DR EMBL; AF050029; AAC41368.1; -.
FT NON_TER 1
FT NON_TER 11
SQ SEQUENCE 11 AA; 1349 MW; 81C12D8EB7341B41 CRC64;

Query Match 32.4%; Score 24; DB 2; Length 11;
Best Local Similarity 66.7%; Pred. No. 4.3e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 IYTRIS 10
DB 3 MTYRLS 8

RESULT 14
O77917
ID O77917 PRELIMINARY; PRT; 11 AA.
AC O77917;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

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DE MHC class II B locus 14 (Fragment).
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8128;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=98315113; PubMed=9649539;
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
RA Figueroa F., Sultmann H., Klein J.;
RT "Linkage relationships and haplotype polymorphism among cichlid MHC
class II B loci.";
RL Genetics 149:1527-1537(1998).
DR EMBL; AF050030; AAC41369.1; -.
FT NON_TER 1
FT NON_TER 11
SQ SEQUENCE 11 AA; 1349 MW; 81C12D8EB7341B41 CRC64;

Query Match 32.4%; Score 24; DB 2; Length 11;
Best Local Similarity 66.7%; Pred. No. 4.3e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 5 ITYRIS 10
DB 3 MTYRLS 8

RESULT 15
O77921 PRELIMINARY; PRT; 11 AA.
AC O77921;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II B locus 14 (Fragment).
OS Pseudotropheus sp. 'Pseudotropheus tropheops complex'.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidei;
OC Cichlidae; Pseudotropheus.
OX NCBI_TaxID=51796;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=98315113; PubMed=9649539;
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
RA Figueroa F., Sultmann H., Klein J.;
RT "Linkage relationships and haplotype polymorphism among cichlid MHC
class II B loci.";
RL Genetics 149:1527-1537(1998).
DR EMBL; AF050034; AAC41373.1; -.
FT NON_TER 1
FT NON_TER 11
SQ SEQUENCE 11 AA; 1349 MW; 81C12D8EB7341B41 CRC64;

Query Match 32.4%; Score 24; DB 2; Length 11;
Best Local Similarity 66.7%; Pred. No. 4.3e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 5 ITYRIS 10
DB 3 MTYRLS 8

Search completed: February 22, 2005, 09:37:45
Job time : 53.6667 secs

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OM protein - protein search, using sw model

Run on: February 22, 2005, 08:52:23 ; Search time 65.6667 Seconds
(without alignments)
88.346 Million cell updates/sec

Title: US-08-991-628-1

Perfect score: 74

Sequence: 1 ARQKITYRISGVGID 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 632537

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	74	100.0	15	2	Aaw04841 Self epit
2	30	40.5	14	4	Aam96744 Human pep
3	29	39.2	14	4	Aam98436 Human pep
4	29	39.2	14	4	Abb56775 Human SNP
5	28	37.8	6	2	Aar90448 Antibody
6	28	37.8	6	2	Aay55175 Anti CD34
7	28	37.8	6	2	Aay55183 Anti CD34
8	28	37.8	6	3	Aay86929 Human hae
9	28	37.8	6	3	Aay86921 Human hae
10	28	37.8	9	8	Adh40843 Human CD6
11	28	37.8	15	8	Adm65292 HLA bindi
12	27	36.5	10	4	Aag86324 Saccharom
13	27	36.5	10	4	Aag86188 Saccharom
14	27	36.5	10	8	Adn70236 Human 273
15	27	36.5	10	8	Adm67283 Human 273
16	27	36.5	10	8	Adn70105 Human 273
17	27	36.5	10	8	Adm67511 Human 273
18	27	36.5	11	8	Adq91410 CDR3 of t
19	27	36.5	13	8	Adm12154 MHC class
20	27	36.5	13	8	Ado38372 Ara h 3 M
21	27	36.5	15	8	Adm12156 MHC class
22	27	36.5	15	8	Adn71740 Human 273
23	27	36.5	15	8	Adn70559 Human 273
24	27	36.5	15	8	Adn71499 Human 273
25	27	36.5	15	8	Adn71122 Human 273

26	27	36.5	15	8	ADN71721	Adn71721 Human 273
27	27	36.5	15	8	ADN70750	Adn70750 Human 273
28	27	36.5	15	8	ADN71576	Adn71576 Human 273
29	27	36.5	15	8	ADN70618	Adn70618 Human 273
30	27	36.5	15	8	ADO38374	Ado38374 Ara h 3 M
31	26.5	35.8	10	4	ABP22244	Abp22244 HIV A03 m
32	26.5	35.8	10	4	ABP14250	Abp14250 HIV A02 s
33	26.5	35.8	10	4	ABP16613	Abp16613 HIV A24 s
34	26.5	35.8	11	4	ABP14257	Abp14257 HIV A02 s
35	26.5	35.8	11	4	ABP25033	Abp25033 HIV DR 3b
36	26	35.1	7	8	ADP47064	Adp47064 Murine li
37	26	35.1	8	8	ADK09053	Adk09053 Human pap
38	26	35.1	9	6	ABP75214	Abp75214 Chlamydia
39	26	35.1	9	6	ABR63363	Abu63363 Human Alz
40	26	35.1	9	7	ABU64342	Abu64342 Human AAC
41	26	35.1	9	8	ADK09054	Adk09054 Human pap
42	26	35.1	10	2	AAR89616	Aar89616 Prostata
43	26	35.1	10	2	AAW33453	Aaw33453 Oligopept
44	26	35.1	10	2	ADG45903	Adg45903 Benign pr
45	26	35.1	10	5	AAE24261	Aae24261 Murine E-

ALIGNMENTS

RESULT 1

AAW04841
ID AAW04841 standard; peptide; 15 AA.
XX
AC AAW04841;
XX
DT 18-FEB-1997 (first entry)
XX
DE Self epitope of desmoglein 3, implicated in autoimmune disease.
XX
KW Tolerisation; self-epitope; antigen; autoimmune disease; autoantigen;
KW HLA; human leukocyte antigen; T-cell; thymocyte; pemphigus vulgaris;
KW desmoglein; multiple sclerosis; herpes simplex virus; adenovirus;
KW phosphomannomutase; human papillomavirus; Epstein-Barr virus;
KW DNA polymerase; influenza; haemagglutinin; reovirus; sigma protein.
XX
OS Homo sapiens.
XX
PN WO9627387-A1.
XX
PD 12-SEP-1996.
XX
PF 07-MAR-1996; 96WO-US003182.
XX
PP 07-MAR-1995; 95US-00400796.
XX
(HARD) HARVARD COLLEGE.
XX
PI Strominger JL, Wucherpfennig KW;
XX
WPI; 1996-425218/42.
XX
DR Pemphigus vulgaris auto-antigens and multiple sclerosis non-self antigens
XX
PT - useful in disease treatment, and method for identification of other
XX
PS self and non-self antigens implicated in auto-immune disease.
XX
CC Claim 1; Page 38; 58pp; English.
XX
CC Pharmaceutical preparations for tolerisation to antigens comprise either
XX
CC an isolated human non-collagen or non-mysin basic protein (MBP)
XX
CC polypeptide which is capable of tolerising an individual to an
XX
CC autoantigen; or an isolated human pathogen polypeptide capable of
XX
CC tolerising an individual to that polypeptide. In both cases, the
XX
CC polypeptide (whether self or non-self) includes an amino acid sequence
XX
CC corresponding to a sequence motif for a MHC class II protein, such as HLA
XX
CC -DR, which is associated with a human autoimmune disease and which binds
XX
CC to the polypeptide to activate autoreactive T-cells in individuals with
XX
CC the autoimmune disease. This peptide is derived from the human desmoglein

CC 3 protein (amino acids 78-93 (sic)) and is implicated as a self epitope
 CC in pemphigus vulgaris. Peptides derived from the human desmoglein protein
 CC are described in AA04841-47

XX SQ Sequence 15 AA;
 Query Match 100.0%; Score 74; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATQKITRISGVGID 15
 Db 1 ATQKITRISGVGID 15

RESULT 2
 AAM96744
 ID AAM96744 standard; peptide; 14 AA.

XX AC AAM96744;
 XX DT 24-JAN-2002 (first entry)
 XX DE Human peptide #19 encoded by a SNP oligonucleotide.
 XX KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KW multifactorial disease; autoimmune disease; infection;
 KW nervous system disease.

XX OS Homo sapiens.
 XX PN WO200147944-A2.
 XX PD 05-JUL-2001.
 XX PF 28-DEC-2000; 2000WO-US035498.
 XX PR 28-DEC-1999; 99US-0173419P.
 XX PT 27-DEC-2000; 2000US-00173419.
 XX PA (CURA-) CURAGEN CORP.

XX PI Shimkets RA, Leach M;
 XX DR WPI; 2001-465210/50.
 XX PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 XX oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
 XX autoimmune diseases and infections.

XX PS Disclosure; Page 3672; 4143pp; English.
 XX CC The present invention relates to oligonucleotides (see AAL26793-AAL34659)
 CC encoding polymorphic variants of proteins related to amylases, amyloid
 CC proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,
 CC polymerase, oncogenes, histones, kinases, colony stimulating factors,
 CC complement related proteins, cytochromes, kinesins, cytokines,
 CC interferons, interleukins, G-protein coupled receptors and thioesterases.
 CC The present sequence is a peptide encoded by one such oligonucleotide.
 CC The oligonucleotides and the peptides encoded by them may be used in the
 CC prevention, diagnosis and treatment of diseases associated with
 CC inappropriate expression of the proteins listed above. Disorders that may
 CC be prevented, diagnosed and/or treated include multifactorial diseases
 CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid
 CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus
 CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
 CC brain, breast, colon and kidney, leukaemia), diseases of the nervous
 CC system and an infection of pathogenic organisms

XX SQ Sequence 14 AA;
 Query Match 40.5%; Score 30; DB 4; Length 14;
 Best Local Similarity 55.6%; Pred. No. 1.8e+02;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 6 TYRISGVGI 14
 Db 1 TWRIQIGI 9

RESULT 3
 AAM98436
 ID AAM98436 standard; peptide; 14 AA.

XX AC AAM98436;
 XX DT 24-JAN-2002 (first entry)
 XX DE Human peptide #1711 encoded by a SNP oligonucleotide.
 XX KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KW multifactorial disease; autoimmune disease; infection;
 KW nervous system disease.

XX OS Homo sapiens.
 XX PN WO200147944-A2.
 XX PD 05-JUL-2001.

XX PF 28-DEC-2000; 2000WO-US035498.
 XX PR 28-DEC-1999; 99US-0173419P.
 XX PT 27-DEC-2000; 2000US-00173419.

XX PA (CURA-) CURAGEN CORP.

XX PI Shimkets RA, Leach M;

XX DR WPI; 2001-465210/50.

XX PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 XX oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
 XX autoimmune diseases and infections.

XX PS Disclosure; Page 4043; 4143pp; English.

XX CC The present invention relates to oligonucleotides (see AAL26793-AAL34659)
 CC encoding polymorphic variants of proteins related to amylases, amyloid
 CC proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,
 CC polymerase, oncogenes, histones, kinases, colony stimulating factors,
 CC complement related proteins, cytochromes, kinesins, cytokines,
 CC interferons, interleukins, G-protein coupled receptors and thioesterases.
 CC The present sequence is a peptide encoded by one such oligonucleotide.
 CC The oligonucleotides and the peptides encoded by them may be used in the
 CC prevention, diagnosis and treatment of diseases associated with
 CC inappropriate expression of the proteins listed above. Disorders that may
 CC be prevented, diagnosed and/or treated include multifactorial diseases
 CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid
 CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus
 CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
 CC brain, breast, colon and kidney, leukaemia), diseases of the nervous
 CC system and an infection of pathogenic organisms

XX SQ Sequence 14 AA;

Query Match 39.2%; Score 29; DB 4; Length 14;
 Best Local Similarity 62.5%; Pred. No. 2.7e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 KITYRISG 11
 | : | : | : |
 DB 1 KLTVRVSG 8

RESULT 4
 ABB56775
 ID ABB56775 standard; peptide; 14 AA.
 XX
 AC ABB56775;
 XX
 DT 05-MAR-2002 (first entry)
 XX
 DE Human SNP related amino acid sequence SEQ ID NO:1340.
 XX
 KW Human; single nucleotide polymorphism; SNP; polymorphism; cytostatic;
 immunosuppressive; anti-inflammatory; neuroprotective; antimicrobial;
 KW autoimmune disease; inflammation; cancer; nervous system disease;
 KW infection; polymorphic protein.
 XX
 OS Homo sapiens.
 XX
 PN WO200138586-A2.
 XX
 PD 31-MAY-2001.
 XX
 PF 22-NOV-2000; 2000WO-US032311.
 XX
 PR 24-NOV-1999; 99US-0167383P.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Shinkets RA, Leach M;
 XX
 DR WPI; 2001-355949/37.
 XX
 PS Isolated human nucleic acids comprising one or more single nucleotide
 polymorphisms, useful for treating a subject suffering from a pathology,
 e.g. autoimmune diseases, ascribed to the presence of a sequence
 polymorphism.
 Claim 1; Page 643; 674pp; English.
 CC ABL00010 to ABL01104 represent human nucleic acid oligonucleotides
 comprising one or more single nucleotide polymorphisms (SNPs). ABB56531
 to ABB56903 represent human peptides encoded by some of the SNP
 oligonucleotides. The sequences from the present invention can have
 immunosuppressive, cytostatic, anti-inflammatory, neuroprotective and
 antimicrobial activities. Nucleic acids, polypeptides, oligonucleotides
 and antibodies from the present invention can be used for treating a
 subject suffering from, at risk for, or suspected of, suffering from a
 pathology ascribed to the presence of a sequence polymorphism. The
 CC pathology may be autoimmune diseases, inflammation, cancer, diseases of
 the nervous system, and infection by pathogenic microorganisms. The SNPs
 are also useful for determining which forms of a characterised
 polymorphism are present in individuals. The antibodies may be used in
 the detection, quantitation and/or cellular or tissue localisation of a
 polymorphic protein (e.g., for use in measuring levels of the polymorphic
 protein within appropriate physiological samples)
 Sequence 14 AA;
 SQ

Query Match 39.2%; Score 29; DB 4; Length 14;
 Best Local Similarity 54.5%; Pred. No. 2.7e+02;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 QKITYRISGVG 13
 | : | : | : |
 DB 3 QBATRLSGSG 13

RESULT 5
 AAR90448
 ID AAR90448 standard; peptide; 6 AA.
 XX
 AC AAR90448;
 XX
 DT 03-SEP-1996 (first entry)
 XX
 DE Antibody 561 displacing peptide #16.
 XX
 KW Antibody; displacement; cell separation system; cell surface antigen; Ag;
 random peptide display library; complementarity determining region; CDR;
 KW antibody; Ab; peptide; CD34 cell; haematopoietic cell; tumour cell;
 KW lymphocyte; high dose therapy; immune system; chemotherapy;
 KW patient-specific vaccine.
 XX
 OS Synthetic.
 XX
 PN WO9534817-A1.
 XX
 PD 21-DEC-1995.
 XX
 PF 13-JUN-1995; 95WO-US007491.
 XX
 PR 14-JUN-1994; 94US-00259427.
 XX
 PA (BAXT) BAXTER INT INC.
 XX
 PI Tseng-Law J, Kobori JA, Al-Abdaly FA, Guillermo R, Helgerson SL;
 Deans RJ;
 XX
 DR WPI; 1996-049806/05.
 XX
 PT Selecting target cells by reacting specific antibody to surface antigen -
 then disrupting the complex formed with peptide displacer, partic. for
 selecting CD34 cells for reconstitution of immune system after anticancer
 treatment.
 Claim 25; Page 155; 170pp; English.
 CC AAR90413-R90468 represent antibody displacing peptides. These sequences
 displace the monoclonal antibody designated 561. These sequences can be
 used in a method to select target cells from a heterogeneous cell
 suspension. In the suspension, there is at least one complex of a cell
 separation system, linked to a primary antibody (Ab) which is bound to
 the cell surface antigen (Ag). The complex is separated from the rest of
 the suspension, and contacted with a peptide (such as this sequence) that
 binds to the Ab, displacing it from the Ag and releasing the cell. These
 sequences can be identified by biopanning random peptide display
 libraries with the Ab, by analysis of potential antigenic peaks of the
 cell surface antigen, or by analysis of the complementarity determining
 regions of the Ab. These sequences can also be used in a method for
 determining the number of specific cells in a composition. The methods
 can be used for positive selection of CD34 haematopoietic cells, and
 removal of undesired tumour cells or lymphocytes from the selected cells.
 The pure CD34 cells are reinfused into a cancer patient after high dose
 therapy to reconstitute the immune system. Cancer cells can also be
 isolated to determine their chemotherapeutic susceptibility, or for the
 production of patient-specific vaccines or antibodies. These sequences
 allow for the recovery of cells from solid supports, in high yield,
 without enzymatic cleavage. They are relatively inexpensive and safe, and
 leave cell surface proteins intact
 Sequence 6 AA;
 SQ

Query Match 37.8%; Score 28; DB 2; Length 6;
 Best Local Similarity 83.3%; Pred. No. 1.8e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 RISGVG 13
 | : | : | : |

Db 1 RVSGVG 6

RESULT 6
 AAY55175
 ID AAY55175 standard; peptide; 6 AA.
 XX
 AC AAY55175;
 XX
 DT 07-JAN-2000 (first entry)
 XX
 DE Anti CD34 antibody 561 releasing peptide SEQ ID NO:69.
 XX
 KW Antibody releasing peptide; CD34; hybridoma; binding; antigen;
 KW cell surface antigen; identification; haematopoietic stem cell; tumour;
 KW cancer; immune system; therapy; displacement.
 XX
 OS Synthetic.
 OS Homo sapiens.
 PN US5968753-A.
 XX
 PD 19-OCT-1999.
 XX
 PF 07-JUN-1995; 95US-00482228.
 XX
 PR 14-JUN-1994; 94US-00259427.
 XX
 PA (NEXE-) NEXELL THERAPEUTICS INC.
 XX
 PI Guillermo R, Helgerson SL, Deans RJ, Tseng-Law J, Kobori JA;
 PI Al-Abdaly FA;
 XX
 DR WPI; 1999-590399/50.
 XX
 PT Short peptides useful for displacing antibodies from cell surface
 PT antigens.
 XX
 PS Claim 7; Col 145; 81pp; English.
 XX
 CC The present invention describes peptides of 4-17 amino acids which
 CC displace either the anti-CD34 monoclonal antibody designated 561, the
 CC anti-CD34 mouse monoclonal antibody produced by the hybridoma ATCC HB-
 CC 11646 (designated 9069), the anti-CD34 antibody produced by hybridoma
 CC ATCC HB-11885 (9079), or the anti-human breast cancer antibody produced
 CC by hybridoma ATCC HB-11884 (9187), from a cell surface antigen on a
 CC target cell. The peptides are useful for displacing antibodies bound to
 CC cell surfaces to release cells that have been positively selected by
 CC antibody-mediated binding to beads or other solid support. AAY55107 to
 CC AAY55319 represent peptides used in the exemplification of the present
 CC invention

Query Match 37.8%; Score 28; DB 2; Length 6;
 Best Local Similarity 83.3%; Pred. No. 1.8e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RVSGVG 13
 Db 1 RVSGVG 6

RESULT 7
 AAY55183
 ID AAY55183 standard; peptide; 6 AA.
 XX
 AC AAY55183;
 XX
 DT 07-JAN-2000 (first entry)
 XX
 DE Anti CD34 antibody 561 releasing peptide SEQ ID NO:77.
 XX

KW Antibody releasing peptide; CD34; hybridoma; binding; antigen;
 KW cell surface antigen; identification; haematopoietic stem cell; tumour;
 KW cancer; immune system; therapy; displacement.
 XX
 OS Synthetic.
 OS Homo sapiens.
 PN US5968753-A.
 XX
 PD 19-OCT-1999.
 XX
 PF 07-JUN-1995; 95US-00482228.
 XX
 PR 14-JUN-1994; 94US-00259427.
 XX
 PA (NEXE-) NEXELL THERAPEUTICS INC.
 XX
 PI Guillermo R, Helgerson SL, Deans RJ, Tseng-Law J, Kobori JA;
 PI Al-Abdaly FA;
 XX
 DR WPI; 1999-590399/50.
 XX
 PT Short peptides useful for displacing antibodies from cell surface
 PT antigens.
 XX
 PS Claim 7; Col 145; 81pp; English.
 XX
 CC The present invention describes peptides of 4-17 amino acids which
 CC displace either the anti-CD34 monoclonal antibody designated 561, the
 CC anti-CD34 mouse monoclonal antibody produced by the hybridoma ATCC HB-
 CC 11646 (designated 9069), the anti-CD34 antibody produced by hybridoma
 CC ATCC HB-11885 (9079), or the anti-human breast cancer antibody produced
 CC by hybridoma ATCC HB-11884 (9187), from a cell surface antigen on a
 CC target cell. The peptides are useful for displacing antibodies bound to
 CC cell surfaces to release cells that have been positively selected by
 CC antibody-mediated binding to beads or other solid support. AAY55107 to
 CC AAY55319 represent peptides used in the exemplification of the present
 CC invention

Query Match 37.8%; Score 28; DB 2; Length 6;
 Best Local Similarity 83.3%; Pred. No. 1.8e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 RVSGVG 13
 Db 1 RVSGVG 6

RESULT 8
 AAY86929
 ID AAY86929 standard; peptide; 6 AA.
 XX
 AC AAY86929;
 XX
 DT 09-MAY-2000 (first entry)
 XX
 DE Human haematopoietic CD34+ cell binding peptide SEQ ID #77.
 XX
 KW Human; haematopoietic CD34+ cell; binding peptide; monoclonal antibody;
 KW non-enzymatic cell selection method; haematopoietic stem cell;
 KW haematopoietic progenitor cell; antibody 561; breast cancer cell;
 KW antibody 9187; cell surface determinant; diagnostic cell based assay.
 XX
 OS Homo sapiens.
 PN US6017719-A.
 XX
 PD 25-JAN-2000.
 XX
 PF 07-JUN-1995; 95US-00482528.
 XX

PR 14-JUN-1994; 94US-00259427.
XX (NEXE-) NEXELL THERAPEUTICS INC.
XX
XX
PI Guillermo R, Helgerson SL, Deans RJ, Tseng-Law J, Kobori JA;
PI Al-Abdaly FA;
XX
XX WPI; 2000-136676/12.
XX
XX Non-enzymatic method for the positive selection of target cells from a
PT heterogeneous cell suspension, useful for selecting human breast cancer
PT cells from a patient's blood or bone marrow.
XX
XX Disclosure; Col 19; 82pp; English.
XX
XX This sequence represents a human haematopoietic CD34+ cell binding
CC peptide, and was used to test the method of the invention. The method is
CC a non-enzymatic method for the positive selection of one or more target
CC cells from a heterogeneous cell suspension, by using specific peptides
CC which effect the displacement and release of a specific target cell from
CC a specific monoclonal antibody. The method is useful for positive
CC selection and specific release of target human haematopoietic
CC stem/progenitor cells bound by the monoclonal anti-CD34 antibodies and
CC the antibody 561. The method is also useful for positive selection and
CC specific release of target human breast cancer cells, bound by the
CC monoclonal anti-breast cancer antibody 9187, from a patient's blood or
CC bone marrow. Identification of peptide epitopes for antibodies which
CC recognise cell surface determinants also allows construction of
CC diagnostic cell based assays. The peptide mediated release is enzyme free
CC and thus leaves the cell surface proteins intact. Moreover, peptide
CC mediated release leaves the target cell free of bound antibody or
CC antibody fragments. The method also produces a high yield of functional
CC target cells and is relatively inexpensive to carry out
XX
XX Sequence 6 AA;
SQ

Query Match 37.8%; Score 28; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.8e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 8 RISGVG 13
DB |:|:|:|
1 RVSGVG 6

RESULT 9
AAY86921
ID AAY86921 standard; peptide; 6 AA.
XX
XX AAY86921;
XX
XX 09-MAY-2000 (first entry)
XX
XX Human haematopoietic CD34+ cell binding peptide SEQ ID #69.
DE
XX Human; haematopoietic CD34+ cell; binding peptide; monoclonal antibody;
KW non-enzymatic cell selection method; haematopoietic stem cell;
KW haematopoietic progenitor cell; antibody 561; breast cancer cell;
KW antibody 9187; cell surface determinant; diagnostic cell based assay.
XX
XX Homo sapiens.
OS
XX US6017719-A.
PN
XX 25-JAN-2000.
PD
XX 07-JUN-1995; 95US-00482528.
PF
XX 14-JUN-1994; 94US-00259427.
PR
XX (NEXE-) NEXELL THERAPEUTICS INC.
PA
XX Guillermo R, Helgerson SL, Deans RJ, Tseng-Law J, Kobori JA;
PI

PI Al-Abdaly FA;
XX
XX WPI; 2000-136676/12.
XX
XX Non-enzymatic method for the positive selection of target cells from a
PT heterogeneous cell suspension, useful for selecting human breast cancer
PT cells from a patient's blood or bone marrow.
XX
XX Example 13; Col 19; 82pp; English.
XX
XX This sequence represents a human haematopoietic CD34+ cell binding
CC peptide, and was used to test the method of the invention. The method is
CC a non-enzymatic method for the positive selection of one or more target
CC cells from a heterogeneous cell suspension, by using specific peptides
CC which effect the displacement and release of a specific target cell from
CC a specific monoclonal antibody. The method is useful for positive
CC selection and specific release of target human haematopoietic
CC stem/progenitor cells bound by the monoclonal anti-CD34 antibodies and
CC the antibody 561. The method is also useful for positive selection and
CC specific release of target human breast cancer cells, bound by the
CC monoclonal anti-breast cancer antibody 9187, from a patient's blood or
CC bone marrow. Identification of peptide epitopes for antibodies which
CC recognise cell surface determinants also allows construction of
CC diagnostic cell based assays. The peptide mediated release is enzyme free
CC and thus leaves the cell surface proteins intact. Moreover, peptide
CC mediated release leaves the target cell free of bound antibody or
CC antibody fragments. The method also produces a high yield of functional
CC target cells and is relatively inexpensive to carry out
XX
XX Sequence 6 AA;
SQ

Query Match 37.8%; Score 28; DB 3; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.8e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 8 RISGVG 13
DB |:|:|:|
1 RVSGVG 6

RESULT 10
ADH40843
ID ADH40843 standard; peptide; 9 AA.
XX
XX ADH40843;
XX
XX 11-MAR-2004 (first entry)
XX
XX Human CD64 HLA binding peptide.
DE
XX human; cytostatic; vaccine; SNP profile; cancer; leukaemia; HLA.
KW
XX Homo sapiens.
OS
XX WO2003106692-A2.
PN
XX 24-DEC-2003.
PD
XX 13-JUN-2003; 2003WO-EP006251.
PF
XX 13-JUN-2002; 2002EP-00013423.
PR
XX (MERE) MERCK PATENT GMBH.
XX
XX Strittmatter W, Moll H;
PI
XX WPI; 2004-082200/08.
DR
XX Providing allelic variant epitope of protein based on single nucleotide
PT polymorphism by defining target protein, screening database of protein,
PT identifying, selecting allelic variant protein, creating variant
PT epitopes.
XX

PS Disclosure; Page 98; 119pp; English.

XX The invention relates to a novel method for providing epitopes of allelic variants of antigenic proteins from specific species based on single nucleotide polymorphism (SNP), by defining target protein/peptide or its subset, screening database of DNA encoding target protein, identifying, selecting allelic peptide/protein variants, expression product or its fragment encoded by DNA sequence having SNP, creating variant epitopes, selecting epitopes binding to MHC protein. A protein of the invention has cytostatic activity, and may have a use in a vaccine. The method is useful for generating a SNP profile of one or more individuals from a given species by applying the method for several protein from the individuals, where the SNP profile was related to disease, preferably cancer. This is useful for diagnosing a disease in an individual by generating the SNP-related polymorphic profile. A method of the invention is useful for transplanting haematopoietic stem cells from a donor to a recipient and treating cancer, preferably leukaemia, and for determining the progression, regression or onset of a treated disease. The present sequence is used in the exemplification of the invention.

XX SQ Sequence 9 AA;

Query Match 37.8%; Score 28; DB 8; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.8e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 TYRISGVG 13
|||:|:
Db 1 TYHCSGMG 8

RESULT 11
ADN65292
ID ADN65292 standard; peptide; 15 AA.
XX AC ADN65292;
XX DT 01-JUL-2004 (first entry)
XX DE HLA binding peptide #1892.
XX KW cytostatic; hepatotropic; virucide; antiinflammatory; anti-HIV;
XX KW gene therapy; vaccine; HLA binding peptide; HTL epitope; liposome;
XX KW prostate specific antigen; prostate specific membrane antigen;
XX KW hepatitis B virus antigen; hepatitis C virus antigen;
XX KW malignant melanoma antigen; Epstein Barr virus; cancer;
XX KW prostate cancer; AIDS; renal carcinoma; cervical carcinoma; lymphoma;
XX KW chondyoma acuminatum.
XX OS Unidentified.
XX PN WO2004031211-A2.
XX PD 15-APR-2004.
XX PF 03-OCT-2003; 2003WO-US031308.
XX PR 03-OCT-2002; 2002US-0416207P.
XX PR 08-OCT-2002; 2002US-0417269P.
XX PA (EPIM-) EPIMMUNE INC.
XX PI Sidney J, Southwood S, Sette A;
XX WPI; 2004-347953/32.
XX PT New composition of peptides and nucleic acids capable of binding Major
XX PT Histocompatibility Complex molecules, useful for diagnosing, preventing
XX PT or treating viral infections or cancer, such as prostate cancer,
XX PT hepatitis B or AIDS.
XX PS Claim 1; SEQ ID NO 1892; 186pp; English.
XX SQ Sequence 10 AA;

CC The invention relates to a novel composition comprising one or more peptides or nucleic acids encoding an HLA binding peptide. The composition further comprises an HTL epitope. It also comprises a spacer molecule, a carrier, an MHC targeting sequence or a lipid. The peptides are incorporated as part of a liposome. The peptide is from an antigen selected from prostate specific antigen (PSA), prostate specific membrane antigen (PSM), hepatitis B virus (HBV) antigen, hepatitis C virus (HCV) antigen, malignant melanoma antigen (MAGE), Epstein Barr virus, human immunodeficiency type-1 (HIV-1), human immunodeficiency type-2 (HIV-2), Papilloma virus, Lassa virus, Mycobacterium tuberculosis (MT), p53, murine p53 (mp53), CEA, HER2/neu, and tyrosine kinase related protein (TKP). The composition is useful for preventing or treating viral infections or cancer, such as prostate cancer, hepatitis B, hepatitis C, AIDS, renal carcinoma, cervical carcinoma, lymphoma, CMV or chondyoma acuminatum. The composition is also used for diagnosing such diseases. This sequence represents a peptide of the invention.

XX SQ Sequence 15 AA;

Query Match 37.8%; Score 28; DB 8; Length 15;
Best Local Similarity 40.0%; Pred. No. 4.5e+02;
Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 2 TOKITYRISG 11
|||:|:
Db 2 TQKLMQING 11

RESULT 12
AAG86324
ID AAG86324 standard; peptide; 10 AA.
XX AC AAG86324;
XX DT 11-SEP-2001 (first entry)
XX DE Saccharomyces cerevisiae peptide, SEQ ID NO: 1273.
XX KW Saccharomyces cerevisiae; complementary peptide; peptide identification;
XX KW drug discovery; drug design.
XX OS Saccharomyces cerevisiae.
XX PN WO200142276-A1.
XX PD 14-JUN-2001.
XX PF 13-DEC-2000; 2000WO-GB004773.
XX PR 13-DEC-1999; 99GB-00029471.
XX PA (PROT-) PROTEOM LTD.
XX PI Roberts GW, Heal JR;
XX WPI; 2001-367863/38.
XX PT Identifying complementary peptides by analysis of protein and nucleotide
XX PT sequence databases, useful in drug design.
XX PS Example 3; Page 205; 488pp; English.
XX CC The invention relates to the identification of complementary peptides by
XX CC analysis of protein and nucleotide sequence databases from higher
XX CC eukaryotic genomes, excluding human and plants. The specific
XX CC complementary peptides interact with their relevant target proteins
XX CC encoded in the eukaryote genome. The peptides may be used as reagents and
XX CC drugs for drug discovery and as lead ligands for drug design and
XX CC development. The present sequence is a complementary peptide from
XX CC Saccharomyces cerevisiae

```
Query Match      36.5%; Score 27; DB 4; Length 10;
Best Local Similarity 83.3%; Pred. No. 4.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY  9 ISGVGI 14
Db  5 ISGVGV 10

RESULT 13
AAG86188
ID  AAG86188 standard; peptide; 10 AA.
XX
AC  AAG86188;
XX
DT  11-SEP-2001 (first entry)
XX
DE  Saccharomyces cerevisiae peptide, SEQ ID NO: 1137.
XX
KW  Saccharomyces cerevisiae; complementary peptide; peptide identification;
KW  drug discovery; drug design.
XX
OS  Saccharomyces cerevisiae.
XX
PN  WO200142276-A1.
XX
PD  14-JUN-2001.
XX
PF  13-DEC-2000; 2000WO-GB004773.
XX
PR  13-DEC-1999; 99GB-00029471.
XX
PA  (PROT-) PROTEOM LTD.
XX
PI  Roberts GW, Heal JR;
XX
WPI; 2001-367863/38.
XX
PT  Identifying complementary peptides by analysis of protein and nucleotide
PT  sequence databases, useful in drug design.
XX
PS  Example 3; Page 186; 488pp; English.
XX
CC  The invention relates to the identification of complementary peptides by
CC  analysis of protein and nucleotide sequence databases from higher
CC  eukaryotic genomes, excluding human and plants. The specific
CC  complementary peptides interact with their relevant target proteins
CC  encoded in the eukaryote genome. The peptides may be used as reagents and
CC  drugs for drug discovery and as lead ligands for drug design and
CC  development. The present sequence is a complementary peptide from
CC  Saccharomyces cerevisiae
XX
SQ  Sequence 10 AA;

Query Match      36.5%; Score 27; DB 4; Length 10;
Best Local Similarity 83.3%; Pred. No. 4.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY  9 ISGVGI 14
Db  5 ISGVGV 10

RESULT 14
ADN70236
ID  ADN70236 standard; peptide; 10 AA.
XX
AC  ADN70236;
XX
DT  01-JUL-2004 (first entry)
XX
DE  Human 273P4B7v.1 protein epitope #4199.
XX

Query Match      36.5%; Score 27; DB 4; Length 10;
Best Local Similarity 83.3%; Pred. No. 4.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY  9 ISGVGI 14
Db  5 ISGVGV 10

RESULT 15
ADN67283
ID  ADN67283 standard; peptide; 10 AA.
XX
AC  ADN67283;
XX
DT  01-JUL-2004 (first entry)
XX
DE  Human 273P4B7v.1 protein epitope #1246.
XX
KW  273P4B7; human; cancer; tumour; epitope.
XX
OS  Homo sapiens.
XX
PN  WO2004016762-A2.
XX
PD  26-FEB-2004.
XX
PF  15-AUG-2003; 2003WO-US025665.
XX
PR  16-AUG-2002; 2002US-0404306P.
XX
PR  01-NOV-2002; 2002US-0423290P.
XX
PA  (AGEN-) AGENSYS INC.
XX
PI  Challita-Bid PM, Paris M, Raitano AB, Jakobovits A, Ge W;
XX
WPI; 2004-203790/19.
XX
PT  New composition comprising 273P4B7 proteins, useful for detecting and
PT  treating cancer by inhibiting the growth or viability of cancer cells.
XX
PS  Claim 1; Fig 2A; 268pp; English.
XX
CC  The invention relates to a composition comprising 273P4B7 proteins. The
CC  composition and proteins are useful for detecting and treating cancer by
CC  inhibiting the growth or viability of cancer cells. The present sequence
CC  represents the amino acid sequence of a human 273P4B7v.1 protein epitope.
CC  Note the epitope sequences are displayed in tables VIII-XLIX.
XX
SQ  Sequence 10 AA;

Query Match      36.5%; Score 27; DB 8; Length 10;
Best Local Similarity 40.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY  5 ITRYISGVGI 14
Db  1 LTTQGVGVGL 10
    :|::|||:
    1 LTTQGVGVGL 10

RESULT 16
ADN67283
ID  ADN67283 standard; peptide; 10 AA.
XX
AC  ADN67283;
XX
DT  01-JUL-2004 (first entry)
XX
DE  Human 273P4B7v.1 protein epitope #1246.
XX
KW  273P4B7; human; cancer; tumour; epitope.
XX
OS  Homo sapiens.
XX
PN  WO2004016762-A2.
XX
PD  26-FEB-2004.
XX
PF  15-AUG-2003; 2003WO-US025665.
XX
PR  16-AUG-2002; 2002US-0404306P.
XX
PR  01-NOV-2002; 2002US-0423290P.
XX
PA  (AGEN-) AGENSYS INC.
XX
PI  Challita-Bid PM, Paris M, Raitano AB, Jakobovits A, Ge W;
XX
WPI; 2004-203790/19.
XX
PT  New composition comprising 273P4B7 proteins, useful for detecting and
PT  treating cancer by inhibiting the growth or viability of cancer cells.
XX
```

PS Claim 1; Fig 2A; 260pp; English.
XX
CC The invention relates to a composition comprising 273P4B7 proteins. The
CC composition and proteins are useful for detecting and treating cancer by
CC inhibiting the growth or viability of cancer cells. The present sequence
CC represents the amino acid sequence of a human 273P4B7v.1 protein epitope.
CC Note the epitope sequences are displayed in tables VIII-XLIX.
XX
SQ Sequence 10 AA;

Query Match 36.5%; Score 27; DB 8; Length 10;
Best Local Similarity 40.0%; Pred. NO. 4.3e+02;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 5 ITYRISGVGI 14
:|::|||:
Db 1 LTTQVGGVGL 10

Search completed: February 22, 2005, 09:24:32
Job time : 68.6667 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 22, 2005, 09:08:09 ; Search time 11.1333 Seconds
(without alignments)
129.633 Million cell updates/sec

Title: US-08-991-628-2

Perfect score: 78

Sequence: 1 FGIFVVDKNTGDIINI 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 2523

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	30.8	15	2 PA0052	protein QF200015 -
2	23	29.5	10	2 A49581	sialokinin I - vel
3	23	29.5	11	2 A40795	glycoprotein H-a -
4	23	29.5	14	2 B58502	36K kidney stone p
5	23	29.5	15	2 PQ0017	terminal protein -
6	22	28.2	14	2 B44854	L-2,4-diaminobutyr
7	22	28.2	15	2 A47146	topoisomerase I -
8	22	28.2	15	2 S62315	cartilage oligomer
9	20	25.6	13	2 A28999	carboxylesterase (
10	20	25.6	14	2 SQ9721	2S albumin small c
11	19	24.4	11	2 S51732	T-cell receptor be
12	19	24.4	11	2 PH0919	aminotransferase c
13	19	24.4	11	4 PC2124	ribosomal protein
14	19	24.4	12	2 S36899	potB protein - Sal
15	19	24.4	12	2 S71034	Ig H chain V-D-J r
16	19	24.4	14	2 PH1614	Ig H chain V-D-J r
17	19	24.4	14	2 PH1617	Trp EG leader pept
18	19	24.4	14	2 A44515	T-cell receptor be
19	19	24.4	15	2 PH0750	T-cell receptor be
20	18	23.1	10	2 S10926	inhibin beta-A cha
21	18	23.1	10	2 A49581	sialokinin II - ye
22	18	23.1	11	2 S23926	major glycoprotein
23	18	23.1	13	2 PH0796	T-cell receptor al
24	18	23.1	13	2 PH0799	T-cell receptor al
25	18	23.1	13	2 PH0783	T-cell receptor al
26	18	23.1	14	2 S22236	lipoxigenase (EC 1
27	18	23.1	14	2 S60353	amylopullulanase -
28	18	23.1	15	2 S43956	Ig mu chain V regi
29	18	23.1	15	2 S47367	T-cell antigen rec

30	18	23.1	15	2 S55312	TSH protein beta c
31	18	23.1	15	2 A35141	T-cell receptor de
32	18	23.1	15	2 PC4213	bphB protein - Com
33	17.5	22.4	15	2 PH1320	Ig heavy chain DJ
34	17	21.8	6	2 A61419	sarcosine dehydrog
35	17	21.8	7	2 S45311	microcin C7 - Esch
36	17	21.8	11	2 PT0211	T-cell receptor al
37	17	21.8	11	2 S45386	low density lipopr
38	17	21.8	12	2 G49410	t-complex polyep
39	17	21.8	12	2 C39109	hypothetical 1.2K
40	17	21.8	12	2 PT0257	Ig heavy chain CRD
41	17	21.8	12	2 PT0216	T-cell receptor be
42	17	21.8	12	2 PH0920	T-cell receptor be
43	17	21.8	12	2 PN0160	ribosomal protein
44	17	21.8	13	1 JTJG3	trimerogen a-13 -
45	17	21.8	13	2 S29488	GTP-binding protei

ALIGNMENTS

RESULT 1

PA0052

protein QF200015 - fungus (Fusarium sporotrichioides) (fragment)

C:Species: Fusarium sporotrichioides

C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001

C:Accession: PA0052

R:Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Taugita, A.

submitted to JPIID, October 1994

A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichi

A:Reference number: PA0051

A:Accession: PA0052

A:Molecule type: protein

A:Residues: 1-15 <CHO>

Query Match 30.8%; Score 24; DB 2; Length 15;

Best Local Similarity 50.0%; Pred. No. 9.1e+02;

Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 IFVVDKNTGDIIN 14

Db 3 IFVVDKNTGDIIN 14

RESULT 2

A49581

sialokinin I - yellow fever mosquito

C:Species: Aedes aegypti (yellow fever mosquito)

C>Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C:Accession: A49581

R:Champagne, D.E.; Ribeiro, J.M.

Proc. Natl. Acad. Sci. U.S.A. 91, 138-142, 1994

A>Title: Sialokinin I and II: vasodilatory tachykinins from the yellow fever mosquito A

A:Reference number: A49581; MUID:94105119; PMID:8278354

A:Accession: A49581

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-10 <CHA>

A:Cross-references: UNIPROT:P42634

A:Experimental source: Rockefeller, salivary gland

A>Note: sequence extracted from NCBI backbone (NCBI:P:141841)

C:Superfamily: unassigned animal peptides

Query Match 29.5%; Score 23; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 8.7e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 NTGD 12

Db 1 NTGD 4

RESULT 3

A40795
glycoprotein H-a - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C>Date: 10-Apr-1992 #sequence_revision 10-Apr-1992 #text_change 31-Dec-1993
C:Accession: A40795
R:Christie, D.L.; Batchelor, D.C.; Palmer, D.J.
J. Biol. Chem. 266, 15679-15683, 1991
A>Title: Identification of kex2-related proteases in chromaffin granules by partial amino acid sequencing
A:Reference number: A40795; MUID:91340701; PMID:1874725
A:Accession: A40795
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-11 <HR>
C:Keywords: glycoprotein

Query Match 29.5%; Score 23; DB 2; Length 11;
Best Local Similarity 55.6%; Pred. No. 9.6e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 7 DKNTGDI 15
Db 3 DINEIDINV 11

RESULT 4
B58502
36K kidney stone protein - unidentified bacterium (fragment)
C:Species: unidentified bacterium
C>Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 10-Jul-1998
C:Accession: B58502
R:Binette, J.P.; Binette, M.B.
submitted to the Protein Sequence Database, October 1996
A:Description: The proteins of kidney and gallbladder stones.
A:Reference number: A58501
A:Accession: B58502
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-14 <BIN>
A:Experimental source: human kidney stone containing Ca ox.monohydrate, 1% struvite, Ca ox.monohydrate
A>Note: tentative identification of 8-Tyr and 9-Thr

Query Match 29.5%; Score 23; DB 2; Length 14;
Best Local Similarity 71.4%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FGIFVVD 7
Db 6 FGTVVD 12

RESULT 5
PQ0017
terminal protein - phase M2 (fragment)
C:Species: phase M2
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C:Accession: PQ0017
R:Matsumoto, K.; Takano, H.; Kim, C.I.; Hirokawa, H.
Gene 84, 247-255, 1989
A>Title: Primary structure of bacteriophage M2 DNA polymerase: conserved segments within the terminal protein
A:Reference number: JQ0161; MUID:90128268; PMID:2515115
A:Accession: PQ0017
A:Molecule type: DNA
A:Residues: 1-15 <MAT>
A:Cross-references: UNIPROT:P19897; GB:M33144; NID:g215507; PIDN:AAA32367.1; PID:g215508
C:Genetics: E
A:Gene: E
C:Superfamily: phage P2A terminal protein

Query Match 29.5%; Score 23; DB 2; Length 15;
Best Local Similarity 60.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GDINI 15

Db 6 GDVNL 10

RESULT 6
B44854
L-2,4-diaminobutyrate decarboxylase (EC 4.1.1.-) - Vibrio alginolyticus (fragment)
C:Species: Vibrio alginolyticus
C>Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: B44854; B41817
R:Yamamoto, S.; Tezuka, Y.; Tougou, K.; Shinoda, S.
J. Gen. Microbiol. 138, 1461-1465, 1992
A>Title: Purification and characterization of L-2,4-diaminobutyrate decarboxylase from *Vibrio alginolyticus*
A:Reference number: A44854; MUID:92381494; PMID:1512577
A:Accession: B44854
A:Molecule type: protein
A:Residues: 1-14 <YAM>
A:Cross-references: UNIPROT:Q9R5I8
A>Note: sequence extracted from NCBI backbone (NCBI:112332)
C:Keywords: carbon-carbon lyase; carboxy-lyase

Query Match 28.2%; Score 22; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 1.8e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 4 FVVDKNTGDI 13
Db 4 FEVDSNIWNI 13

RESULT 7
A47146
topoisomerase I - vaccinia virus (fragment)
C:Species: vaccinia virus
C>Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 09-Jul-2004
C:Accession: A47146
R:Klemperer, N.; Traktman, P.
J. Biol. Chem. 268, 15887-15899, 1993
A>Title: Biochemical analysis of mutant alleles of the vaccinia virus topoisomerase I
A:Reference number: A47146; MUID:93340198; PMID:8393454
A:Accession: A47146
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-15 <KLE>
A:Cross-references: UNIPROT:Q9JFB0; GB:L13447
C:Superfamily: vaccinia virus DNA topoisomerase

Query Match 28.2%; Score 22; DB 2; Length 15;
Best Local Similarity 38.5%; Pred. No. 2e+03;
Matches 5; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 2 GIFVVDKNTGDI 14
Db 1 GIRIKDLRTYGVN 13

RESULT 8
S66215
cartilage oligomeric matrix protein - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C>Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C:Accession: S66215
R:Hauser, N.; Paulsson, M.; Kale, A.A.; DiCesare, P.E.
FEBS Lett. 368, 307-310, 1995
A>Title: Tendon extracellular matrix contains pentameric thrombospondin-4 (TSP-4).
A:Reference number: S66214; MUID:95354859; PMID:7628627
A:Accession: S66215
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <HAU>

Query Match 28.2%; Score 22; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 2e+03;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 NTGGIN 14
| | | |
Db 8 NGGDFN 13

RESULT 9
A26999
carboxylesterase (EC 3.1.1.1), intestinal - *Caenorhabditis elegans* (fragment)
C:Species: *Caenorhabditis elegans*
C>Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 09-Jul-2004
C:Accession: A26999
R:McGhee, J.D.
Biochemistry 26, 4101-4107, 1987
A:Title: Purification and characterization of a carboxylesterase from the intestine of *C. elegans*
A:Reference number: A26999; MUID:88000636; PMID:3651439
A:Accession: A26999
A:Molecule type: protein
A:Residues: 1-13 <MCG>
A:Cross-references: UNIPROT:Q7M3Q8
C:Keywords: carboxylic ester hydrolase; intestine

Query Match 25.6%; Score 20; DB 2; Length 13;
Best Local Similarity 33.3%; Pred. No. 3.6e+03;
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 VVDKNGDI 13
| | | | |
Db 3 IVEHNGKV 11

RESULT 10
S09721
2S albumin small chain nIII - rape (fragments)
C:Species: *Brassica napus* (rape)
C>Date: 19-Mar-1997 #sequence_revision 13-Mar-1998 #text_change 13-Mar-1998
C:Accession: S09721
R:Moncalve, R.I.; Menendez-Arias, L.; Lopez-Otin, C.; Rodriguez, R.
FEBS Lett. 263, 209-212, 1990
A:Title: beta-Turns as structural motifs for the proteolytic processing of seed proteins
A:Reference number: S09720; MUID:90242974; PMID:2185951
A:Accession: S09721
A:Molecule type: protein
A:Residues: 1-9;10-14 <MON>
A:Experimental source: seed

Query Match 25.6%; Score 20; DB 2; Length 14;
Best Local Similarity 40.0%; Pred. No. 3.9e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 GIFVVDKNG 11
| | | | |
Db 3 GPFRIKQSG 12

RESULT 11
S51732
T-cell receptor alpha chain joining region - human (fragment)
C:Species: *Homo sapiens* (man)
C>Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 05-Nov-1999
C:Accession: S51732
R:Durinovic-Bello, I.; Steinle, A.; Ziegler, A.G.; Schendel, D.J.
submitted to the EMBL Data Library, November 1993
A:Reference number: S51732
A:Accession: S51732
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-11 <DUR>
A:Cross-references: EMBL:228343; NID:g607116; PIDN:CAA82197.1; PID:g607117
C:Keywords: T-cell receptor

Query Match 24.4%; Score 19; DB 2; Length 11;

Best Local Similarity 50.0%; Pred. No. 4.4e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 KNTGDI 13
| | | | |
Db 4 ENTGKL 9

RESULT 12
PH0919
T-cell receptor beta chain V-D-J region (isolate 5) - rat (fragment)
C:Species: *Rattus norvegicus* (Norway rat)
C>Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C:Accession: PH0919
R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic arthritis
A:Reference number: PH0919; MUID:92078857; PMID:1836012
A:Accession: PH0919
A:Molecule type: mRNA
A:Residues: 1-11 <GOL>
A:Experimental source: concanavalin A-activated lymphoblast
A:Note: the authors translated the codon CAG for residue 11 as Glu
C:Keywords: T-cell receptor

Query Match 24.4%; Score 19; DB 2; Length 11;
Best Local Similarity 75.0%; Pred. No. 4.4e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 KNTG 11
| | | | |
Db 7 RNTG 10

RESULT 13
PC2124
aminotransferase chimera DY376 - synthetic (fragment)
C:Species: synthetic
C>Date: 28-May-1999 #sequence_revision 28-May-1999 #text_change 28-May-1999
C:Accession: PC2124
R:Wiyazawa, K.; Kawaguchi, S.; Okamoto, A.; Kato, R.; Ogawa, T.; Kuramitsu, S.
J. Biochem. 115, 568-577, 1994
A:Title: Construction of aminotransferase chimeras and analysis of their substrate specificity
A:Reference number: JX0315; MUID:94334304; PMID:8056774
A:Accession: PC2124
A:Molecule type: DNA
A:Residues: 1-11 <MIY>
C:Comment: This is a chimeric enzyme of *Escherichia coli* aspartate aminotransferase (EC 2.3.1.27) and *Thermoplasma volcanum* (EC 2.3.1.27)
C:Genetics: *Thermoplasma volcanum*
A:Gene: aspC; tyrB
C:Keywords: aminotransferase

Query Match 24.4%; Score 19; DB 4; Length 11;
Best Local Similarity 40.0%; Pred. No. 4.4e+03;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 FGIV 5
| | | | |
Db 7 FGIV 11

RESULT 14
S36899
ribosomal protein S6 - *Mycobacterium bovis* (fragment)
C:Species: *Mycobacterium bovis*
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Jan-1995
C:Accession: S36899
R:Ohara, N.; Kimura, M.; Higashi, Y.; Yamada, T.
FEBS Lett. 331, 9-14, 1993
A:Title: Isolation and amino acid sequence of the 30S ribosomal protein S19 from *Mycobacterium bovis*
A:Reference number: S36887; MUID:94009653; PMID:8405418
A:Accession: S36899

A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-12 <OHA>
C;Keywords: protein biosynthesis; ribosome

Query Match 24.4%; Score 19; DB 2; Length 12;
Best Local Similarity 57.1%; Pred. No. 4.8e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 FGIFVVD 7
: | | | |
Db 4 YEIMVVD 10

RESULT 15

S71034
potB protein - Salmonella typhimurium (fragment)
C;Species: Salmonella typhimurium
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S71034
R;Stein, M.A.; Leung, K.Y.; Zwick, M.; Garcia-del Portillo, P.; Finlay, B.B.
Mol. Microbiol. 20, 151-164, 1996
A;Title: Identification of a Salmonella virulence gene required for formation of filamentous phage
A;Reference number: S71033; MUID:97014378; PMID:8861213
A;Accession: S71034
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-12 <STE>
A;Cross-references: UNIPROT:Q56060; EMBL:U51867; NID:g1272352; PIDN:AAA97466.1; PID:g1272352
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1996
C;Genetics:
A;Gene: potB

Query Match 24.4%; Score 19; DB 2; Length 12;
Best Local Similarity 30.0%; Pred. No. 4.8e+03;
Matches 3; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 5 VVDKNTGDIIN 14
::: | | |
Db 2 LLNKKVSDIS 11

Search completed: February 22, 2005, 09:46:23
Job time : 12.1333 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: February 22, 2005, 08:53:13 ; Search time 52.6 Seconds
(without alignments)
146.030 Million cell updates/sec

Title: US-08-991-628-2

Perfect score: 78

Sequence: 1 FGIFVDRKNTGDINI 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 6622

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	27	34.6	2 Q8JLG6	Q8JLG6 ashbya goss
2	25	32.1	13 2 P97140	P97140 borrelia bu
3	25	32.1	15 2 Q9RAP6	Q9RAP6 brevundimon
4	24	30.8	13 2 Q8WV56	Q8WV56 homo sapien
5	23	29.5	10 1 TKS1_AEDAE	P42634 aedes aegypt
6	23	29.5	12 2 Q9TQY5	Q9TQY5 bos taurus
7	23	29.5	14 2 Q9S8X6	Q9S8X6 glycine max
8	23	29.5	14 2 Q65CH4	Q65CH4 sinaloa tom
9	23	29.5	15 1 TERM_BPM2	P19897 bacterioph
10	22	28.2	11 2 Q997C1	Q997C1 east africa
11	22	28.2	14 2 Q9E5I8	Q9E5I8 vibrio algi
12	22	28.2	15 2 Q75LP0	Q75LP0 homo sapien
13	21	26.9	12 2 Q65UX6	Q65UX6 photobacter
14	21	26.9	13 2 Q9UPB5	Q9UPB5 homo sapien
15	21	26.9	13 2 Q6LBD3	Q6LBD3 vibrio harv
16	21	26.9	13 2 Q6VFN6	Q6VFN6 photobacter
17	21	26.9	14 1 UC18_MAIZE	P80624 zea mays (m
18	21	26.9	14 1 UN46_CLOPA	P81362 clostridium
19	21	26.9	14 2 Q9RPG9	Q9RPG9 listeria mo
20	21	26.9	15 2 Q7S362	Q7S362 neurospora
21	21	26.9	15 2 Q9S8D4	Q9S8D4 cynara card
22	20	25.6	9 1 UPAG_HUMAN	P30092 homo sapien
23	20	25.6	11 2 P83128	P83128 bos indicus
24	20	25.6	12 1 PA2B_VIPBO	P31859 vipera beru
25	20	25.6	13 2 Q7M3Q8	Q7M3Q8 caenorhabdi
26	20	25.6	13 2 Q9THS3	Q9THS3 bryopsis sp
27	20	25.6	15 2 Q9R597	Q9R597 micrococcus
28	20	25.6	15 2 Q9RFPZ5	Q9RFPZ5 mycoplasma
29	19	24.4	10 2 Q9S936	Q9S936 beta vulgar
30	19	24.4	13 2 Q53693	Q53693 streptomyce
31	19	24.4	14 1 LPW_RHIME	P18854 rhizobium m

32 19 24.4 14 2 Q9G3C0 Q9G3C0 calliphora
33 19 24.4 15 1 UC28_MAIZE P80634 zea mays (m
34 19 24.4 15 2 Q69FJ1 Q69FJ1 stemphylium
35 19 24.4 15 2 Q86TJ6 Q86TJ6 homo sapien
36 19 24.4 15 2 Q9TR52 Q9TR52 bos taurus
37 19 24.4 15 2 Q9S8I1 Q9S8I1 volvox cart
38 18 23.1 8 2 Q6SE42 Q6SE42 drosophila
39 18 23.1 9 2 Q70Y81 Q70Y81 plectranthu
40 18 23.1 10 1 TKS2_AEDAE P42635 aedes aegypt
41 18 23.1 11 2 Q9UAR8 Q9UAR8 aedes aegypt
42 18 23.1 11 2 Q7M2M1 Q7M2M1 bos taurus
43 18 23.1 11 2 Q77910 Q77910 orochromis
44 18 23.1 12 1 HCYB_MEGCR Q10584 megathura c
45 18 23.1 13 2 Q69GD7 Q69GD7 pleospora t

ALIGNMENTS

RESULT 1
Q8JLG6 PRELIMINARY; PRT; 12 AA.
AC Q8JLG6;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE YEL062 (Fragment).
GN Name=YEL062;
OS Ashbya gossypii (Yeast) (Eremothecium gossypii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Eremothecium.
OX NCBI_TaxID=33169;
RN [1]
RP SEQUENCE FROM N.A.
RA Alberti-Sequi C, Dietrich F., Philippsen P.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBAJ databases.
DR EMBL; AF378568; AAN87135.1; -;
FT NON_TER 1
SQ SEQUENCE 12 AA; 1294 MW; 2EE79139285B5B18 CRC64;

Query Match 34.6%; Score 27; DB 2; Length 12;
Best Local Similarity 62.5%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 KNTGDINI 15
|||:
DB 2 KGTGEYNI 9

RESULT 2
P97140 PRELIMINARY; PRT; 13 AA.
AC P97140;
DT 01-MAY-1997 (TRENBLrel. 03, Created)
DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)
DT 01-NOV-1998 (TRENBLrel. 08, Last annotation update)
DE Flagellin protein (Fragment).
GN Name=flaB;
OS Borrelia burgdorferi (Lyme disease spirochete).
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=212;
RX MEDLINE=97312006; PubMed=9168617;
RA Ge Y., Old I.G., Girons I.S., Charon N.W.;
RT "The flgK motility operon of Borrelia burgdorferi is initiated by a
sigma 70-like promoter."
RL Microbiology 143:1681-1690(1997).
DR EMBL; U66699; AAB58987.1; -;
DR GO; GO:0019861; C:flagellum; IEA.
KW Flagellum.
FT NON_TER 13 13

SQ SEQUENCE 13 AA; 1386 MW; 188978372FFCA1A4 CRC64;
 Query Match 32.1%; Score 25; DB 2; Length 13;
 Best Local Similarity 40.0%; Pred. No. 2.8e+03;
 Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 5 VVDKNTGGIN 14
 Db 2 IINHTSAIN 11
 RESULT 3
 Q9R4P6 PRELIMINARY; PRT; 15 AA.
 AC Q9R4P6;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE Ribosomal protein S21 (Fragment).
 OS Brevundimonas diminuta (Pseudomonas).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales;
 OC Caulobacteraceae; Brevundimonas.
 OX NCBI_TaxID=293;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95244309; PubMed=7727274;
 RA Ochi K.;
 RT "Comparative ribosomal protein sequence analyses of a phylogenetically
 defined genus, Pseudomonas, and its relatives.";
 RL Int. J. Syst. Bacteriol. 45:268-273(1995).
 SQ SEQUENCE 15 AA; 1713 MW; 012C57185EBD3CA CRC64;
 Query Match 32.1%; Score 25; DB 2; Length 15;
 Best Local Similarity 71.4%; Pred. No. 3.3e+03;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3 IFVVDKN 9
 Db 3 IFVVDNN 9
 RESULT 4
 ID Q8WV56 PRELIMINARY; PRT; 13 AA.
 AC Q8WV56;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Epithelial sodium channel beta-3 subunit (Fragment).
 GN Name=SCNN1B;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=11934701;
 RA Thomas C.P., Loftus R.W., Liu K.Z., Itani O.A.;
 RT "Genomic organization of the 5' end of human beta-ENaC and preliminary
 characterization of its promoter.";
 RL Am. J. Physiol. Renal Physiol. 282:F998-F999(2002).
 DR EMBL; AF260228; AAL48197.1;
 DR GO; GO:0005216; F:ion channel activity; IEA.
 KW Ionic channel.
 FT NON TER 13
 FT NON TER 13
 SQ SEQUENCE 13 AA; 1437 MW; 1716D00275917724 CRC64;
 Query Match 30.8%; Score 24; DB 2; Length 13;
 Best Local Similarity 62.5%; Pred. No. 4.2e+03;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 7 DKNTGGIN 14
 SQ SEQUENCE 14 AA; 1437 MW; 1716D00275917724 CRC64;
 Query Match 30.8%; Score 24; DB 2; Length 13;
 Best Local Similarity 62.5%; Pred. No. 4.2e+03;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 7 DKNTGGIN 14

Db 4 DENIGDKN 11
 RESULT 5
 TKSI_AEDAE STANDARD; PRT; 10 AA.
 AC P42634;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Sialokinin I.
 OS Aedes aegypti (Yellowfever mosquito).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
 OX NCBI_TaxID=7159;
 RN [1]
 RP SEQUENCE.
 RX STRAIN=Rockefeller; TISSUE=Salivary gland;
 MEDLINE=94105119; PubMed=8278354;
 RA Champagne D.E., Ribeiro J.M.C.;
 RT "Sialokinin I and II: vasodilatory tachykinins from the yellow fever
 mosquito Aedes aegypti.";
 RL Proc. Natl. Acad. Sci. U.S.A. 91:138-142(1994).
 CC -!- FUNCTION: Vasodilatory peptide. May activate macrophages at the
 site of feeding.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the tachykinin family.
 DR PIR; A49581; A49581.
 DR InterPro; IPR002040; Tachy Neurokinin.
 DR PROSITE; PS00267; TACHYKININ; 1.
 KW Amidation; Direct protein sequencing; Neuropeptide; Tachykinin.
 FT MOD RES 10 10 Methionine amide.
 SQ SEQUENCE 10 AA; 1145 MW; 3DCFDE6B59C33AA8 CRC64;
 Query Match 29.5%; Score 23; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.6e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 NTGD 12
 Db 1 NTGD 4
 RESULT 6
 Q9TQY5 PRELIMINARY; PRT; 12 AA.
 AC Q9TQY5;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Glycoprotein H-A N-TERMINAL, GPH-A N-TERMINAL=KEX2/subtilisin-related
 DE protease (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=91340701; PubMed=1874725;
 RA Christie D.L., Batchelor D.C., Palmer D.J.;
 RT "Identification of kex2-related proteases in chromaffin granules by
 partial amino acid sequence analysis.";
 RL J. Biol. Chem. 266:15679-15683(1991).
 FT NON TER 1
 FT NON TER 1
 FT NON TER 12
 FT NON TER 12
 SQ SEQUENCE 12 AA; 1374 MW; 0BDF36703B5B1440 CRC64;
 Query Match 29.5%; Score 23; DB 2; Length 12;
 Best Local Similarity 55.6%; Pred. No. 5.6e+03;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 7 DKNTGGIN 15

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Db      4 DINEIDIN 12
RESULT 7
Q9S8X6 PRELIMINARY; PRT; 14 AA.
ID Q9S8X6
AC Q9S8X6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Vegetative storage protein 94 peptide 1, VSP94-LIPOXYGENASE
DE (fragment).
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE.
RX MEDLINE=92361246; PubMed=1822994;
RA Tranbarger T.J., Franceschi V.R., Hildebrand D.P., Grimes H.D.;
RT "The soybean 94-kilodalton vegetative storage protein is a
RT lipoxigenase that is localized in paraveinal mesophyll cell
RT vacuoles.";
RL Plant Cell 3:973-987(1991).
FT NON_TER 1 1
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1541 MW; 98EB730EA6A8785A CRC64;
Query Match 29.5%; Score 23; DB 2; Length 14;
Best Local Similarity 71.4%; Pred. No. 6.7e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 KNTGGIN 14
Db 3 KNVLDIN 9
RESULT 8
Q65CH4 PRELIMINARY; PRT; 14 AA.
ID Q65CH4
AC Q65CH4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Coat protein (Fragment).
GN Name=AVI;
OS Sinaloa tomato leaf curl virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=71186;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NII;
RA Rojas A., Kvarnheden A., Rodriguez D., Valkonen J.P.T.;
RT "A mixture of begomoviruses in severe leaf curl-affected tomatoes in
RT Nicaragua.";
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ508778; CAD48516.1; -.
KW Coat protein.
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1573 MW; 571284313A0594D3 CRC64;
Query Match 29.5%; Score 23; DB 2; Length 14;
Best Local Similarity 55.6%; Pred. No. 6.7e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 VDKNTGGIN 14
Db 5 VDKATAWN 13
RESULT 9

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TERM BPM2 STANDARD; PRT; 15 AA.
ID TERM BPM2
AC P19897;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE DNA terminal protein (Protein GP3) (Fragment).
GN Name=3; Synonyms=E;
OS Bacteriophage M2.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
OC phi-29-like viruses.
OX NCBI_TaxID=10751;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90128268; PubMed=2515115; DOI=10.1016/0378-1119(89)90498-8;
RA Matsumoto K., Takano H., Kim C.I., Hirokawa H.;
RT "Primary structure of bacteriophage M2 DNA polymerase: conserved
RT segments within protein-priming DNA polymerases and DNA polymerase I
RT of Escherichia coli.";
RL Gene 84:247-255(1989).
CC -1- FUNCTION: DNA terminal protein is linked to the 5' ends of both
CC strands of the genome through a phosphodiester bond between the
CC beta-hydroxyl group of a serine residue and the 5'-phosphate of
CC the terminal deoxyadenylate. This protein is essential for DNA
CC replication and is involved in the priming of DNA elongation.
CC
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CC
CC EMBL; M33144; AAA32367.1; -.
DR PIR; PQ0017; PQ0017.
DR InterPro; IPR008770; PHI-29_GP3.
DR Pfam; PF05435; PHI-29_GP3; 1.
KW Covalent protein-DNA linkage; DNA priming; DNA replication;
KW Early protein.
FT NON_TER 1 1
FT SITE 5 7 Cell attachment site (Potential).
SQ SEQUENCE 15 AA; 1797 MW; D3CBAFF8759DEA06 CRC64;
Query Match 29.5%; Score 23; DB 1; Length 15;
Best Local Similarity 60.0%; Pred. No. 7.2e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 11 GDINI 15
Db 6 GDVNL 10
RESULT 10
Q997C1 PRELIMINARY; PRT; 11 AA.
ID Q997C1
AC Q997C1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Coat protein (Fragment).
OS East African cassava mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=62079;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21103006; PubMed=11172108;
RA Pita J.S., Fondong V.N., Sangare A., Otim-Nape G.W., Ogwal S.,
RA Fauquet C.M.;
RT "Recombination, pseudorecombination and synergism of geminiviruses are
RT determinant keys to the epidemic of severe cassava mosaic disease in
RT Uganda.";
RL J. Gen. Virol. 82:655-665(2001).

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DR EMBL; AF230374; AAK26738.1; -;
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 KW Coat protein.
 FT NON TER 11
 SQ SEQUENCE 11 AA; 1216 MW; 7751D0695AA86774 CRC64;
 Query Match 28.2%; Score 22; DB 2; Length 11;
 Best Local Similarity 50.0%; Pred. No. 7.6e+03;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 Qy 6 VDKNTGDIINI 15
 Db 1 MSKRPGDIII 10
 RESULT 11
 ID Q9RS18 PRELIMINARY; PRT; 14 AA.
 AC Q9RS18;
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
 DE L-2,4-diaminobutyrate decarboxylase (Fragment).
 OS Vibrio alginolyticus.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrio.
 OX NCBI_TaxID=663;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92381494; PubMed=1512577;
 RA Yanamoto S., Tsuzaki Y., Tougou K., Shinoda S.;
 RT "Purification and characterization of L-2,4-diaminobutyrate
 RT decarboxylase from *Acinetobacter calcoaceticus*.";
 RL J. Gen. Microbiol. 138:1461-1465(1992).
 DR PIR; B44854; B44854.
 SQ SEQUENCE 14 AA; 1643 MW; 9F1B13DD35168ABA CRC64;
 Query Match 28.2%; Score 22; DB 2; Length 14;
 Best Local Similarity 50.0%; Pred. No. 9.9e+03;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 Qy 4 FVVDKNTGDI 13
 Db 4 FEVDNINWNI 13
 RESULT 12
 ID Q75LP0 PRELIMINARY; PRT; 15 AA.
 AC Q75LP0;
 DT 05-JUL-2004 (TRENBLrel. 27, Created)
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
 DE Hypothetical protein ARP3BETA (Fragment).
 GN Name=ARP3BETA;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22737999; PubMed=12853948; DOI=10.1038/nature01782;
 RA Hillier L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H.,
 RA Wagner-McPherson C., Layman D., Maas J., Jaeger S., Walker R.,
 RA Wyllie K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,
 RA Fewell G.A., Delehaunty K.D., Miner T.L., Nash W.E., Cordes M., Du H.,
 RA Sun H., Edwards J., Bradshaw-Cordum H., Ali J., Andrews S., Isak A.,
 RA Vanbrunt A., Nguyen C., Du F., Lamar B., Courtney L., Kalicki J.,
 RA Ozersky P., Bielicki L., Scott K., Holmes A., Harkins R., Harris A.,
 RA Strong C.M., Hou S., Tomlinson C., Dauphin-Kohlberg S.,
 RA Kozlowski-Reilly A., Leonard S., Rohlfing T., Rock S.M.,
 RA Tin-Wollam A.M., Abbott A., Minx P., Maupin R., Strommatt C.,

RA Latreille P., Miller N., Johnson D., Murray J., Woessner J.P.,
 RA Wendl M.C., Yang S.P., Schultz B.R., Wallis J.W., Spieth J.,
 RA Bieri T.A., Nelson J.O., Berkowicz N., Wohlmann P.B., Cook L.L.,
 RA Hickenbotham M.T., Eldred J., Williams D., Bedell J.A., Mardis E.R.,
 RA Clifton S.W., Chissoe S.L., Marra M.A., Raymond C., Haugen E.,
 RA Gillett W., Zhou Y., James R., Phelps K., Iadonato S., Bubb K.,
 RA Simms E., Levy R., Clendenning J., Kaul R., Kent W.J., Furey T.S.,
 RA Baertsch R.A., Brent M.R., Keibler E., Flicek P., Bork P., Suyama M.,
 RA Bailey J.A., Portnoy M.E., Torrents D., Chinwalla A.T., Gish W.R.,
 RA Eddy S.R., McPherson J.D., Olson M.V., Eichler E.E., Green E.D.,
 RA Waterston R.H., Wilson R.K.;
 RT "The DNA sequence of human chromosome 7.";
 RL Nature 424:157-164(2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Armstrong J., Doebber A., Haakenson W., Meyer R., VanBrunt A.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Waterston R.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Wilson R.;
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC092180; AAS07430.1; -;
 KW Hypothetical protein.
 FT NON TER 15
 SQ SEQUENCE 15 AA; 1407 MW; 8234E644327988F7 CRC64;
 Query Match 28.2%; Score 22; DB 2; Length 15;
 Best Local Similarity 71.4%; Pred. No. 1.1e+04;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 5 VVDKNTG 11
 Db 9 VVDGCTG 15
 RESULT 13
 ID Q6SJK6 PRELIMINARY; PRT; 12 AA.
 AC Q6SJK6;
 DT 05-JUL-2004 (TRENBLrel. 27, Created)
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
 DE Acyl-protein synthetase (Fragment).
 GN Name=luxE;
 OS Photobacterium mondopomensis.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Photobacterium.
 OX NCBI_TaxID=48408;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Seaf1.1.1;
 RC PubMed=15034641;
 RX Ast J.C., Dunlap P.V.;
 RA "Phylogenetic analysis of the lux operon distinguishes two
 RT evolutionarily distinct clades of *Photobacterium leiognathi*.";
 RL Arch. Microbiol. 181:352-361(2004).
 DR EMBL; AY456751; AAS16492.1; -;
 FT NON TER 12
 SQ SEQUENCE 12 AA; 1365 MW; 526E500A93A05AA7 CRC64;
 Query Match 26.9%; Score 21; DB 2; Length 12;
 Best Local Similarity 44.4%; Pred. No. 1.2e+04;
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 Qy 5 VVDKNTGDI 13
 Db 4 LLDIDTNDI 12

RESULT 14

Q9UPES PRELIMINARY; PRT; 13 AA.
AC Q9UPES5;
DT 01-WAY-2000 (TrEMBLrel. 13, Created)
DT 01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Inosine monophosphatase 2 (Fragment).
GN Name=IMPA2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97463449; PubMed=9322233;
RA Yoshikawa T., Turner G., Esterling L.E., Sanders A.R.,
RA Detera-Wadleigh S.D.;
RT "A novel human myo-inositol monophosphatase gene, IMP.18p, maps to a
RT susceptibility region for bipolar disorder.";
RL Mol. Psychiatry 2:393-397(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20284187;
RA Yoshikawa T., Padigaru M., Karkera J.D., Sharma M., Berrettini W.H.,
RA Esterling L.E., Detera-Wadleigh S.D.;
RT "Genomic structure and novel variants of myo-inositol monophosphatase
RT 2.";
RL Mol. Psychiatry 5:165-171(2000).
DR EMBL; AF025886; RAD22138.1;
DR EMBL; AF025885; AAD22138.1; JOINED.
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1331 MW; 89C724C8E3457865 CRC64;

Query Match 26.9%; Score 21; DB 2; Length 13;

Best Local Similarity 27.3%; Pred. No. 1.3e+04; Matches 3; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 5 VVDKNTGDINI 15
| : | : | :
DB 2 VIDTSGGPLDL 12

RESULT 15

Q6LBZ3 PRELIMINARY; PRT; 13 AA.
AC Q6LBZ3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Luciferase (Fragment).
GN Name=luxB;
OS Vibrio harveyi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=669;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B392;
RX MEDLINE=83117801; PubMed=6571986;
RA Cohn D.H., Ogden R.C., Abelson J.N., Baldwin T.O., Nealson K.H.,
RA Simon M.I., Mileham A.J.;
RT "Cloning of the Vibrio harveyi luciferase genes: use of a synthetic
RT oligonucleotide probe.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:120-123(1983).
DR EMBL; V01424; CAA24694.1; -.
FT NON_TER 13
FT NON_TER 13
SQ SEQUENCE 13 AA; 1596 MW; C59F081F3C7E29C9 CRC64;

Query Match 26.9%; Score 21; DB 2; Length 13;

Best Local Similarity 42.9%; Pred. No. 1.3e+04; Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 FGIFVVD 7
| : | : | :
DB 3 FGLFFLN 9

Search completed: February 22, 2005, 09:37:48
Job time : 55.6667 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 22, 2005, 08:52:23 ; Search time 65.6667 Seconds
(without alignments)
88.346 Million cell updates/sec

Title: US-08-991-628-2

Perfect score: 78
Sequence: 1 FGIFVVDKNTGSDINI 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 632537

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	78	100.0	15	2	AAW04842 Self epit
2	46	59.0	11	3	AAY61458 Cadherin-
3	42	53.8	10	3	AAY61455 Cadherin-
4	42	53.8	11	3	AAY61477 Cadherin-
5	42	53.8	11	3	AAY61636 Cadherin-
6	40	51.3	9	3	AAY61486 Cadherin-
7	40	51.3	9	3	AAY61370 Cadherin-
8	40	51.3	9	3	AAY61678 Cadherin-
9	40	51.3	9	5	ABB45631 Non-class
10	40	51.3	11	3	AAY61438 Cadherin-
11	40	51.3	11	3	AAY61413 Cadherin-
12	40	51.3	11	3	AAY61428 Cadherin-
13	39	50.0	11	3	AAY63733 Desmoglei
14	39	50.0	11	3	AAY61076 Cadherin-
15	39	50.0	11	5	ABB45785 Desmoglei
16	38	48.7	10	3	AAY63730 Desmoglei
17	38	48.7	10	3	AAY61474 Cadherin-
18	38	48.7	10	3	AAY61633 Cadherin-
19	38	48.7	10	5	ABB45782 Desmoglei
20	38	48.7	11	3	AAY62189 Cadherin-
21	37	47.4	9	8	ADQ13125 Hepatitis
22	37	47.4	9	8	ADQ13126 Hepatitis
23	37	47.4	10	3	AAY61073 Cadherin-
24	37	47.4	10	5	ABJ08003 Hepatitis
25	37	47.4	10	5	ABJ08418 Hepatitis

ALIGNMENTS

RESULT 1

AAW04842					
ID	AAW04842	standard; peptide; 15 AA.			
XX	AC	AAW04842;			
XX	DT	18-FEB-1997 (first entry)			
XX	DB	Self epitope of desmoglein 3, implicated in autoimmune disease.			
XX	KW	Tolerisation; self-epitope; antigen; autoimmune disease; autoantigen;			
XX	KW	HLA; human leukocyte antigen; T-cell; thymocyte; pemphigus vulgaris;			
XX	KW	desmoglein; multiple sclerosis; herpes simplex virus; adenovirus;			
XX	KW	phosphomannomutase; human papillomavirus; Epstein-Barr virus;			
XX	KW	DNA polymerase; influenza; haemagglutinin; reovirus; sigma protein.			
XX	OS	Homo sapiens.			
XX	PN	WO9627387-A1.			
XX	PD	12-SEP-1996.			
XX	PF	07-MAR-1996; 96WO-US003182.			
XX	PA	07-MAR-1995; 95US-00400796.			
XX	PI	(HARD) HARVARD COLLEGE.			
XX	PI	Strominger JL, Wucherpfennig KW;			
XX	PT	WPI; 1996-425218/42.			
XX	PT	Pemphigus vulgaris auto-antigens and multiple sclerosis non-self antigens			
XX	PT	- useful in disease treatment, and method for identification of other			
XX	PT	self and non-self antigens implicated in auto-immune disease.			
XX	XX	Claim 1; Page 38; 50pp; English.			
XX	XX	Pharmaceutical preparations for tolerisation to antigens comprise either			
XX	XX	an isolated human non-collagen or non-mysin basic protein (MBP)			
XX	XX	polypeptide which is capable of tolerising an individual to an			
XX	XX	autoantigen; or an isolated human pathogen polypeptide capable of			
XX	XX	tolerising an individual to that polypeptide. In both cases, the			
XX	XX	polypeptide (whether self or non-self) includes an amino acid sequence			
XX	XX	corresponding to a sequence motif for a MHC class II protein, such as HLA			
XX	XX	-DR, which is associated with a human autoimmune disease and which binds			
XX	XX	to the polypeptide to activate autoreactive T-cells in individuals with			
XX	XX	the autoimmune disease. This peptide is derived from the human desmoglein			

Adk38959 Hepatitis
Abj08409 Hepatitis
Abj07987 Hepatitis
Abj09323 Hepatitis
Abj08966 Hepatitis
Abj09353 Hepatitis
Abj09974 Hepatitis
Abj09258 Hepatitis
Adk39235 Hepatitis
Adk39349 Hepatitis
Aay61675 Cadherin-
Aay61367 Cadherin-
Aay61483 Cadherin-
Aay61452 Cadherin-
Aay61410 Cadherin-
Aay61427 Cadherin-
Aay61437 Cadherin-
Aay61965 Cadherin-
Aay63718 Desmoglei
Abb45770 Desmoglei

26 37 47.4 10 8 ADK38959
27 37 47.4 11 5 ABJ08409
28 37 47.4 11 5 ABJ07987
29 37 47.4 15 5 ABJ09323
30 37 47.4 15 5 ABJ08966
31 37 47.4 15 5 ABJ09353
32 37 47.4 15 5 ABJ09974
33 37 47.4 15 5 ABJ09258
34 37 47.4 15 8 ADK39235
35 37 47.4 15 8 ADK39349
36 36 46.2 8 3 AAY61675
37 36 46.2 8 3 AAY61367
38 36 46.2 8 3 AAY61483
39 36 46.2 9 3 AAY61452
40 36 46.2 10 3 AAY61410
41 36 46.2 10 3 AAY61427
42 36 46.2 10 3 AAY61437
43 36 46.2 11 3 AAY61965
44 36 46.2 11 3 AAY63718
45 36 46.2 11 5 ABB45770

CC 3 protein (amino acids 97-111) and is implicated as a self epitope in
 CC pemphigus vulgaris. Peptides derived from the human desmoglein protein
 CC are described in AA04841-47
 XX
 SQ Sequence 15 AA;
 Query Match 100.0%; Score 78; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.1e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FGIFVVDKNTGDIINI 15
 DB 1 FGIFVVDKNTGDIINI 15
 RESULT 2
 ID AAY61458 standard; peptide; 11 AA.
 XX
 AC AAY61458;
 XX
 DT 02-MAR-2000 (first entry)
 XX
 DE Cadherin-7 cell adhesion recognition cyclic peptide SEQ ID NO:1343.
 XX
 KW Modulation; nonclassical cadherin mediated cell adhesion; CAR;
 KW inhibition; cadherin extracellular domain; cell adhesion recognition;
 KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;
 KW cadherin-14; cadherin-15; T-cadherin; PB-cadherin;
 KW cadherin related neuronal receptor; LI-cadherin; protocadherin;
 KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
 KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
 KW neurological disease; cyclic.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 XX
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1..11
 FT /note= "the terminal residues are condensed with each
 FT other to form a cyclic peptide"
 XX
 XX
 PN WO9957149-A2.
 XX
 PD 11-NOV-1999.
 XX
 XX
 PF 05-MAY-1999; 99WO-CA000363.
 XX
 XX
 PR 05-MAY-1998; 98US-00073040.
 PR 06-NOV-1998; 98US-00187859.
 PR 20-JAN-1999; 99US-00234395.
 PR 08-MAR-1999; 99US-00264516.
 XX
 XX (ADHE-) ADHEREX TECHNOLOGIES INC.
 XX
 XX Blaschuk OW, Gour BJ, Byers S;
 XX WPI; 2000-038791/03.
 XX
 XX New cadherin modulating agents, used for modulating nonclassical cadherin
 XX mediated functions for treating e.g. cancers, obesity, rheumatoid
 XX arthritis, multiple sclerosis, diabetes or a neurological disease.
 XX
 XX Claim 36; Page 172; 252pp; English.
 XX
 XX The present invention describes cadherin modulating agents (MA)
 XX comprising peptides which comprise a nonclassical cadherin cell adhesion
 XX recognition (CAR) sequence. The MAs can be used for modulating
 XX nonclassical cadherin-mediated functions. They can be used for e.g.
 XX inhibiting adhesion of nonclassical-cadherin expressing cells in a
 XX mammal, enhancing delivery of a drug through the skin of a mammal,
 XX enhancing delivery of a drug to a tumour in a mammal, treating cancer in
 XX a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting

CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
 CC expressing cell, preventing or treating obesity in a mammal, stimulating
 CC blood vessel regression in a mammal, enhancing drug delivery to the
 CC central nervous system, treating a demyelinating neurological disease,
 CC increasing vasopermeability in a mammal, enhancing adhesion of
 CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in
 CC a mammal, or preventing pregnancy in a mammal. They can also be used for
 CC e.g. enhancing or directing neurite outgrowth, facilitating wound healing
 CC or reducing scar tissue, or enhancing adhesion of foreign tissue in a
 CC mammal. They can also be used for treating e.g. psoriasis, arthritis, age
 CC related macular degeneration, multiple sclerosis and diabetes. The
 CC products can also be used for detection and diagnosis and in bioreactors.
 CC AAY60592 to AAY64572 represent specifically claimed peptides, and
 CC AAY64573 to AAY64643 and AAZ33183 to AAZ33186 represent sequences used in
 CC the exemplification of the present invention
 XX
 SQ Sequence 11 AA;
 Query Match 59.0%; Score 46; DB 3; Length 11;
 Best Local Similarity 70.0%; Pred. No. 0.34;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 3 IFVVDKNTGD 12
 DB 2 IFIDNTGD 11
 RESULT 3
 ID AAY61455 standard; peptide; 10 AA.
 XX
 AC AAY61455;
 XX
 DT 02-MAR-2000 (first entry)
 XX
 DE Cadherin-7 cell adhesion recognition cyclic peptide SEQ ID NO:1340.
 XX
 KW Modulation; nonclassical cadherin mediated cell adhesion; CAR;
 KW inhibition; cadherin extracellular domain; cell adhesion recognition;
 KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;
 KW cadherin-14; cadherin-15; T-cadherin; PB-cadherin;
 KW cadherin related neuronal receptor; LI-cadherin; protocadherin;
 KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
 KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
 KW neurological disease; cyclic.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1..10
 FT /note= "the terminal residues are condensed with each
 FT other to form a cyclic peptide"
 XX
 XX
 PN WO9957149-A2.
 XX
 PD 11-NOV-1999.
 XX
 XX
 PF 05-MAY-1999; 99WO-CA000363.
 XX
 XX
 PR 05-MAY-1998; 98US-00073040.
 PR 06-NOV-1998; 98US-00187859.
 PR 20-JAN-1999; 99US-00234395.
 PR 08-MAR-1999; 99US-00264516.
 XX
 XX (ADHE-) ADHEREX TECHNOLOGIES INC.
 XX
 XX Blaschuk OW, Gour BJ, Byers S;
 XX WPI; 2000-038791/03.
 XX
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 XX mediated functions for treating e.g. cancers, obesity, rheumatoid

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 CC mammal, enhancing delivery of a drug through the skin of a mammal,
 CC enhancing delivery of a drug to a tumour in a mammal, treating cancer in
 CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting
 CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
 CC expressing cell, preventing or treating obesity in a mammal, stimulating
 CC blood vessel regression in a mammal, enhancing drug delivery to the
 CC central nervous system, treating a demyelinating neurological disease,
 CC increasing vasopermeability in a mammal, enhancing adhesion of
 CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in
 CC a mammal, or preventing pregnancy in a mammal. They can also be used for
 CC e.g. enhancing or directing neurite outgrowth, facilitating wound healing
 CC or reducing scar tissue, or enhancing adhesion of foreign tissue in a
 CC mammal. They can also be used for treating e.g. psoriasis, arthritis, age
 CC -related macular degeneration, multiple sclerosis and diabetes. The
 CC products can also be used for detection and diagnosis and in bioreactors.
 CC AAY60592 to AAY64572 represent specifically claimed peptides, and
 CC AAY64573 to AAY64643 and AA233183 to AA233186 represent sequences used in
 CC the exemplification of the present invention
 XX Sequence 10 AA;
 SQ

Query Match 53.8%; Score 42; DB 3; Length 10;
 Best Local Similarity 66.7%; Pred. No. 1.6;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 FVVDKNTGD 12
 |:::|
 Db 2 FIIDNTGD 10

RESULT 4
 AAY61477
 ID AAY61477 standard; peptide; 11 AA.
 AC AAY61477;
 XX
 DT 02-MAR-2000 (first entry)
 XX Cadherin-7 cell adhesion recognition cyclic peptide SEQ ID NO:1363.
 DE
 XX Modulation; nonclassical cadherin mediated cell adhesion; CAR;
 KW inhibition; cadherin extracellular domain; cell adhesion recognition;
 KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;
 KW cadherin-14; cadherin-15; T-cadherin; PB-cadherin;
 KW cadherin related neuronal receptor; Li-cadherin; protocadherin;
 KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
 KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
 KW neurological disease; cyclic.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX

Key Location/Qualifiers
 FT Modified-site 1..11
 FT /note= "the terminal residues are condensed with each
 FT other to form a cyclic peptide"
 XX
 XX WO957149-A2.
 PN
 XX 11-NOV-1999.
 PD
 XX
 XX 05-MAY-1999; 99WO-CA000363.
 PF
 XX 05-MAY-1998; 98US-00073040.
 PR

PR 06-NOV-1998; 98US-00187859.
 PR 20-JAN-1999; 99US-00234395.
 PR 08-MAR-1999; 99US-00264516.
 XX
 PA (ADHE-) ADHEREX TECHNOLOGIES INC.
 XX Blaschuk OW, Gour BJ, Byers S;
 PI WPI; 2000-038791/03.
 XX
 DR New cadherin modulating agents, used for modulating nonclassical cadherin
 PT mediated functions for treating e.g. cancers, obesity, rheumatoid
 PT arthritis, multiple sclerosis, diabetes or a neurological disease.
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 CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting
 CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
 CC expressing cell, preventing or treating obesity in a mammal, stimulating
 CC blood vessel regression in a mammal, enhancing drug delivery to the
 CC central nervous system, treating a demyelinating neurological disease,
 CC increasing vasopermeability in a mammal, enhancing adhesion of
 CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in
 CC a mammal, or preventing pregnancy in a mammal. They can also be used for
 CC e.g. enhancing or directing neurite outgrowth, facilitating wound healing
 CC or reducing scar tissue, or enhancing adhesion of foreign tissue in a
 CC mammal. They can also be used for treating e.g. psoriasis, arthritis, age
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 CC AAY60592 to AAY64572 represent specifically claimed peptides, and
 CC AAY64573 to AAY64643 and AA233183 to AA233186 represent sequences used in
 CC the exemplification of the present invention
 XX Sequence 11 AA;
 SQ

Query Match 53.8%; Score 42; DB 3; Length 11;
 Best Local Similarity 60.0%; Pred. No. 1.7;
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 3 IFVVDKNTGD 12
 |:::|
 Db 2 IFIIDENTGE 11

RESULT 5
 AAY61636
 ID AAY61636 standard; peptide; 11 AA.
 XX
 AC AAY61636;
 XX
 XX 02-MAR-2000 (first entry)
 DT
 XX Cadherin-7 cell adhesion recognition cyclic peptide SEQ ID NO:1522.
 DE
 XX Modulation; nonclassical cadherin mediated cell adhesion; CAR;
 KW inhibition; cadherin extracellular domain; cell adhesion recognition;
 KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;
 KW cadherin-14; cadherin-15; T-cadherin; PB-cadherin;
 KW cadherin related neuronal receptor; Li-cadherin; protocadherin;
 KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
 KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
 KW neurological disease; cyclic.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX

Query Match 51.3%; Score 40; DB 3; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.8e+06;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 IFVVDKNTG 11
 DB 1 IFIIDNTG 9

RESULT 8
 AAY61678
 ID AAY61678 standard; peptide; 9 AA.
 XX
 AC AAY61678;
 XX
 DT 02-MAR-2000 (first entry)
 DE Cadherin-7 cell adhesion recognition cyclic peptide SEQ ID NO:1564.
 XX
 KW Modulation; nonclassical cadherin mediated cell adhesion; CAR;
 KW inhibition; cadherin extracellular domain; cell adhesion recognition;
 KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;
 KW cadherin-14; cadherin-15; T-cadherin; PB-cadherin;
 KW cadherin related neuronal receptor; LI-cadherin; protocadherin;
 KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
 KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
 KW neurological disease; cyclic.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PF Key Location/Qualifiers
 FT Modified-site 1..9
 FT /note= "the terminal residues are condensed with each
 FT other to form a cyclic peptide"
 XX
 PN WO9957149-A2.
 XX
 PD 11-NOV-1999.
 XX
 PF 05-MAY-1999; 99WO-CA000363.
 XX
 PR 05-MAY-1998; 98US-00073040.
 PR 06-NOV-1998; 98US-00187859.
 PR 20-JAN-1999; 99US-00234395.
 PR 08-MAR-1999; 99US-00264516.
 XX
 PA (ADHE-) ADHEREX TECHNOLOGIES INC.
 XX
 PI Blaschuk OW, Gour BJ, Byers S;
 XX
 DR WPI; 2000-038791/03.
 XX
 PT New cadherin modulating agents, used for modulating nonclassical cadherin
 PT mediated functions for treating e.g. cancers, obesity, rheumatoid
 PT arthritis, multiple sclerosis, diabetes or a neurological disease.
 XX
 PS Claim 33; Page 170; 252pp; English.
 XX
 CC The present invention describes cadherin modulating agents (MA)
 CC comprising peptides which comprise a nonclassical cadherin cell adhesion
 CC recognition (CAR) sequence. The MAs can be used for modulating
 CC nonclassical cadherin-mediated functions. They can be used for e.g.
 CC inhibiting adhesion of nonclassical-cadherin expressing cells in a
 CC mammal, enhancing delivery of a drug through the skin of a mammal,
 CC enhancing delivery of a drug to a tumour in a mammal, treating cancer in
 CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting
 CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
 CC expressing cell, preventing or treating obesity in a mammal, stimulating
 CC blood vessel regression in a mammal, enhancing drug delivery to the
 CC central nervous system, treating a demyelinating neurological disease,
 CC increasing vasopermeability in a mammal, enhancing adhesion of
 CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in
 CC a mammal, or preventing pregnancy in a mammal. They can also be used for
 CC e.g. enhancing or directing neurite outgrowth, facilitating wound healing
 CC or reducing scar tissue, or enhancing adhesion of foreign tissue in a
 CC mammal. They can also be used for treating e.g. psoriasis, arthritis, age
 CC related macular degeneration, multiple sclerosis and diabetes. The
 CC products can also be used for detection and diagnosis and in bioreactors.
 CC AAY60592 to AAY64572 represent specifically claimed peptides, and
 CC AAY64573 to AAY64643 and AAZ33183 to AAZ33186 represent sequences used in
 CC the exemplification of the present invention
 XX
 SQ Sequence 9 AA;

CC a mammal, or preventing pregnancy in a mammal. They can also be used for
 CC e.g. enhancing or directing neurite outgrowth, facilitating wound healing
 CC or reducing scar tissue, or enhancing adhesion of foreign tissue in a
 CC mammal. They can also be used for treating e.g. psoriasis, arthritis, age
 CC -related macular degeneration, multiple sclerosis and diabetes. The
 CC products can also be used for detection and diagnosis and in bioreactors.
 CC AAY60592 to AAY64572 represent specifically claimed peptides, and
 CC AAY64573 to AAY64643 and AAZ33183 to AAZ33186 represent sequences used in
 CC the exemplification of the present invention
 XX
 SQ

Sequence 9 AA;

Query Match 51.3%; Score 40; DB 3; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.8e+06;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 IFVVDKNTG 11
 ||:|:|
 Db 1 IFIIDNTG 9

RESULT 9
 ABB45631
 ID ABB45631 standard; peptide; 9 AA.

XX AC ABB45631;

XX DT 30-JAN-2002 (first entry)

XX DE Non-classical cadherin CAR sequence SEQ ID NO 375.

XX KW Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
 KW cystostatic; antiapoptotic; wound healing; reduce scar tissue; skin graft;
 KW organ implant; autoimmune blistering disorder; cancer; apoptosis.
 XX OS Synthetic.

XX PN WO200172956-A2.

XX PD 04-OCT-2001.

XX PF 27-MAR-2001; 2001WO-IB001400.

XX PR 27-MAR-2000; 2000US-00535852.

XX PA (ADHE-) ADHEREX TECHNOLOGIES INC.

XX PI Blaschuk OW, Symonds JW, Gour BJ;

XX PS WPI; 2002-025778/03.

XX PT Modulating agents for inhibiting or enhancing desmosomal cadherin
 PT mediated cell adhesion, useful for facilitating wound healing and/or
 PT reducing scar tissue, treating cancer and inducing apoptosis.

XX PS Disclosure; Page 21; 127pp; English.

XX The invention relates to modulating agents for inhibiting or enhancing
 CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
 CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
 CC (ABB4531-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
 CC sequence, a substance such as an antibody or antigen-binding fragment
 CC that specifically binds a desmosomal cadherin CAR sequence and/or a
 CC polynucleotide encoding a polypeptide that comprises a desmosomal
 CC cadherin CAR sequence or analogue. The modulating agents have
 CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
 CC facilitate wound healing and/or reduce scar tissue, for enhancing
 CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
 CC treating an autoimmune blistering disorder and to treat cancer (e.g.
 CC carcinoma, leukaemia or melanoma) and induce apoptosis

XX Sequence 9 AA;

Query Match 51.3%; Score 40; DB 5; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.8e+06;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 IFVVDKNTG 11
 ||:|:|
 Db 1 IFIIDNTG 9

RESULT 10
 AAY61438
 ID AAY61438 standard; peptide; 11 AA.

XX AC AAY61438;

XX DT 02-MAR-2000 (first entry)

XX DE Cadherin-7 cell adhesion recognition cyclic peptide SEQ ID NO:3913.

XX KW Modulation; nonclassical cadherin mediated cell adhesion; CAR;
 KW inhibition; cadherin extracellular domain; cell adhesion recognition;
 KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;
 KW cadherin-14; cadherin-15; T-cadherin; PS-cadherin;
 KW cadherin related neuronal receptor; LI-cadherin; protocadherin;
 KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
 KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
 KW neurological disease; cyclic.

XX OS Synthetic.

XX OS Homo sapiens.

XX X Key Location/Qualifiers

FT Modified-site 1..11
 FT /note= "the terminal residues are condensed with each
 FT other to form a cyclic peptide"

XX PN WO9957149-A2.

XX PD 11-NOV-1999.

XX PF 05-MAY-1999; 99WO-CA000363.

XX PR 05-MAY-1998; 98US-00073040.

XX PR 06-NOV-1998; 98US-00187859.

XX PR 20-JAN-1999; 99US-00234395.

XX PR 08-MAR-1999; 99US-00264516.

XX PA (ADHE-) ADHEREX TECHNOLOGIES INC.

XX PI Blaschuk OW, Gour BJ, Byers S;

XX PS WPI; 2000-038791/03.

XX PT New cadherin modulating agents, used for modulating nonclassical cadherin
 PT mediated functions for treating e.g. cancers, obesity, rheumatoid
 PT arthritis, multiple sclerosis, diabetes or a neurological disease.

XX PS Claim 36; Page 171; 252pp; English.

XX The present invention describes cadherin modulating agents (MA)
 CC comprising peptides which comprise a nonclassical cadherin cell adhesion
 CC recognition (CAR) sequence. The MAs can be used for modulating
 CC nonclassical cadherin-mediated functions. They can be used for e.g.
 CC inhibiting adhesion of nonclassical-cadherin expressing cells in a
 CC mammal, enhancing delivery of a drug through the skin of a mammal,
 CC enhancing delivery of a drug to a tumour in a mammal, treating cancer in
 CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting
 CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
 CC expressing cell, preventing or treating obesity in a mammal, stimulating
 CC blood vessel regression in a mammal, enhancing drug delivery to the
 CC central nervous system, treating a demyelinating neurological disease,
 CC increasing vasopermeability in a mammal, enhancing adhesion of
 CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in

CC a mammal, or preventing pregnancy in a mammal. They can also be used for
 CC e.g. enhancing or directing neurite outgrowth, facilitating wound healing
 CC or reducing scar tissue, or enhancing adhesion of foreign tissue in a
 CC mammal. They can also be used for treating e.g. psoriasis, arthritis, age
 CC related macular degeneration, multiple sclerosis and diabetes. The
 CC products can also be used for detection and diagnosis and in bioreactors.
 CC AAY60592 to AAY64572 represent specifically claimed peptides, and
 CC AAY64573 to AAY64643 and AA233183 to AA233186 represent sequences used in
 CC the exemplification of the present invention
 XX
 SQ Sequence 11 AA;

Query Match 51.3%; Score 40; DB 3; Length 11;
 Best Local Similarity 66.7%; Pred. No. 3.9;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 IFVVDKNTG 11
 ||:|:|
 Db 2 IFIDNTG 10

RESULT 11

AAV61413
 ID AAY61413 standard; peptide; 11 AA.

XX
 AC AAY61413;

DT 02-MAR-2000 (first entry)

DE Cadherin-7 cell adhesion recognition cyclic peptide SEQ ID NO:1317.

XX Modulation; nonclassical cadherin mediated cell adhesion; CAR;
 KW inhibition; cadherin extracellular domain; cell adhesion recognition;
 KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;
 KW cadherin-14; cadherin-15; T-cadherin; PB-cadherin;
 KW cadherin related neuronal receptor; LI-cadherin; protocadherin;
 KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
 KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
 KW neurological disease; cyclic.

XX Synthetic.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Disulfide-bond 1..11

PN WO9957149-A2.

XX 11-NOV-1999.

XX 05-MAY-1999; 99WO-CA000363.

XX 05-MAY-1998; 98US-00073040.

PR 06-NOV-1998; 98US-00187859.

PR 20-JAN-1999; 99US-00234395.

PR 08-MAR-1999; 99US-00264516.

XX (ADHE-) ADHEREX TECHNOLOGIES INC.

XX Blaschuk OW, Gour BJ, Byers S;

XX WPI; 2000-038791/03.

XX New cadherin modulating agents, used for modulating nonclassical cadherin
 PT mediated functions for treating e.g. cancers, obesity, rheumatoid
 PT arthritis, multiple sclerosis, diabetes or a neurological disease.

PS Claim 36; Page 171; 252pp; English.

XX The present invention describes cadherin modulating agents (MA)

CC comprising peptides which comprise a nonclassical cadherin cell adhesion
 CC recognition (CAR) sequence. The MA can be used for modulating
 CC nonclassical cadherin-mediated functions. They can be used for e.g.

CC inhibiting adhesion of nonclassical-cadherin expressing cells in a
 CC mammal, enhancing delivery of a drug through the skin of a mammal,
 CC enhancing delivery of a drug to a tumour in a mammal, treating cancer in
 CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting
 CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
 CC expressing cell, preventing or treating obesity in a mammal, stimulating
 CC blood vessel regression in a mammal, enhancing drug delivery to the
 CC central nervous system, treating a demyelinating neurological disease,
 CC increasing vasopermeability in a mammal, enhancing adhesion of
 CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in
 CC a mammal, or preventing pregnancy in a mammal. They can also be used for
 CC e.g. enhancing or directing neurite outgrowth, facilitating wound healing
 CC or reducing scar tissue, or enhancing adhesion of foreign tissue in a
 CC mammal. They can also be used for treating e.g. psoriasis, arthritis, age
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 CC products can also be used for detection and diagnosis and in bioreactors.
 CC AAY60592 to AAY64572 represent specifically claimed peptides, and
 CC AAY64573 to AAY64643 and AA233183 to AA233186 represent sequences used in
 CC the exemplification of the present invention
 XX
 SQ Sequence 11 AA;

Query Match 51.3%; Score 40; DB 3; Length 11;

Best Local Similarity 66.7%; Pred. No. 3.9;

Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 IFVVDKNTG 11

||:|:|

Db 2 IFIDNTG 10

RESULT 12

AAV61428

ID AAY61428 standard; peptide; 11 AA.

XX
 AC AAY61428;

DT 02-MAR-2000 (first entry)

DE Cadherin-7 cell adhesion recognition cyclic peptide SEQ ID NO:3903.

XX Modulation; nonclassical cadherin mediated cell adhesion; CAR;
 KW inhibition; cadherin extracellular domain; cell adhesion recognition;
 KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;
 KW cadherin-14; cadherin-15; T-cadherin; PB-cadherin;
 KW cadherin related neuronal receptor; LI-cadherin; protocadherin;
 KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
 KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
 KW neurological disease; cyclic.

XX Synthetic.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 1..11

FT /note= "the terminal residues are condensed with each
 FT other to form a cyclic peptide"

XX WO9957149-A2.

XX 11-NOV-1999.

XX 05-MAY-1999; 99WO-CA000363.

XX 05-MAY-1998; 98US-00073040.

PR 06-NOV-1998; 98US-00187859.

PR 20-JAN-1999; 99US-00234395.

PR 08-MAR-1999; 99US-00264516.

XX (ADHE-) ADHEREX TECHNOLOGIES INC.

XX Blaschuk OW, Gour BJ, Byers S;

XX

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DR WPI; 2000-038791/03.
XX
XX New cadherin modulating agents, used for modulating nonclassical cadherin
PT -mediated functions for treating e.g. cancers, obesity, rheumatoid
PT arthritis, multiple sclerosis, diabetes or a neurological disease.
XX
XX Claim 36; Page 171; 252pp; English.
XX
XX The present invention describes cadherin modulating agents (MA)
CC comprising peptides which comprise a nonclassical cadherin cell
CC recognition (CAR) sequence. The MAs can be used for modulating
CC nonclassical cadherin-mediated functions. They can be used for e.g.
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CC mammal, enhancing delivery of a drug through the skin of a mammal,
CC enhancing delivery of a drug to a tumour in a mammal, treating cancer in
CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting
CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
CC expressing cell, preventing or treating obesity in a mammal, stimulating
CC blood vessel regression in a mammal, enhancing drug delivery to the
CC central nervous system, treating a demyelinating neurological disease,
CC increasing vasopermeability in a mammal, enhancing adhesion of
CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in
CC a mammal, or preventing pregnancy in a mammal. They can also be used for
CC e.g. enhancing or directing neurite outgrowth, facilitating wound healing
CC or reducing scar tissue, or enhancing adhesion of foreign tissue in a
CC mammal. They can also be used for treating e.g. psoriasis, arthritis, age
CC -related macular degeneration, multiple sclerosis and diabetes. The
CC products can also be used for detection and diagnosis and in bioreactors.
CC AAY60592 to AAY64572 represent specifically claimed peptides, and
CC AAY64573 to AAY64643 and AA233183 to AA233186 represent sequences used in
CC the exemplification of the present invention
XX
XX Sequence 11 AA;
XX
XX Query Match 51.3%; Score 40; DB 3; Length 11;
XX Best Local Similarity 66.7%; Pred. No. 3.9;
XX Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 3 IFVVDKNTG 11
XX ||:|:|:|
XX Db 2 IFIIDNTG 10
XX
XX RESULT 13
XX AAY63733
XX ID AAY63733 standard; peptide; 11 AA.
XX
XX AC AAY63733;
XX
XX DT 02-MAR-2000 (first entry)
XX
XX DE Desmoglein cell adhesion recognition cyclic peptide SEQ ID NO:3185.
XX
XX KW Modulation; nonclassical cadherin mediated cell adhesion; CAR;
XX inhibition; cadherin extracellular domain; cell adhesion recognition;
XX OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;
XX cadherin-14; cadherin-15; T-cadherin; PB-cadherin;
XX cadherin related neuronal receptor; LI-cadherin; protocadherin;
XX desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
XX rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
XX neurological disease; cyclic.
XX
XX OS Synthetic.
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX Modified-site 1..11
XX FT /note= "the terminal residues are condensed with each
XX FT other to form a cyclic peptide"
XX
XX FN WO9957149-A2.
XX
XX 11-NOV-1999.
XX

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XX PF 05-MAY-1999; 99WO-CA000363.
XX
XX PR 05-MAY-1998; 98US-00073040.
XX PR 06-NOV-1998; 98US-00187859.
XX PR 20-JAN-1999; 99US-00234395.
XX PR 08-MAR-1999; 99US-00264516.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
XX Blaschuk OW, Gour BJ, Byers S;
XX
XX WPI; 2000-038791/03.
XX
XX New cadherin modulating agents, used for modulating nonclassical cadherin
PT -mediated functions for treating e.g. cancers, obesity, rheumatoid
PT arthritis, multiple sclerosis, diabetes or a neurological disease.
XX
XX Claim 90; Page 208; 252pp; English.
XX
XX The present invention describes cadherin modulating agents (MA)
CC comprising peptides which comprise a nonclassical cadherin cell
CC recognition (CAR) sequence. The MAs can be used for modulating
CC nonclassical cadherin-mediated functions. They can be used for e.g.
CC inhibiting adhesion of nonclassical-cadherin expressing cells in a
CC mammal, enhancing delivery of a drug through the skin of a mammal,
CC enhancing delivery of a drug to a tumour in a mammal, treating cancer in
CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting
CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
CC expressing cell, preventing or treating obesity in a mammal, stimulating
CC blood vessel regression in a mammal, enhancing drug delivery to the
CC central nervous system, treating a demyelinating neurological disease,
CC increasing vasopermeability in a mammal, enhancing adhesion of
CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in
CC a mammal, or preventing pregnancy in a mammal. They can also be used for
CC e.g. enhancing or directing neurite outgrowth, facilitating wound healing
CC or reducing scar tissue, or enhancing adhesion of foreign tissue in a
CC mammal. They can also be used for treating e.g. psoriasis, arthritis, age
CC -related macular degeneration, multiple sclerosis and diabetes. The
CC products can also be used for detection and diagnosis and in bioreactors.
CC AAY60592 to AAY64572 represent specifically claimed peptides, and
CC AAY64573 to AAY64643 and AA233183 to AA233186 represent sequences used in
CC the exemplification of the present invention
XX
XX Sequence 11 AA;
XX
XX Query Match 50.0%; Score 39; DB 3; Length 11;
XX Best Local Similarity 50.0%; Pred. No. 5.8;
XX Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 3 IFVVDKNTGD 12
XX :|:|:|:|
XX Db 2 MFIINRNTGD 11
XX
XX RESULT 14
XX AAY61076
XX ID AAY61076 standard; peptide; 11 AA.
XX
XX AC AAY61076;
XX
XX DT 02-MAR-2000 (first entry)
XX
XX DE Cadherin-6 cell adhesion recognition cyclic peptide SEQ ID NO:1022.
XX
XX KW Modulation; nonclassical cadherin mediated cell adhesion; CAR;
XX inhibition; cadherin extracellular domain; cell adhesion recognition;
XX OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;
XX cadherin-14; cadherin-15; T-cadherin; PB-cadherin;
XX cadherin related neuronal receptor; LI-cadherin; protocadherin;
XX desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
XX rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
XX neurological disease; cyclic.
XX

```

XX Synthetic.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH Modified-site 1..11
FT /note= "the terminal residues are condensed with each
FT other to form a cyclic peptide"
XX
XX WO9957149-A2.
PN
XX
XX 11-NOV-1999.
PD
XX
XX 05-MAY-1999; 99WO-CA000363.
PF
XX 05-MAY-1998; 98US-00073040.
PR 06-NOV-1998; 98US-00197859.
PR 20-JAN-1999; 99US-00234395.
PR 08-MAR-1999; 99US-00264516.
XX
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
PA
XX Blaschuk OW, Gour BJ, Byers S;
PI
XX WPI; 2000-038791/03.
DR
XX New cadherin modulating agents, used for modulating nonclassical cadherin
PT mediated functions for treating e.g. cancers, obesity, rheumatoid
PT arthritis, multiple sclerosis, diabetes or a neurological disease.
PT
XX
PS Claim 27; Page 166; 252pp; English.
XX
XX The present invention describes cadherin modulating agents (MA)
CC comprising peptides which comprise a nonclassical cadherin cell adhesion
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CC nonclassical cadherin-mediated functions. They can be used for e.g.
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CC mammal, enhancing delivery of a drug through the skin of a mammal,
CC enhancing delivery of a drug to a tumour in a mammal, treating cancer in
CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting
CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
CC expressing cell, preventing or treating obesity in a mammal, stimulating
CC blood vessel regression in a mammal, enhancing drug delivery to the
CC central nervous system, treating a demyelinating neurological disease,
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CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in
CC a mammal, or preventing pregnancy in a mammal. They can also be used for
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CC or reducing scar tissue, or enhancing adhesion of foreign tissue in a
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CC AAY60592 to AAY64572 represent specifically claimed peptides, and
CC AAY64573 to AAY64643 and AAZ33183 to AAZ33186 represent sequences used in
CC the exemplification of the present invention
XX
XX Sequence 11 AA;

Query Match 50.0%; Score 39; DB 3; Length 11;
Best Local Similarity 50.0%; Pred. No. 5.8;
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 3 IFVVDKNTGTD 12
Db 2 LFIINRTGTD 11

RESULT 15
ABB45785
ID ABB45785 standard; peptide; 11 AA.
XX
XX ABB45785;
XX

DT 30-JAN-2002 (first entry)
XX
XX Desmoglein CAR sequence cyclic peptide SEQ ID NO 529.
XX
XX Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
KW cytostatic; antiapoptotic; wound healing; reduce scar tissue; skin graft;
KW organ implant; autoimmune blistering disorder; cancer; apoptosis; cyclic.
XX
XX Synthetic.
XX
XX WO200172956-A2.
PN
XX 04-OCT-2001.
PD
XX 27-MAR-2001; 2001WO-IB001400.
PF
XX 27-MAR-2000; 2000US-00535852.
PR
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
PA
XX Blaschuk OW, Symonds JM, Gour BJ;
PI
XX WPI; 2002-025778/03.
DR
XX Modulating agents for inhibiting or enhancing desmosomal cadherin
PT mediated cell adhesion, useful for facilitating wound healing and/or
PT reducing scar tissue, treating cancer and inducing apoptosis.
PT
XX Claim 18; Page 98; 127pp; English.
XX
XX The invention relates to modulating agents for inhibiting or enhancing
CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
CC sequence, a substance such as an antibody or antigen-binding fragment
CC that specifically binds a desmosomal cadherin CAR sequence and/or a
CC polynucleotide encoding a polypeptide that comprises a desmosomal
CC cadherin CAR sequence or analogue. The modulating agents have
CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
CC facilitate wound healing and/or reduce scar tissue, for enhancing
CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
CC treating an autoimmune blistering disorder and to treat cancer (e.g.
CC carcinoma, leukaemia or melanoma) and induce apoptosis
XX
XX Sequence 11 AA;

Query Match 50.0%; Score 39; DB 5; Length 11;
Best Local Similarity 50.0%; Pred. No. 5.8;
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 3 IFVVDKNTGTD 12
Db 2 MFIINRTGTD 11

Search completed: February 22, 2005, 09:24:33
Job time : 66.6667 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 22, 2005, 09:08:09 ; Search time 11.1333 Seconds
(without alignments)
129.633 Million cell updates/sec

Title: US-08-991-628-3

Perfect score: 71

Sequence: 1 LNSKIAFKIVSQEPA 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 2523

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	35.2	10	2 S66458	ferredoxin - Rhizo
2	23	32.4	14	2 A49018	myosin heavy chain
3	20	28.2	14	2 PH0795	T-cell receptor al
4	20	28.2	14	2 PH0776	T-cell receptor al
5	20	28.2	15	2 PA0097	starch phosphoryla
6	19	26.8	10	2 F44644	neurotoxin-ascosia
7	19	26.8	12	2 S71034	potB protein - Sal
8	19	26.8	13	2 S57571	T cell receptor al
9	19	26.8	13	2 E42762	proteasome endopep
10	19	26.8	13	2 G44644	neurotoxin-ascosia
11	19	26.8	15	2 PS0452	32K protein 3306 -
12	18	25.4	10	2 PT0309	Ig heavy chain CRD
13	18	25.4	10	2 A24407	amcyanin - Paraco
14	18	25.4	11	2 E60691	phycobilisome 8K l
15	18	25.4	12	2 D28551	hypothetical prote
16	18	25.4	12	2 S27024	Na+/K+-exchanging
17	18	25.4	14	2 PH0801	T-cell receptor al
18	18	25.4	15	2 PQ0174	stylar glycoprotei
19	18	25.4	15	2 PS0251	15K protein 5106 -
20	18	25.4	15	2 PA0054	protein OF200017 -
21	18	25.4	15	2 A32971	heparin-binding le
22	17.5	24.6	15	2 PT0222	Ig heavy chain CR
23	17	23.9	3	3 A33802	thyrotropin-releas
24	17	23.9	10	2 PH0807	T-cell receptor al
25	17	23.9	11	2 G61497	seed protein ws-23
26	17	23.9	12	2 A55837	5-aminoimidazole r
27	17	23.9	13	2 H64124	hypothetical prote
28	17	23.9	13	2 PL0157	Ig kappa chain V-I
29	17	23.9	13	2 B56864	dipeptidyl-peptida

VCAM-1 5'UTR bindi
acetyl-CoA carboxy
insulin-like growt
protein OA100044 -
T-cell receptor al
cytochrome-c oxida
rpsa protein - Erw
Atpase R1 subunit
gene NF2 protein -
ubiquinol-cytochro
glycine reductase
eledoisin - musky
eledoisin - curled
beta-D-galactosida
beta-glucosidase (
phospholipase A2 (
30 17 23.9 13 2 A59387
31 17 23.9 14 2 S35267
32 17 23.9 14 2 JH0516
33 17 23.9 15 2 PA0046
34 17 23.9 15 2 PH0782
35 17 23.9 15 2 S77987
36 16 22.5 8 2 S37141
37 16 22.5 9 2 D48186
38 16 22.5 9 2 I54379
39 16 22.5 9 2 PC7073
40 16 22.5 10 2 B39308
41 16 22.5 11 1 E00C
42 16 22.5 11 1 E00C
43 16 22.5 11 2 S53436
44 16 22.5 11 2 PQ0231
45 16 22.5 12 2 A29169

ALIGNMENTS

RESULT 1

S66458
ferredoxin - Rhizobium meliloti (fragment)
C:Species: Rhizobium meliloti

C>Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C:Accession: S66458
R:Riedel, K.U.; Jouanneau, Y.; Masepohl, B.; Puehler, A.; Klipp, W.

A:Title: A Rhizobium meliloti ferredoxin (FdXn) purified from Escherichia coli donates

A:Reference number: S66458; MUID:95377307; PMID:7649175

A:Accession: S66458

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-10 <RIE>

C:Genetics:

A:Gene: fdxN

Query Match 35.2%; Score 25; DB 2; Length 10;

Best Local Similarity 50.0%; Pred. No. 2e+02;

Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 AFKIVSQE 13

|||||:

Db 1 AFKIIASQ 8

RESULT 2

A49018
myosin heavy chain, fast skeletal muscle type X - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)

C>Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 13-Aug-1999
C:Accession: A49018; S32161
R:DeNardi, C.; Ausoni, S.; Moretti, P.; Gorza, L.; Velleca, M.; Schiaff

J. Cell Biol. 123, 823-835, 1993

A:Title: Type 2X-myosin heavy chain is coded by a muscle fiber type-specific and develop

A:Reference number: A49018; MUID:94043465; PMID:8227143

A:Accession: A49018

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-14 <DEN>

A:Cross-references: GB:X72591; NID:g288645; PIDN:CAA51189.1; PID:g288646

R:DeNardi, C.; Ausoni, S.; Moretti, P.; Gorza, L.; Velleca, M.; Merlie, J.; Buckingham,

submitted to the EMBL Data Library, March 1993

A:Description: Type 2X myosin heavy chain is coded by a muscle fiber type-specific and

A:Reference number: S32161

A:Accession: S32161

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-14 <DEN2>

A:Cross-references: EMBL:X72591; NID:g288645; PIDN:CAA51189.1; PID:g288646

C:Superfamily: myosin heavy chain; myosin motor domain homology

C:Keywords: skeletal muscle

Query Match 32.4%; Score 23; DB 2; Length 14;
Best Local Similarity 66.7%; Pred. No. 6.7e+02; Indels 0; Gaps 0;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KIVSQE 13
||:|:
Db 9 KIISSE 14
||:|:

RESULT 3
PH0795
T-cell receptor alpha chain (K1 V-alpha-4.3) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PH0795
R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A;Title: T cell receptor genes in a series of class I major histocompatibility complex-I allelic exclusion and antigen-specific repertoire.
A;Reference number: PH0746; MUID:92078846; PMID:1836010
A;Accession: PH0795
A;Molecule type: mRNA
A;Residues: 1-14 <CAS>
A;Cross-references: EMBL:X60900
A;Experimental source: T lymphocyte
C;Keywords: T-cell receptor

Query Match 28.2%; Score 20; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 2.5e+03; Indels 1; Gaps 0;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 NSKIAT 7
||:|:
Db 8 NAKLTF 13
||:|:

RESULT 4
PH0776
T-cell receptor alpha chain (M1 V-alpha-8.F3.3) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PH0776
R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A;Title: T cell receptor genes in a series of class I major histocompatibility complex-I allelic exclusion and antigen-specific repertoire.
A;Reference number: PH0746; MUID:92078846; PMID:1836010
A;Accession: PH0776
A;Molecule type: mRNA
A;Residues: 1-14 <CAS>
A;Cross-references: EMBL:X60873
A;Experimental source: T lymphocyte
C;Keywords: T-cell receptor

Query Match 28.2%; Score 20; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 2.5e+03; Indels 1; Gaps 0;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 NSKIAT 7
||:|:
Db 8 NAKLTF 13
||:|:

RESULT 5
PA0097
starch phosphorylase (EC 2.4.1.1) - fungus (Fusarium sporotrichioides) (fragment)
N;Alternate names: maltodextrin phosphorylase
C;Species: Fusarium sporotrichioides
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C;Accession: PA0097
R;Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JIPID, October 1994

A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichioides
A;Reference number: PA0051
A;Accession: PA0097
A;Molecule type: protein
A;Residues: 1-15 <CHO>
C;Keywords: glycosyltransferase; hexosyltransferase

Query Match 28.2%; Score 20; DB 2; Length 15;
Best Local Similarity 40.0%; Pred. No. 2.7e+03; Indels 5; Gaps 0;
Matches 4; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 3 SKIAPKIVSQ 12
:|:|:
Db 2 NKPFVFTITGQ 11
:|:|:

RESULT 6
F44644
neurotoxin-associated protein type B Hn+ 35K chain, band 3a - Clostridium botulinum (fragment)
C;Species: Clostridium botulinum
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C;Accession: F44644
R;Somers, E.; DasGupta, B.R.
J. Protein Chem. 10, 415-425, 1991
A;Title: Clostridium botulinum types A, B, C1, and E produce proteins with or without heat-labile neurotoxin
A;Reference number: A44644; MUID:92143938; PMID:1781887
A;Contents: type B
A;Accession: F44644
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <SOW>
A;Cross-references: UNIPROT:Q9R5N6
A;Note: sequence extracted from NCBI backbone (NCBIP:83787)
C;Keywords: hemagglutinin

Query Match 26.8%; Score 19; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 2.7e+03; Indels 1; Gaps 0;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LNSKI 5
||:|:
Db 5 LNDKI 9
||:|:

RESULT 7
S71034
potB protein - Salmonella typhimurium (fragment)
C;Species: Salmonella typhimurium
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S71034
R;Stein, M.A.; Leung, K.Y.; Zwick, M.; Garcia-del Portillo, F.; Finlay, B.B.
Mol. Microbiol. 20, 151-164, 1996
A;Title: Identification of a Salmonella virulence gene required for formation of filaments
A;Reference number: S71033; MUID:97014378; PMID:8861213
A;Accession: S71034
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-12 <STG>
A;Cross-references: UNIPROT:Q56060; EMBL:U51867; NID:G1272352; PIDN:AAA97466.1; PID:G1272352
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1996
C;Genetics:
A;Gene: potB

Query Match 26.8%; Score 19; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 3.2e+03; Indels 1; Gaps 0;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LNSKIA 6
||:|:
Db 3 LNKKVS 8
||:|:

RESULT 8

S57571
T cell receptor alpha chain V-J region (clone PP7 and others) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 19-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 05-Nov-1999
C:Accession: S57571; S57573; S57576
R:Burrows, S.R.; Silins, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Argast, V.P.
submitted to the EMBL Data Library, June 1995
A:Description: T cell receptor repertoire for a viral epitope in humans is diversified
A:Reference number: S57494
A:Accession: S57571
A:Molecule type: mRNA
A:Residues: 1-13 <BUR>
A:Cross-references: EMBL:Z49948; NID:G887496; PIDN:CAA90219.1; PID:G887497
A:Experimental source: clone PP7
A:Accession: S57573
A:Molecule type: mRNA
A:Residues: 1-13 <BUL>
A:Cross-references: EMBL:Z49950; NID:G887500; PIDN:CAA90221.1; PID:G887501
A:Experimental source: clone TFI
A:Accession: S57576
A:Molecule type: mRNA
A:Residues: 1-13 <BUW>
A:Cross-references: EMBL:Z49952; NID:G887512; PIDN:CAA90223.1; PID:G887513
A:Experimental source: clone RL16
C:Keywords: T-cell receptor

Query Match 26.8%; Score 19; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 NSKIAP 7
| | |
DB 7 NEKLTF 12

RESULT 9
E42762
proteasome endopeptidase complex (EC 3.4.25.1) subunit 13 - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C>Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 17-Feb-2003
C:Accession: E42762
R:Dieck, L.R.; Moomaw, C.R.; Pramanik, B.C.; DeMartino, G.N.; Slaughter, C.A.
Biochemistry 31, 7347-7355, 1992
A>Title: Identification and localization of a cysteinyl residue critical for the trypsin
A:Reference number: A42762; MUID:92378961; PMID:1510924
A:Accession: E42762
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-13 <DIC>
A>Note: sequence extracted from NCBI backbone (NCBIP:112180)
C:Keywords: hydrolase

Query Match 26.8%; Score 19; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

DB 1 LNSKIAPVQSQ 12
| | | | |
1 MDPEXLPETISQ 12

RESULT 10
G44644
neurotoxin-associated protein type B Hn+ 35K chain, band 3b - Clostridium botulinum (fra
C:Species: Clostridium botulinum
C>Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C:Accession: G44644
R:Somers, E.; DasGupta, B.R.
J. Protein Chem. 10, 415-425, 1991
A>Title: Clostridium botulinum types A, B, C1, and E produce proteins with or without he
A:Reference number: A44644; MUID:92413938; PMID:1781887
A:Contents: type B
A:Accession: G44644

A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-13 <SOM>
A:Cross-references: UNIPROT:O9RSN5
A>Note: sequence extracted from NCBI backbone (NCBIP:83785)
C:Keywords: hemagglutinin

Query Match 26.8%; Score 19; DB 2; Length 13;
Best Local Similarity 80.0%; Pred. No. 3.5e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LNSKI 5
| | |
DB 8 LNDKI 12

RESULT 11
PS0452
32K protein 3306 - rice (strain Nihonbare) (fragment)
C:Species: Oryza sativa (rice)
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 11-Apr-1995
C:Accession: PS0452
R:Tsuigita, A.; Miyatake, N.
submitted to JIPID, April 1993
A:Reference number: PS0208
A:Accession: PS0452
A:Molecule type: protein
A:Residues: 1-15 <TSU>
A:Experimental source: bran, strain Nihonbare
C:Comment: molecular weight 32K, pI 5.3.

Query Match 26.8%; Score 19; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 4.1e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 FKIVSQEP 14
| | | | |
DB 7 FPILLQXP 14

RESULT 12
PT0309
Ig heavy chain CRD3 region (clone 6-94) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0309
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A>Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0309
A:Molecule type: DNA
A:Residues: 1-10 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotrimer; immunoglobulin

Query Match 25.4%; Score 18; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 NSKIAP 7
| | |
DB 5 NSRAAY 10

RESULT 13
A24407
amicyanin - Paracoccus denitrificans (fragment)
C:Species: Paracoccus denitrificans
C>Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 09-Jul-2004
C:Accession: A24407
R:Husain, M.; Davidson, V.L.
Biochemistry 25, 2431-2436, 1986

A;Title: Properties of Paracoccus denitrificans amicyanin.
 A;Reference number: A24407; MUID:86243362; PMID:3718960
 A;Accession: A24407
 A;Molecule type: protein
 A;Residues: 1-10 <HUS>
 A;Cross-references: UNIPROT:P22364

Query Match 25.4%; Score 18; DB 2; Length 10;
 Best Local Similarity 66.7%; Pred. No. 4.1e+03;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 IVSQEP 14
 | | | |
 Db 5 IPSQSP 10

RESULT 14
 E60691
 phycobilisome 8K linker protein - Synechococcus sp. (PCC 7002) (fragment)
 C;Species: Synechococcus sp.
 C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 07-May-1999
 C;Accession: E60691
 R;Bryant, D.A.; de Lorimier, R.; Guglielmi, G.; Stevens Jr., S.E.
 Arch. Microbiol. 153, 550-560, 1990
 A;Title: Structural and compositional analyses of the phycobilisomes of Synechococcus sp.
 A;Reference number: A60691; MUID:90314662; PMID:2164365
 A;Accession: E60691
 A;Molecule type: protein
 A;Residues: 1-11 <BRY>
 C;Comment: This protein, one of the eleven components detected in this species of the ph
 C;Keywords: photosystem II

Query Match 25.4%; Score 18; DB 2; Length 11;
 Best Local Similarity 50.0%; Pred. No. 4.5e+03;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 FKIVSQEP 14
 | | | : |
 Db 4 FKITACVP 11

RESULT 15
 D28551
 hypothetical protein 4 - Streptococcus mutans (strain GS-5) (fragment)
 C;Species: Streptococcus mutans
 C;Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 15-Oct-1999
 C;Accession: D28551
 R;Shiroza, T.; Kuramitsu, H.K.
 J. Bacteriol. 170, 810-816, 1988
 A;Title: Sequence analysis of the Streptococcus mutans fructosyltransferase gene and fla
 A;Reference number: A91892; MUID:88115184; PMID:2828325
 A;Accession: D28551
 A;Molecule type: DNA
 A;Residues: 1-12 <SHI>
 A;Cross-references: GB:M18954; MID:g153635; PIDN:AAA88586.1; PID:g1196927

Query Match 25.4%; Score 18; DB 2; Length 12;
 Best Local Similarity 37.5%; Pred. No. 5e+03;
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 NSKIAPKI 9
 | | | : :
 Db 3 NKKIRIL 10

Search completed: February 22, 2005, 09:46:24
 Job time : 12.1333 secs

Result No.	Score	Query			ID	Description
		Match	Length	DB		
1	26	33.6	15	1	Q6GWV7	Q6gwv7 bos taurus
2	24	36.8	13	1	PROX ORYSA	P83647 oryza sativa
3	23	32.4	13	2	Q957T7	Q957t7 trichopsis
4	23	32.4	14	2	Q06415	Q06415 rattus ratt
5	22	31.0	9	2	Q70YA2	Q70ya2 alvesia rose
6	22	31.0	14	1	UC15 MAIZE	P80621 zea mays (m
7	22	31.0	14	2	Q06414	Q06414 rattus ratt
8	22	31.0	15	1	THBI BOTJA	P84026 bothrops ja
9	21	29.6	15	2	Q91XV8	Q91xv8 rattus norv
10	20	28.2	9	2	Q45533	Q45533 bacillus su
11	20	28.2	10	2	Q9QVK8	mus sp. mep
12	20	28.2	11	2	Q34380	Q34380 drosophila
13	20	28.2	13	2	Q9ZE21	Q9ze21 buchnera ap
14	20	28.2	14	2	Q16118	Q16118 homo sapien
15	20	28.2	14	2	Q6SE52	Q6se52 drosophila
16	20	28.2	14	2	Q93202	Q93202 porcine cir
17	20	28.2	14	2	Q77NR3	Q77nr3 porcine cir
18	20	28.2	14	2	Q77RC0	Q77rc0 porcine cir
19	20	28.2	14	2	Q77RM6	Q77rm6 porcine cir
20	20	28.2	14	2	Q77S02	Q77s02 porcine cir
21	20	28.2	14	2	Q77S09	Q77s09 porcine cir
22	20	28.2	14	2	Q77S13	Q77s13 porcine cir
23	19	26.8	10	1	CX81_CANFA	P61904 canis famli
24	19	26.8	10	2	Q83YL7	Q83yl7 acinetobact
25	19	26.8	10	2	Q9R5N4	Q9r5n4 clostridium
26	19	26.8	10	2	Q9R5N6	Q9r5n6 clostridium
27	19	26.8	11	2	Q9L4P7	Q9l4f7 bacillus ce
28	19	26.8	13	1	BP37_LEUMA	P81754 leucophaea
29	19	26.8	13	2	Q93A39	Q93a39 enterococcu
30	19	26.8	13	2	Q55234	Q55234 synecocyst
31	19	26.8	13	2	Q9R5N5	Q9r5n5 clostridium

```
Query Match          36.6%; Score 26; DB 2; Length 15;
Best Local Similarity 33.3%; Pred. No. 1.2e+03;
Matches 5; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
```

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RESULT 2
PROX ORYSA
ID PROX ORYSA STANDARD; PRRT; 13 AA.
AC P83647;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Probable proflin LP04 (Fragments).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. Indica / IR64; TISSUE=Panicle;
RA Hosseini Salekdeh S.G., Bennett J.;
RT "Proteome analysis of rice panicle.";
RL Submitted (JUL-2003) to Swiss-Prot.
CC -1- FUNCTION: Binds to actin and affects the structure of the
CC cytoskeleton. At high concentrations, proflin prevents the
CC polymerization of actin, whereas it enhances it at low
CC concentrations. By binding to PIP2, it inhibits the formation
CC IP3 and DG (By similarity)
CC

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CC -|- SUBUNIT: Occurs in many kinds of cells as a complex with monomeric
CC actin in a 1:1 ratio.
CC -|- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 4.4, its MW is: 14.0 kDa.
CC -|- SIMILARITY: Belongs to the profilin family.
DR InterPro: IPR002097; Profilin.
DR PROSITE: PS00414; PROFILIN; PARTIAL.
KW Actin-binding; Cytoskeleton; Direct protein sequencing;
KW Multigene family.
FT NON_TER 1 1
FT NON_TER 5 6
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1362 MW; 0A3022E0E52C68B CRC64;

Query Match 33.8%; Score 24; DB 1; Length 13;
Best Local Similarity 30.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 5 IAFKIVSOEP 14
Db 4 LAYWVIOGEP 13

RESULT 3
Q957T7 ID Q957T7 PRELIMINARY; PRT; 13 AA.
AC Q957T7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome b (Fragment).
OS Trichopsis pumila (Pygmy gourami).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
OC Anabantoidae; Belontiidae; Trichopsis.
OX NCBI_TaxID=159454;
RN [1]
RP SEQUENCE FROM N.A.
RA Wang T.Y., Tzeng C.S., Shen S.C.;
RT "Conservation and Phylogeography of Taiwan Paradise Fish, Macropodus
RT opercularis Linnaeus.";
RL Acta Zool. Taiwanica 10:121-134(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Wang T.Y., Tzeng C.S., Shen S.C.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF359378; AAK51458.1; -
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 1 1
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1443 MW; 55430C67982AAB17 CRC64;

Query Match 32.4%; Score 23; DB 2; Length 13;
Best Local Similarity 62.5%; Pred. No. 3.8e+03;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LNSKIAFK 8
Db 6 LEDKILFK 13

RESULT 4
Q06415 ID Q06415 PRELIMINARY; PRT; 14 AA.
AC Q06415;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE 2X myosin heavy chain (Fragment).
OS Rattus rattus (Black rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10117;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Diaphragm;
RX MEDLINE=94043465; PubMed=8227143; DOI=10.1083/jcb.123.4.823;
RA DeNardi C., Ausoni S., Moretti P., Gorza L., Velleca M.,
RA Buckingham M., Schiaffino S.;
RT "type 2X Myosin Heavy Chain is coded by a muscle fiber type-specific
RT and developmentally regulated gene.";
RL J. Cell Biol. 123:823-835(1993).
DR EMBL; X72591; CAA51189.1; -
FT NON_TER 1 1
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1655 MW; F1C0536CD7B6AF1 CRC64;

Query Match 32.4%; Score 23; DB 2; Length 14;
Best Local Similarity 66.7%; Pred. No. 4.1e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 8 KIVSOE 13
Db 9 KIIFEE 14

RESULT 5
Q70YA2 ID Q70YA2 PRELIMINARY; PRT; 9 AA.
AC Q70YA2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Ribosomal protein (Fragment).
GN Name=rp16;
OS Alvania rosmarinifolia.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Alvania.
OX NCBI_TaxID=204103;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15019625; DOI=10.1016/j.ympev.2003.08.002;
RA Paton A., Springate D.A., Sudde S., Otieno D., Grayer R., Harley M.M.,
RA Willis P., Simonds M.S.J., Powell M.P., Savolainen V.;
RT "Phylogeny and evolution of basilis and allies (Ocimeae, Labiatae)
RT based on three plastid DNA regions.";
RL Mol. Phylogenet. Evol. 31:277-299(2004).
DR EMBL; AJ505329; CAD45452.1; -
DR GO; GO:0003735; P:structural constituent of ribosome; IEA.
KW Ribosomal protein.
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 979 MW; 0DF006C5B721F2C0 CRC64;

Query Match 31.0%; Score 22; DB 2; Length 9;
Best Local Similarity 80.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 10 VSOEP 14
Db 5 LSQEP 9

RESULT 6
UC15 MAIZE ID UC15 MAIZE STANDARD; PRT; 14 AA.
AC P80621;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Unknown protein from 2D-PAGE of etiolated coleoptile (Spot 245)
DE (Fragment).
OS Zea mays (Maize).

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OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Fernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -|- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 4.8, its MW is: 35.7 kDa.
DR Maize-2DPAGE; P80621; COLEOPTILE.
DR MaizeDB; 123947; -.
KW Direct protein sequencing.
FT NON_TER 1
FT NON_TER 14
SQ SEQUENCE 14 AA; 1396 MW; C68949275F404CD2 CRC64;

Query Match 31.0%; Score 22; DB 1; Length 14;
Best Local Similarity 42.9%; Pred. No. 6.4e+03;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 9 IVSQEPA 15
DB 8 VAAEPEA 14
: : : : :

RESULT 7
Q06414 PRELIMINARY; PRT; 14 AA.
AC Q06414; Q06918;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE 2B myosin heavy chain (2A myosin heavy chain) (Fragment).
OS Rattus rattus (Black rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10117;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=diaphragm;
RX MEDLINE=94043465; PubMed=8227143; DOI=10.1083/jcb.123.4.823;
RA Denardi C., Ausoni S., Moretti P., Gorza L., Velleca M.,
RA Buckingham M., Schiaffino S.;
RT "Type 2X Myosin Heavy Chain is coded by a muscle fiber type-specific
RT and developmentally regulated gene.";
RL J. Cell Biol. 123:823-835(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=diaphragm;
RA Schiaffino S.;
RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; X72590; CAA51188.1; -.
DR EMBL; X72589; CAA51187.1; -.
FT NON_TER 1
FT NON_TER 14
SQ SEQUENCE 14 AA; 1641 MW; F1C0536CC526AF1 CRC64;

Query Match 31.0%; Score 22; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 8 KIVSQE 13
DB 9 KVISSE 14
: : : : :

RESULT 8
THBI_BOTJA STANDARD; PRT; 15 AA.
ID THBI_BOTJA

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AC P84026;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Thrombin inhibitor subunit I (Fragment).
OS Bothrops jararaca (Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodactylia; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8724;
RN [1]
RP SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, SUBUNIT,
RP AND GLYCOSYLATION.
RC TISSUE=Plasma;
RX PubMed=12927776; DOI=10.1016/S0006-291X(03)01464-5;
RA Tanaka-Azevedo A.M., Tanaka A.S., Sano-Martins I.S.;
RT "A new blood coagulation inhibitor from the snake Bothrops jararaca
RT plasma: isolation and characterization.";
RL Biochem. Biophys. Res. Commun. 308:706-712(2003).
CC -|- FUNCTION: Binds to thrombin and inhibits blood coagulant activity.
CC Does not inhibit the serine protease activity of thrombin or
CC platelet aggregation activity. May bind to the heparin recognition
CC exosite.
CC -|- SUBUNIT: Heteropolymer of subunit I and subunit II.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Plasma.
CC -|- PTM: Glycosylated.
KW Blood coagulation; Direct protein sequencing; Glycoprotein.
FT NON_TER 1
FT NON_TER 15
SQ SEQUENCE 15 AA; 1651 MW; CE8E339D80419137 CRC64;

Query Match 31.0%; Score 22; DB 1; Length 15;
Best Local Similarity 50.0%; Pred. No. 6.9e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 7 PKIVSQEP 14
DB 3 PPAVNQKP 10
: : : : :

RESULT 9
Q91XV8 PRELIMINARY; PRT; 15 AA.
AC Q91XV8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE 20alpha-hydroxysteroid dehydrogenase (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Nakajima T., Yasuda K., Okada H., Sanezumi M., Osaki T., Kanzaki H.,
RA Nishizawa M., Ito S.;
RT "Expression of 20alpha-HSD (hydroxysteroid dehydrogenase) in
RT endometrium.";
RL J. Fertilization and Implantation 17:186-187(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Nishizawa M., Nakajima T., Ito S.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB028066; BAB62013.1; -.
FT NON_TER 15
FT NON_TER 15
SQ SEQUENCE 15 AA; 1732 MW; B452E70F45C4822F CRC64;

Query Match 29.6%; Score 21; DB 2; Length 15;
Best Local Similarity 80.0%; Pred. No. 1.1e+04;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 LNSKI 5
   :||||
Db 1 MNSKI 5

RESULT 10
Q45533 PRELIMINARY; PRT; 9 AA.
AC Q45533;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE Hypothetical protein (Fragment).
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=W168;
RX MEDLINE=92041654; PubMed=1938941;
RA Fuhrer D.K., Ordal G.W.;
RT "Bacillus subtilis Chen, a homolog of CheA, the central regulator of
RT chemotaxis in Escherichia coli.";
RL J. Bacteriol. 173:7443-7448(1991).
DR EMBL; M57894; AAA22312.1; -.
KW Hypothetical protein.
FT NON TER
SQ SEQUENCE 9 AA; 966 MW; 8780C6C5A7618F6C5 CRC64;

Query Match 28.2%; Score 20; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 VSQEP 15
   :|||
Db 1 ISQHP 6

RESULT 11
Q9QVK8 PRELIMINARY; PRT; 10 AA.
AC Q9QVK8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE MEPRIN-METALLOENDOPEPTIDASE (Fragment).
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE.
RX MEDLINE=91363409; PubMed=1888759; DOI=10.1016/0167-4838(91)90032-U;
RA Flannery A.V., Macadam G.C., Beynon R.J.;
RT "Immunological characterisation of different meprin species in mice.";
RL Biochim. Biophys. Acta 1079:119-122(1991).
FT NON TER
FT NON TER
SQ SEQUENCE 10 AA; 1163 MW; DD6436144731B2C9 CRC64;

Query Match 28.2%; Score 20; DB 2; Length 10;
Best Local Similarity 44.4%; Pred. No. 1.1e+04;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 5 IAFKIVSQE 13
   :|||
Db 1 IAFVTLNEE 9

RESULT 12
Q34380 PRELIMINARY; PRT; 11 AA.
AC Q34380;

QY 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE NADH dehydrogenase subunit 1 (Fragment).
GN Name=mt:ND1; Synonyms=ND1;
OS Drosophila subobscura (Fruit fly).
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Sphyroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7241;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95106285; PubMed=7528808;
RA Barrio E., Latorre A., Moya A.;
RT "Phylogeny of the Drosophila obscura species group deduced from
RT mitochondrial DNA sequences.";
RL J. Mol. Evol. 39:478-488(1994).
DR EMBL; U07287; AAA76625.1; -.
FLYBase; FBgn0012956; Deub(mt:ND1.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER
SQ SEQUENCE 11 AA; 1264 MW; 46AEP494C7272053 CRC64;

Query Match 28.2%; Score 20; DB 2; Length 11;
Best Local Similarity 66.7%; Pred. No. 1.2e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 IAPKIV 10
   :|||
Db 1 IGFKIL 6

RESULT 13
Q9ZEZ1 PRELIMINARY; PRT; 13 AA.
AC Q9ZEZ1;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE 2-isopropylmalate synthase (EC 4.1.3.12) (Fragment).
GN Name=leuA;
OS Buchnera aphidicola.
OC Plasmid pBP1.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
OX NCBI_TaxID=9;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99028904; PubMed=9812361;
RA Silva F.J., Van Ham R.C.H.J., Sabater B., Latorre A.;
RT "Structure and evolution of the leucine plasmids carried by the
RT endosymbiont (Buchnera aphidicola) from aphids of the family
RT Aphididae.";
RL FEWS Microbiol. Lett. 168:43-49(1998).
DR EMBL; AJ006877; CAA07302.1; -.
DR GO; GO:0016829; F:lyase activity; IEA.
KW Lyase; Plasmid.
FT NON TER
FT NON TER
SQ SEQUENCE 13 AA; 1538 MW; 1BD1D0320390C050 CRC64;

Query Match 28.2%; Score 20; DB 2; Length 13;
Best Local Similarity 60.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNSKI 5
   :|||
Db 1 MNSKV 5

RESULT 14
Q16118

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ID Q16118 PRELIMINARY; PRT; 14 AA.
AC Q16118;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Cyclic adenosine 3',5'-monophosphate response element binding protein
DE (Fragment).
DE
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94158910; PubMed=8114764;
RA Waeber G., Meyer T.E., LeSieur M., Hermann H.L., Gerard N.,
RT Habener J.H.;
RT "Developmental stage-specific expression of cyclic adenosine 3',5'-
RT monophosphate response element binding protein CREB during
RT spermatogenesis involves alternative exon splicing.";
RL Mol. Endocrinol. 7:1501-1501(1993).
DR EMBL; S68577; AAB2985.2; -;
FT NON TER 1
SQ SEQUENCE 14 AA; 1698 MW; C42ECDBE36B7CEB6 CRC64;

Query Match 28.2%; Score 20; DB 2; Length 14;
Best Local Similarity 66.7%; Pred. NO. 1.6e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 KIVSOR 13
DB 3 KIVKQD 8

RESULT 15

Q6SE52 PRELIMINARY; PRT; 14 AA.
AC Q6SE52;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Pgi (Fragment).
OS Drosophila simulans (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7240;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14762063; DOI=10.1101/gr.1329204;
RA Hailigan D.L., Eyre-Walker A., Andolfatto P., Keightley P.D.;
RT "Patterns of evolutionary constraints in intronic and intergenic DNA
RT of Drosophila."
RL Genome Res. 14:273-279(2004).
DR EMBL; AY459549; AAR23007.1; -;
FT NON TER 14
SQ SEQUENCE 14 AA; 1456 MW; 2C83E49CCD8E7E37 CRC64;

Query Match 28.2%; Score 20; DB 2; Length 14;
Best Local Similarity 57.1%; Pred. NO. 1.6e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LNSKIAP 7
DB 8 LNQERAP 14

Search completed: February 22, 2005, 09:37:49
Job time : 53.6667 secs

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OM protein - protein search, using sw model

Run on: February 22, 2005, 08:52:23 ; Search time 65.6667 Seconds
(without alignments)
88.346 Million cell updates/sec

Title: US-08-991-628-3

Perfect score: 71
Sequence: 1 LNSKIAPKIVSQEPA 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 385760381 residues

Total number of hits satisfying chosen parameters: 632537

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	71	100.0	15	2 AAW04843	AAW04843 Self epit
2	71	100.0	15	2 AAW64815	Aaw64815 Desmoglei
3	71	100.0	15	2 AAW78814	Aaw78814 Desmoglei
4	71	100.0	15	3 AAB33625	MHC class
5	71	100.0	15	4 AAG93721	Human des
6	71	100.0	15	5 AAO17033	Desmoglei
7	71	100.0	15	6 ABU96577	MHC class
8	71	100.0	15	8 ADQ14318	Human des
9	71	100.0	15	8 AD41700	Desmoglei
10	71	100.0	15	8 ADS14310	Desmoglei
11	31	43.7	15	5 ABB04739	Human hep
12	31	43.7	15	8 ADJ34233	Human sec
13	30	42.3	15	8 ADL26206	Synthetic
14	30	42.3	15	8 ADL26187	Synthetic
15	29	40.8	15	2 AAW85386	Helper T-
16	29	40.8	15	2 AAW85174	Helper T-
17	29	40.8	15	3 AAB13871	L2/HNK1 c
18	29	40.8	15	3 ADL26192	Synthetic
19	28	39.4	10	5 AAE24272	Murine B-
20	27	38.0	10	4 AAB73139	Tumour an
21	27	38.0	10	8 ADQ35117	Novel pep
22	27	38.0	10	8 ADQ35116	Novel pep
23	27	38.0	11	8 ADQ35123	Novel pep
24	27	38.0	15	5 ABP55461	Human zin
25	27	38.0	15	8 ADL26185	Synthetic

ALIGNMENTS

RESULT 1

AAW04843
ID AAW04843 standard; peptide; 15 AA.

AC AAW04843;

XX 18-FEB-1997 (first entry)

DE Self epitope of desmoglein 3, implicated in autoimmune disease.

KW Tolerisation; self-epitope; antigen; autoimmune disease; autoantigen;
KW HLA; human leukocyte antigen; T-cell; thymocyte; pemphigus vulgaris;
KW desmoglein; multiple sclerosis; herpes simplex virus; adenovirus;
KW phosphomannomutase; human papillomavirus; Epstein-Barr virus;
KW DNA polymerase; influenza; haemagglutinin; reovirus; sigma protein.

XX Homo sapiens.

XX WO9627387-A1.

XX 12-SEP-1996.

XX 07-MAR-1996; 96WO-US003182.

XX 07-MAR-1995; 95US-00400796.

XX (HARD) HARVARD COLLEGE.

XX Strominger JL, Wucherpfennig KW;

XX WPI; 1996-425218/42.

XX Pemphigus vulgaris auto-antigens and multiple sclerosis non-self antigens
- useful in disease treatment, and method for identification of other
self and non-self antigens implicated in auto-immune disease.

XX Claim 1; Page 39; 58pp; English.

XX Pharmaceutical preparations for tolerisation to antigens comprise either
an isolated human non-collagen or non-mysin basic protein (MBP)
polypeptide which is capable of tolerising an individual to an
autoantigen; or an isolated human pathogen polypeptide capable of
tolerising an individual to that polypeptide. In both cases, the
polypeptide (whether self or non-self) includes an amino acid sequence
corresponding to a sequence motif for a MHC class II protein, such as HLA
-DR, which is associated with a human autoimmune disease and which binds
to the polypeptide to activate autoreactive T-cells in individuals with
the autoimmune disease. This peptide is derived from the human desmoglein

CC 3 protein (amino acids 190-204) and is implicated as a self epitope in
CC pemphigus vulgaris. Peptides derived from the human desmoglein protein
CC are described in AA04841-47
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 71; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNSKIAFKIVSQEPA 15
|||||
Db 1 LNSKIAFKIVSQEPA 15

RESULT 2
AAW64815
ID AAW64815 standard; peptide; 15 AA.
XX
AC AAW64815;
XX
DT 29-SEP-1998 (first entry)
XX
DE Desmoglein-3 190-204.
XX
KW Desmoglein; DG; gene therapy; pemphigus vulgaris; microparticle;
KW autoantigen; autoimmune disease; MHC.
XX
OS Homo sapiens.
XX
PN US5783567-A.
XX
PD 21-JUL-1998.
XX
PF 22-JAN-1997; 97US-00787547.
XX
PR 22-JAN-1997; 97US-00787547.
XX
PA (PANG-) PANGAEA PHARM INC.
XX
PI Langer RS, Hedley ML, Curley JM;
XX
PS WPI; 1998-427077/36.
XX
DR
XX
PT Microparticle encapsulated nucleic acids - for recombinant expression of
PT proteins e.g. in gene therapy.
XX
PS Disclosure; Col 4; 42pp; English.
XX
CC The patent describes a new preparation of microparticles each comprising
CC a polymeric matrix and a nucleic acid. The polymeric matrix consists of
CC one or more synthetic polymers having a solubility in water of less than
CC 1 mg/l (e.g. poly-lactic-co-glycolic acid); and at least 90% of the
CC microparticles have a diameter of less than 100 microns. The
CC microparticles are useful for the delivery of nucleic acids to phagocytic
CC cells. In one embodiment the microparticles are less than 20 microns in
CC diameter and the nucleic acid (preferably in closed circular form)
CC includes an expression control sequence operatively linked to a coding
CC sequence, where the expression product of the coding sequence is a
CC polypeptide having a length and a sequence which permits it to bind to an
CC MHC class I or II molecule. The expression product is thus an effective
CC stimulator of an immune response in mammals. The present sequence, an
CC antigenic portion of desmoglein 3, is an example of an MHC class II
CC peptide which can be expressed by the nucleic acid. It is associated with
CC pemphigus vulgaris
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 71; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNSKIAFKIVSQEPA 15
|||||
Db 1 LNSKIAFKIVSQEPA 15

Db 1 LNSKIAFKIVSQEPA 15
|||||

RESULT 3
AAW78814
ID AAW78814 standard; peptide; 15 AA.
XX
AC AAW78814;
XX
DT 17-NOV-1998 (first entry)
XX
DE Desmoglein 3 protein fragment 190-204.
XX
KW Microparticle; delivery; polymeric matrix; autoantigen; tumour antigen;
KW class II associated peptide; pathogen; gene therapy; genetic disease;
KW infection; downregulation; immune response.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO9831398-A1.
XX
PD 23-JUL-1998.
XX
PF 22-JAN-1998; 98WO-US001499.
XX
PR 22-JAN-1997; 97US-00787547.
PR 06-JAN-1998; 98US-00003253.
XX
PA (PANG-) PANGAEA PHARM INC.
XX
PI Hedley ML, Curley JM, Langer RS, Lunsford LB;
XX
DR WPI; 1998-427556/36.
XX
PT New preparations of microparticles - comprising a synthetic polymer
PT matrix and nucleic acid comprising an expression vector for use in gene
PT therapy.
XX
PS Disclosure; Page 8; 101pp; English.
XX
CC A microparticle preparation (MP) has been developed, consisting of
CC microparticles having a diameter of less than 100 mu m. The MP comprises:
CC (a) a polymeric matrix (PM) consisting of one or more synthetic polymers
CC having a solubility in water of less than 1 mg/l; and (b) an expression
CC vector selected from RNA molecules (at least 50% of which are closed
CC circles) or circular plasmid DNA (at least 50% of which are supercoiled).
CC Also described is a MP of at most 20 microns in diameter, comprising: (a)
CC a PM; and (b) a NAM comprising an expression control sequence operatively
CC linked to a coding sequence, where the coding sequence encodes an
CC expression product selected from: (i) a polypeptide at least 7 amino
CC acids in length, having a sequence identical to the sequence of: (i) a
CC fragment of a naturally-occurring mammalian protein; or (ii) a fragment
CC of a naturally-occurring protein from an infectious agent which infects a
CC mammal; (2) a peptide having a length and sequence which permits it to
CC bind to an MHC class I or II molecule; and (3) the polypeptide or the
CC peptide linked to a trafficking sequence. AAW69763 to AAW69765, and
CC AAW78793 to AAW78897 are peptide fragments for use in the present
CC invention. The MPs are highly effective vehicles for the delivery of
CC polynucleotides into phagocytic cells. They can be used for gene therapy,
CC e.g. for treating genetic diseases, infections or tumours or for
CC downregulating an immune response
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 71; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNSKIAFKIVSQEPA 15
|||||
Db 1 LNSKIAFKIVSQEPA 15


```
RESULT 4
AAB33625
ID AAB33625 standard; peptide; 15 AA.
XX
AC AAB33625;
XX
DT 26-JAN-2001 (first entry)
XX
DE MHC class II associated immunogenic peptide SEQ ID 24.
XX
KW Microparticle; nucleic acid delivery; immunogenic peptide; MHC I; MHC II;
KW major histocompatibility complex; vaginal tissue; mucosal tissue.
XX
OS Unidentified.
XX
PN WO200053161-A2.
XX
PD 14-SEP-2000.
XX
PF 10-MAR-2000; 2000WO-US006578.
XX
PR 11-MAR-1999; 99US-00266463.
PR 27-MAY-1999; 99US-00321346.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Lunsford LB, Putnam D, Hedley ML;
XX
DR WPI; 2000-638130/61.
XX
PT Microparticles useful for administering a nucleic acid into the mucosal
PT tissue preferably vaginal tissue of an animal, comprises a polymeric
PT matrix, a lipid and a nucleic acid molecule.
XX
PS Claim 25; Page 11; 96pp; English.
XX
CC The present invention relates to microparticles which are less than 20
CC microns in diameter, which comprise a polymeric matrix, a lipid and a
CC nucleic acid molecule. The microparticle is specifically not encapsulated
CC in a liposome and does not comprise a cell. The nucleotide sequence
CC encodes an expression product that binds to major histocompatibility
CC complex (MHC) type I or II molecules. Peptides AAB33602-B33647 represent
CC MHC class II associated immunogenic peptides, and AAB33648-B33710
CC represent MHC class I associated immunogenic peptides. The peptides are
CC examples of the expression products of the nucleotide sequences which can
CC be included in the microparticles of the invention. Sequences AAB33711-
CC B33716 represent alternative expression products and nuclear localisation
CC signals also used in the invention. The microparticles are useful for
CC administering a nucleic acid into the mucosal tissue preferably vaginal
CC tissue of an animal
XX
SQ Sequence 15 AA;
Query Match 100.0%; Score 71; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LNSKIAFKIVSQEPA 15
DB 1 LNSKIAFKIVSQEPA 15
RESULT 5
AAG93721
ID AAG93721 standard; peptide; 15 AA.
XX
AC AAG93721;
XX
DT 17-SEP-2001 (first entry)
XX
DE Human desmoglein 3 peptide 1.
```

```
XX Continuous flow production; microparticle; gene therapy;
KW antisense therapy; vaccination; treatment; autoimmune disease;
KW immune response modulation.
XX
OS Homo sapiens.
XX
PN WO200136583-A1.
XX
PD 25-MAY-2001.
XX
PF 17-NOV-2000; 2000WO-US031770.
XX
PR 19-NOV-1999; 99US-00443654.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Hedley ML, Hsu Y, Tyo M;
XX
DR WPI; 2001-425203/45.
XX
CC Continuous production of microparticles containing nucleic acid for e.g.
CC gene therapy, comprises mixing a solution of polymeric material and
CC nucleic acid with a surfactant solution, removing solvent and drying.
XX
PS Disclosure; Page 9; 47pp; English.
XX
CC The present sequence is that of a peptide of the invention. The invention
CC relates to a method for scalable, continuous flow production of a nucleic
CC acid containing microparticle that maintains the structural integrity of
CC the associated nucleic acid and results in a microparticle having purity
CC suitable for introduction into an animal host. Microparticles prepared
CC according to the method can be used for delivery of a nucleic acid for
CC gene therapy, antisense therapy, vaccination, treatment of autoimmune
CC disease and either specific or non-specific modulation of an immune
CC response. The microparticles may also be used to deliver nucleic acid
CC encoding a protein or peptide useful in any kind of therapy. The method
CC is economical, aseptic and scalable. The method also enables control over
CC the size of microparticles. The microparticles produced are free of
CC impurities such as organic solvents and are readily dispersed in a wide
CC range of dispersing agents
XX
SQ Sequence 15 AA;
Query Match 100.0%; Score 71; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LNSKIAFKIVSQEPA 15
DB 1 LNSKIAFKIVSQEPA 15
RESULT 6
AAO17033
ID AAO17033 standard; peptide; 15 AA.
XX
AC AAO17033;
XX
DT 29-MAY-2002 (first entry)
XX
DE Desmoglein 3 residues 190-204 SEQ ID NO: 30.
XX
KW Alpha-MSH; inflammation; autoimmune disease; gene therapy; sepsis;
KW alpha-melanocyte stimulating hormone; rheumatoid arthritis; asthma;
KW cirrhosis; dermatitis; psoriasis; inflammatory bowel disease;
KW immunosuppressive; antiinflammatory; antirheumatic; antiarthritic;
KW antiasthmatic; antibacterial; dermatological; antipsoriatic;
KW antidiabetic; ophthalmological; neuroprotective; multiple sclerosis;
KW diabetes; uveitis; coeliac disease.
XX
OS Unidentified.
```

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PN WO200206316-A2.
XX
PD 24-JAN-2002.
XX
XX
PF 16-JUL-2001; 2001WO-US022263.
XX
XX 14-JUL-2000; 2000US-0218381P.
XX 18-AUG-2000; 2000US-0226382P.
PR 06-OCT-2000; 2000US-0238380P.
PR 29-DEC-2000; 2000US-0258764P.
PR 14-JUN-2001; 2001US-0298317P.
XX
XX (ZYCO-) ZYCOS INC.
XX
XX Hedley ML, Urban R, Aziz N, Chen H, Etemad-Moghadam B, Yin P;
XX WPI; 2002-195801/25.
XX
XX Novel nucleic acid encoding fusion protein comprising alpha-melanocyte
XX stimulating hormone concatamer or its analog, for treating inflammatory
XX or autoimmune disorders.
XX
XX Disclosure; Page 26; 89pp; English.
XX
XX The present invention relates to a nucleic acid comprising a sequence
XX encoding a fusion polypeptide having an alpha-melanocyte stimulating
XX hormone (MSH) concatamer. The sequences are useful for treating an
XX individual suffering from, or at risk of, a disorder of the immune system
XX e.g. inflammatory disorder or autoimmune disorder, including rheumatoid
XX arthritis, asthma, sepsis, cirrhosis, dermatitis, psoriasis, contact
XX hypersensitivity, inflammatory bowel disease, autoimmune encephalitis,
XX multiple sclerosis, diabetes, lupus, uveitis and coeliac disease. The
XX present sequence is a peptide described in the exemplification of the
XX invention
XX
XX Sequence 15 AA;
SQ
    Query Match      100.0%; Score 71; DB 5; Length 15;
    Best Local Similarity 100.0%; Pred. No. 2.3e-06;
    Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNSKIAPKIVSQEPA 15
   |||||
DB 1 LNSKIAPKIVSQEPA 15
   |||||

RESULT 7
ABU96577
ID ABU96577 standard; peptide; 15 AA.
XX
XX AC ABU96577;
XX
XX DT 12-AUG-2003 (first entry)
XX
XX DE MHC class II associated desmoglein 3 peptide 190-204.
XX
XX KW Microparticle; microsphere; polynucleotide delivery; phagocytic cell;
XX tumour; viral infection; bacterial infection; fungal infection;
XX protozoan infection; gene therapy; major histocompatibility complex;
XX MHC class II.
XX
XX OS Unidentified.
XX
XX FN US2002182258-A1.
XX
XX PD 05-DEC-2002.
XX
XX PF 18-JUL-2001; 2001US-00909460.
XX
XX 22-JAN-1997; 97US-0035983P.
PR 06-JAN-1998; 98US-00003253.
PR 22-JAN-1998; 98WO-US001499.
PR 11-MAR-1999; 99US-00266463.

PR 27-MAY-1999; 99US-00321346.
XX
XX (ZYCO-) ZYCOS INC.
XX
XX Lunsford LB, Putnam D, Hedley ML;
XX
XX WPI; 2003-438782/41.
XX
XX Microparticles, useful as vehicles for delivery of polynucleotides to
XX phagocytic cells, comprises polymeric matrix, lipid, and nucleic acid
XX molecule.
XX
XX Disclosure; Page 3; 37pp; English.
XX
XX The invention relates to a microparticle (microsphere) less than 20
XX microns in diameter that comprises: (1) a polymeric matrix; (2) a lipid;
XX and (3) a nucleic acid molecule. The microparticle is not encapsulated in
XX a liposome and the microparticle does not comprise a cell. The
XX microparticles are used as vehicles for the delivery of polynucleotides
XX into phagocytic cells. The microparticles can be used to express antigens
XX to treat tumour cells or viral, bacterial, fungal or protozoan
XX infections. The microparticles can be made without adversely affecting
XX nucleic acid integrity. The present sequence represents the amino acid
XX sequence of a major histocompatibility complex, MHC, class II associated
XX peptide
XX
XX Sequence 15 AA;
SQ
    Query Match      100.0%; Score 71; DB 6; Length 15;
    Best Local Similarity 100.0%; Pred. No. 2.3e-06;
    Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LNSKIAPKIVSQEPA 15
   |||||
DB 1 LNSKIAPKIVSQEPA 15
   |||||

RESULT 8
ADQ14318
ID ADQ14318 standard; peptide; 15 AA.
XX
XX AC ADQ14318;
XX
XX DT 07-OCT-2004 (first entry)
XX
XX DE Human desmoglein 3 (DSG3) antigenic determinant (residues 190-204).
XX
XX KW Notch signalling; modulator; antigen; antigenic determinant;
XX immunomodulator; immune disorder; immune response; immune tolerance;
XX peripheral T-cell activation; regulatory T-cell; T reg; tumour; cancer;
XX autoimmune disorder; allergy; transplant rejection; immunosuppressive;
XX cytostatic; antiallergic; vaccine; human; autoantigen; desmoglein 3;
XX DSG3; pemphigus; MHC class II peptide; major histocompatibility complex;
XX antigenic determinant; epitope.
XX
XX OS Homo sapiens.
XX
XX FN WO2004060262-A2.
XX
XX PD 22-JUL-2004.
XX
XX PF 07-JAN-2004; 2004WO-GB0000046.
XX
XX 07-JAN-2003; 2003GB-00000234.
PR 23-JAN-2003; 2003GB-00001510.
PR 23-JAN-2003; 2003GB-00001512.
PR 23-JAN-2003; 2003GB-00001513.
PR 23-JAN-2003; 2003GB-00001515.
PR 23-JAN-2003; 2003GB-00001518.
PR 23-JAN-2003; 2003GB-00001519.
PR 23-JAN-2003; 2003GB-00001521.
PR 23-JAN-2003; 2003GB-00001522.
PR 23-JAN-2003; 2003GB-00001524.

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PR 23-JAN-2003; 2003GB-00001526.
 PR 23-JAN-2003; 2003GB-00001527.
 PR 23-JAN-2003; 2003GB-00001529.
 PR 22-MAR-2003; 2003GB-00006621.
 PR 04-APR-2003; 2003WO-GB001525.
 PR 24-MAY-2003; 2003GB-00012062.
 PR 01-AUG-2003; 2003WO-GB003285.
 PR 03-OCT-2003; 2003GB-00023130.
 XX
 PA (LORA-) LORANTIS LTD.
 XX
 XX Bodmer MW, Briend ECP, Champion BR, Lennard AC, McKenzie GJ;
 PI Tugal T, Ward GA, Young LL;
 PI
 XX WPI; 2004-534298/51.
 XX
 XX New product for modulating the immune system, comprises a pharmaceutical
 PT support matrix bearing modulators of Notch signaling, and an antigen or
 PT antigenic determinant, or a polynucleotide coding for the antigen or
 PT determinant.
 PT
 XX Disclosure; Page 126; 294pp; English.
 XX
 XX The invention relates to a product comprising (1) a pharmaceutical
 CC support matrix for in vivo administration bearing modulators of Notch
 CC signalling (especially a Delta or Serrate/Jagged protein or fragment or
 CC homologue thereof); and (2) an antigen or antigenic determinant, or
 CC polynucleotide encoding an antigen or antigenic determinant. The product
 CC acts as a combined preparation for modulation of the immune system or for
 CC modulation of an immune response to the antigen or antigenic determinant.
 CC The invention also relates to a pharmaceutical composition comprising the
 CC product; a particle with a maximum linear dimension of less than 500
 CC (preferably 30-70) nm having several bound modulators of Notch signalling
 CC; a method of modulating Notch signalling; methods of treating an immune
 CC disorder, for reducing an immune response, for promoting immune tolerance
 CC in a mammal, and a method for increasing an immune response to a tumour
 CC or pathogen antigen or its antigenic determinant in a mammal. The
 CC composition and methods are useful for modulating peripheral T-cell
 CC activation, for generating regulatory T-cells (T reg's), for reducing an
 CC immune response to an antigen or antigenic determinant, for promoting
 CC immune tolerance to an antigen or antigenic determinant, or for treating
 CC tumours, autoimmune diseases, allergies or transplant rejection. The
 CC present sequence represents an antigenic determinant derived from a human
 CC autoantigen which may be used in a product of the invention.
 XX
 XX Sequence 15 AA;
 SQ
 Query Match 100.0%; Score 71; DB 8; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.3e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 LNSKIAPKIVSORPA 15
 Db 1 LNSKIAPKIVSORPA 15
 |||||
 RESULT 9
 ADR41700
 ID ADR41700 standard; peptide; 15 AA.
 XX
 AC ADR41700;
 XX
 XX 21-OCT-2004 (first entry)
 DT
 XX Desmoglein 3 (DSG3) (aa 190-204), class II MHC associated autoantigen.
 DE
 XX DSG3; Desmoglein 3; autoantigen; notch signalling pathway;
 KW autoimmune disorder; bystander effect; suppression; DSL domain;
 KW EGF domain; Goodpasture's disease; Wegener's granulomatosis; anaemia;
 KW thrombocytopenia; gastritis; hepatitis; vasculitis; scleroderma;
 KW myositis; arthritis; Systemic lupus erythematosus; SLE; cirrhosis;
 KW Sjogren's syndrome; hepatic fibrosis; liver cirrhosis; thyroiditis;
 KW dermatitis; placental dysfunction; eclampsia;

KW inflammatory related gynaecological disease; neurodegenerative disorder;
 KW Alzheimer's disease; Parkinson's disease; Huntington disease;
 KW encephalitis; psychiatric disorder; Down's syndrome; stroke; exogenous;
 KW bystander antigen; multiple sclerosis; delta serrate lag;
 XX inflammatory bowel disease; notch receptor.
 OS Homo sapiens.
 OS Synthetic.
 XX WO2004064863-A1.
 PN
 XX 05-AUG-2004.
 PD
 XX 23-JAN-2004; 2004WO-GB000263.
 PF
 XX 23-JAN-2003; 2003GB-00001510.
 PR 23-JAN-2003; 2003GB-00001512.
 PR 23-JAN-2003; 2003GB-00001513.
 PR 23-JAN-2003; 2003GB-00001515.
 PR 23-JAN-2003; 2003GB-00001518.
 PR 23-JAN-2003; 2003GB-00001519.
 PR 23-JAN-2003; 2003GB-00001521.
 PR 23-JAN-2003; 2003GB-00001522.
 PR 23-JAN-2003; 2003GB-00001524.
 PR 23-JAN-2003; 2003GB-00001526.
 PR 23-JAN-2003; 2003GB-00001527.
 PR 23-JAN-2003; 2003GB-00001529.
 PR 04-APR-2003; 2003WO-GB001525.
 PR 24-MAY-2003; 2003GB-00012062.
 PR 01-AUG-2003; 2003WO-GB003285.
 PR 03-OCT-2003; 2003GB-00023130.
 PR 07-JAN-2004; 2004WO-GB000046.
 XX (LORA-) LORANTIS LTD.
 PA
 XX Champion BR, Ragno S, Young LL;
 PI WPI; 2004-562091/54.
 XX
 XX New product having a modulator of the Notch signaling pathway, useful for
 PT modulating an immune response in autoimmune disorders, such as anemia,
 PT gastritis, hepatitis, scleroderma and myositis.
 XX
 XX Disclosure; Page 66; 244pp; English.
 PS
 XX The invention relates to the modulation of immune function through a
 CC notch signalling pathway for the prevention of autoimmune diseases. It
 CC has been found that the notch signalling pathway provides a bystander
 CC effect or bystander suppression effect, which can be used in a wide
 CC variety of ways to suppress unwanted immune responses in immune diseases
 CC and disorders. Autoimmune diseases are characterised by immune responses
 CC that are directed against self antigens. T lymphocytes are activated upon
 CC recognition of a self antigen and/or a foreign antigen as a complex with
 CC self major histocompatibility complex (MHC) gene products on the surface
 CC of antigen presenting cells (APC). The invention provides the method of
 CC modulating of an immune response, modulator information and a
 CC pharmaceutical kit for suppression of an immune response. The modulator
 CC of the notch signalling pathway is an agent which activates the notch
 CC receptor or a polynucleotide which codes for such an agent. It comprises
 CC a protein or polypeptide comprising a notch ligand DSL (delta serrate
 CC lag) domain, notch ligand EGF domain, optionally all or part of a notch
 CC ligand N terminal domain, and optionally one or more heterologous amino
 CC acid or a polynucleotide sequences. The modulator can be a fusion protein
 CC comprising a segment of a notch ligand extracellular domain and an
 CC immunoglobulin Fc segment. The disorders include Goodpasture's disease,
 CC Wegener's granulomatosis, autoimmune anaemia, thrombocytopenia,
 CC gastritis, autoimmune hepatitis, inflammatory bowel disease, autoimmune
 CC vasculitis, scleroderma, myositis, autoimmune arthritis, Systemic Lupus
 CC Erythematosus (SLE) or Sjogren's syndrome, hepatic fibrosis, liver
 CC cirrhosis, thyroiditis, dermatitis, placental dysfunction, eclampsia,
 CC cirrhosis related gynaecological diseases, neurodegenerative disorders
 CC (such as Alzheimer's disease, Parkinson's disease, Huntington disease)
 CC encephalitis, psychiatric disorders, Down's syndrome, stroke, multiple

CC sclerosis, etc. The invention discloses a method for generating immune
 CC suppression at a disease locus by administering an exogenous antigen. It
 CC also provides the use of modulator or activator of notch signalling in
 CC simultaneous, separate or sequential combination with a bystander antigen
 CC or antigenic determinant for reducing an immune response to a target
 CC antigen. The presented protein sequence is the desmoglein 3 (DSG3) (aa
 CC 190-204), class II MHC associated autoantigen.

XX Sequence 15 AA;

Query Match 100.0%; Score 71; DB 8; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.3e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNSKIAPKIVSQEPA 15

Db 1 LNSKIAPKIVSQEPA 15

RESULT 10
 ADS14310
 ID ADS14310 standard; peptide; 15 AA.

XX AC ADS14310;

DT 16-DEC-2004 (first entry)

DE Desmoglein 3 antigenic peptide residues 190-204.

XX Cytostatic; Immunosuppressive; Antidiabetic; Neuroprotective;
 KW Antiarthritic; Antirheumatic; Antiallergic; Vaccine; Notch signaling;
 KW Notch; Notch ligand; Delta protein; Serrate protein; Jagged protein;
 KW multiple sclerosis; rheumatoid arthritis; diabetes; allergy;
 KW immune disorder; autoimmune disease; graft rejection; cancer;
 KW organ transplant; desmoglein 3.

XX Unidentified.

FN WO2004083372-A2.

PD 30-SEP-2004.

XX 22-MAR-2004; 2004WO-GB001229.

XX 21-MAR-2003; 2003GB-00006582.

PR 21-MAR-2003; 2003GB-00006583.

PR 22-MAR-2003; 2003GB-00006621.

PR 22-MAR-2003; 2003GB-00006622.

PR 22-MAR-2003; 2003GB-00006624.

PR 22-MAR-2003; 2003GB-00006626.

PR 22-MAR-2003; 2003GB-00006640.

PR 22-MAR-2003; 2003GB-00006644.

PR 22-MAR-2003; 2003GB-00006650.

PR 22-MAR-2003; 2003GB-00006651.

PR 22-MAR-2003; 2003GB-00006654.

XX (LORA-) LORANTIS LTD.

PA Champion BR, Ragno S;

XX WPI; 2004-709927/69.

DR Particle capable of being inserted into or taken up by cell useful for
 PT modulating immune response to antigen in subject, comprises
 PT polynucleotide coding for modulator of Notch signaling, and
 PT polynucleotide coding for antigen.

XX Disclosure; Page 118; 278pp; English.

XX The present invention relates to a particle (I) capable of being inserted
 CC into or taken up by a cell comprising (i) a polynucleotide coding for a
 CC modulator of Notch signaling, and (ii) a polynucleotide coding for an
 CC antigen or antigenic determinant. The first polynucleotide sequence codes

CC for a Notch ligand such as a Delta or Serrate/Jagged protein or its
 CC fragment, derivative, homologue, analogue or allelic variant, or for a
 CC protein which comprises a Notch ligand DSL domain and at least one Notch
 CC ligand EGF-like domain and optionally a membrane binding or transmembrane
 CC domain. The first and second sequences are operably linked to one or more
 CC promoters or enhancers or polyadenylation sequences. The antigen or
 CC antigenic determinant is an allergen, autoantigen, Major
 CC Histocompatibility complex (MHC) (transplant) antigen, pathogen antigen,
 CC tumour antigen or their antigenic determinant. (I) is useful for
 CC modulating an immune response to an antigen in a subject. Pharmaceutical
 CC compositions comprising (I) are useful for treating or preventing
 CC conditions mediated by T cells, such as multiple sclerosis, rheumatoid
 CC arthritis, diabetes, allergy, for treating immune disorders such as
 CC autoimmune diseases of graft rejection such as allograft rejection,
 CC treating cancer and organ transplants. The present sequence is a
 CC desmoglein 3 antigenic peptide (a class II MHC-associated autoantigen
 CC peptide), which can be used as an antigen to prepare the particle of the
 CC invention.

XX Sequence 15 AA;

Query Match 100.0%; Score 71; DB 8; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.3e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LNSKIAPKIVSQEPA 15

Db 1 LNSKIAPKIVSQEPA 15

RESULT 11

ABB04739

ID ABB04739 standard; peptide; 15 AA.

XX AC ABB04739;

XX 11-MAR-2002 (first entry)

DE Human heparan sulfate 3-O-sulfotransferase 19 peptide SEQ ID NO:7.

XX Human; heparan sulfate 3-O-sulfotransferase 19; haemorrhagic disease;
 KW thrombus embolism; haemopathy; myocardial infarction; tumour;
 KW inflammation; immunological disease; HIV infection.

XX Homo sapiens.

XX CN1311305-A.

XX 05-SEP-2001.

XX 02-MAR-2000; 2000CN-00111794.

XX 02-MAR-2000; 2000CN-00111794.

XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.

XX Mao Y, Xie Y;

XX WPI; 2002-049921/07.

XX New polypeptide-heparan sulfate 3-O-sulfotransferase 19 and
 PT polynucleotide for coding such polypeptide.

XX Example 6; Page 19 (Disclosure); 34pp; Chinese.

XX The present invention describes human heparan sulfate 3-O-
 CC sulfotransferase 19 protein (I). The present invention also describes a
 CC method of applying (I) in the treatment of various diseases, such as
 CC haemorrhagic diseases, thrombus embolism, other haemopathy, myocardial
 CC infarction, various tumours, inflammation, immunological diseases and HIV
 CC infection. The present invention also describes the agonist resisting (I)
 CC and its treatment effect. The present sequence represents the N-terminal
 CC peptide of (I) which is used in an example from the present invention

XX Sequence 15 AA;
SQ

Query Match 43.7%; Score 31; DB 5; Length 15;
Best Local Similarity 42.9%; Pred. No. 96;
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 LNSKIAPKIVSQEP 14
Db 1 MNSSIKLLIIVREP 14

RESULT 12
ADJ34233
ID ADJ34233 standard; protein; 15 AA.
XX
AC ADJ34233;
XX
DT 06-MAY-2004 (first entry)
XX
XX Human secreted protein NOV9e.
XX
XX Human; NOVX; secreted protein; cancer; diabetes; obesity;
KW endocrine disorder; CNS disorder; inflammatory disorder; gene therapy.
XX
XX Homo sapiens.
OS
XX WO2004000997-A2.
XX
XX 31-DEC-2003.
XX
XX 04-JUN-2003; 2003WO-US017512.
XX
XX 19-MAR-2002; 2002US-0365491P.
PR 04-JUN-2002; 2002US-0385504P.
PR 05-JUN-2002; 2002US-0386041P.
PR 06-JUN-2002; 2002US-0386453P.
PR 06-JUN-2002; 2002US-0386816P.
PR 07-JUN-2002; 2002US-0386974P.
PR 07-JUN-2002; 2002US-0387002P.
PR 10-JUN-2002; 2002US-0387540P.
PR 11-JUN-2002; 2002US-0387659P.
PR 12-JUN-2002; 2002US-0387934P.
PR 13-JUN-2002; 2002US-0389123P.
PR 17-JUN-2002; 2002US-0389729P.
PR 17-JUN-2002; 2002US-0389742P.
PR 19-JUN-2002; 2002US-0390066P.
PR 17-JUL-2002; 2002US-0396708P.
PR 12-AUG-2002; 2002US-0402832P.
PR 13-AUG-2002; 2002US-0403486P.
PR 14-AUG-2002; 2002US-0403522P.
PR 15-AUG-2002; 2002US-0403748P.
PR 06-NOV-2002; 2002US-0387037P.
PR 03-JUN-2003; 2003US-00454246.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Anderson DW, Boldog FL, Burgess CE, Casman SJ, Edinger SR;
PI Eisen A, Ellerman K, Gerlach VL, Gorman L, Guo X, Gusev VY, Ji W;
PI Li L, MacDougall JR, Malyankar UM, Millet I, Ort T, Padigar M;
PI Prayaga SK, Patturajan M, Pena CEA, Peyman JA, Rieger DK;
PI Rothenberg ME, Sciorio P, Shenoy SG, Smithson G, Spytek KA, Stone DJ;
PI Taupier RJ, Tchernev VT, Vernet CAM, Voss EZ, Zerhusen BD, Zhong M;
XX WPI; 2004-082483/08.
DR N-PSDB; ADJ34232.
XX
XX New isolated NOVX polypeptides useful for treating, preventing and
PT diagnosing pathological conditions with NOVX-associated disorders, such
PT as cancer, obesity, diabetes and inflammatory or CNS diseases.
XX
XX Claim 1; SEQ ID NO 122; 418pp; English.
XX

The invention relates to a new isolated polypeptide (designated NOVX) comprising one of 141 fully defined sequences, their mature forms, a protein comprising one or more conservative substitutions or having at least 95% identity to one of the 141 proteins. Also included are a composition comprising NOVX (or a NOVX nucleic acid molecule (NA)), a kit comprising the composition of NOVX in one or more containers, an isolated nucleic acid molecule encoding a NOVX protein, producing NOVX (comprising polypeptide, where the cell comprises a vector comprising NOVX NA), identifying an agent that binds to NOVX, identifying a potential therapeutic agent for use in the treatment of a pathology that is related to aberrant expression or physiological interactions of NOVX, screening for a modulator of activity of or latency or predisposition to a pathology associated with NOVX, modulating the activity of NOVX, treating or preventing a pathology associated with NOVX, treating a pathological state in a mammal, a vector comprising the NOVX nucleic acid molecule, a cell comprising the vector, an antibody that immunospecifically binds to NOVX, determining the presence or amount of NOVX or the nucleic acid molecule in a sample, and determining the presence of or predisposition to a disease associated with altered levels of expression of NOVX or the nucleic acid molecule in a first mammalian subject. The methods and compositions of the present invention are useful for the diagnosis and treatment of disorders associated with aberrant expression or activity of the NOVX polypeptide, such as cancer, diabetes, obesity, and endocrine, CNS and inflammatory disorders. They can also be used in various detection and screening assays, chromosome mapping, tissue typing, gene therapy and predictive medicine. The present sequence represents a NOVX protein.

XX Sequence 15 AA;
SQ

Query Match 43.7%; Score 31; DB 8; Length 15;
Best Local Similarity 66.7%; Pred. No. 96;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 NSKIAPKIV 10
Db 2 NSKVAFPSAV 10

RESULT 13
ADL26206
ID ADL26206 standard; peptide; 15 AA.
XX
AC ADL26206;
XX
XX 17-JUN-2004 (first entry)
XX
XX Synthetic peptide B121 derived from a conserved region of HCV.
DE HCV; hepatitis C virus; virucide; vaccine; MHC; HLA;
KW major histocompatibility complex; human leukocyte antigen.
XX
XX Synthetic.
XX
XX WO2004024182-A2.
XX
XX 25-MAR-2004.
XX
XX 27-AUG-2003; 2003WO-EP009482.
XX
XX 13-SEP-2002; 2002AT-00001376.
PR 27-FEB-2003; 2003WO-EP002005.
PR 11-JUL-2003; 2003EP-00450171.
XX
XX (INTE-) INTERCELL AG.
XX
XX Buschle M, Habel A, Klade C, Mattner F, Otava O, Vytvytska O;
PI Zauner W, Zinke S, Kirlappos H;
XX WPI; 2004-269899/25.
DR
XX Isolating Hepatitis C Virus peptides (HPe) which have a binding capacity

PT to a MHC/HLA molecule or a complex comprising the HCV-peptide and the
 PT molecule by separating the complex from the HCV-peptides which do not
 XX bind to the molecule.

PS Example 1; Page 31; 73pp; English.

XX The invention relates to a novel method for isolating Hepatitis C Virus
 CC (HCV) peptides (HPs). The method of the invention has virucide activity,
 CC and may be useful in producing a vaccine. The method is useful for
 CC isolating Hepatitis C Virus peptides (HPs) which have a binding capacity
 CC to a MHC/HLA molecule or a complex comprising the HCV-peptide and the
 CC MHC/HLA molecule for preparing a vaccine against HCV infection. The T
 CC cells, a T cell clone or a T cell population or preparation is useful for
 CC identifying heteroclitic epitopes or for preparing a composition for
 CC treating HCV infection. The present sequence represents a synthetic
 CC peptide derived from a conserved region of HCV.

XX Sequence 15 AA;

Query Match 42.3%; Score 30; DB 8; Length 15;
 Best Local Similarity 66.7%; Pred. No. 1.5e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 IAFKIVSOE 13
 Db 7 VAFKIMSGE 15
 :||||:|

RESULT 14
 ADL26187
 ID ADL26187 standard; peptide; 15 AA.

XX AC ADL26187;
 XX 17-JUN-2004 (first entry)
 XX Synthetic peptide B102 derived from a conserved region of HCV.
 XX HCV; hepatitis C virus; virucide; vaccine; MHC; HLA;
 KW major histocompatibility complex; human leukocyte antigen.

XX OS Synthetic.
 XX WO2004024182-A2.
 XX 25-MAR-2004.
 XX 27-AUG-2003; 2003WO-EP009482.
 XX 13-SEP-2002; 2002AT-00001376.
 PR 27-FEB-2003; 2003WO-EP002005.
 PR 11-JUL-2003; 2003EP-00450171.
 XX (INTE-) INTERCELL AG.
 XX Buschle M, Habel A, Klade C, Mattner F, Otava O, Vytvytska O;
 PI Zauner W, Zinke S, Kirlappos H;
 XX WPI; 2004-269899/25.
 DR Isolating Hepatitis C Virus peptides (HPs) which have a binding capacity
 PT to a MHC/HLA molecule or a complex comprising the HCV-peptide and the
 PT molecule by separating the complex from the HCV-peptides which do not
 PT bind to the molecule.

XX Example 1; Page 31; 73pp; English.

XX The invention relates to a novel method for isolating Hepatitis C Virus
 CC (HCV) peptides (HPs). The method of the invention has virucide activity,
 CC and may be useful in producing a vaccine. The method is useful for
 CC isolating Hepatitis C Virus peptides (HPs) which have a binding capacity
 CC to a MHC/HLA molecule or a complex comprising the HCV-peptide and the
 CC MHC/HLA molecule for preparing a vaccine against HCV infection. The T

CC cells, a T cell clone or a T cell population or preparation is useful for
 CC identifying heteroclitic epitopes or for preparing a composition for
 CC treating HCV infection. The present sequence represents a synthetic
 CC peptide derived from a conserved region of HCV.

XX Sequence 15 AA;

Query Match 42.3%; Score 30; DB 8; Length 15;
 Best Local Similarity 66.7%; Pred. No. 1.5e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 IAFKIVSOE 13
 Db 7 VAFKIMSGE 15
 :||||:|

RESULT 15
 AAW85386
 ID AAW85386 standard; peptide; 15 AA.

XX AC AAW85386;
 XX 16-FEB-1999 (first entry)
 XX Helper T-cell class II peptide derived from EXP1 protein.
 XX Helper T-cell peptide; human leukocyte antigen; HLA; DR4w4; DR1; DR7;
 KW cytotoxic T lymphocyte; CTL; hepatitis; autoimmune disease;
 KW acquired immune deficiency syndrome; malaria; cancer;
 KW allograft rejection; allergy; Lyme disease; hepatitis;
 KW post-streptococcal endocarditis; glomerulonephritis;
 KW food hypersensitivity.

XX OS Synthetic.
 OS Plasmodium falciparum.
 XX WO9832456-A1.
 XX 30-JUL-1998.
 XX 23-JAN-1998; 98WO-US001373.
 XX 23-JAN-1997; 97US-0036713P.
 PR 07-FEB-1997; 97US-0037432P.
 XX (EPIM-) EPIMMUNE INC.
 XX Sette A, Sidney J, Southwood S;
 XX WPI; 1998-427679/36.
 DR Composition containing peptide that induces cytotoxic T lymphocyte
 PT response, and helper peptide - can bind to human leukocyte antigen
 PT alleles, used to treat or prevent cancers, parasitic infections and
 PT autoimmune disease.

XX Disclosure; Page 41; 51pp; English.

XX AAW85284-451 represent helper T-cell class II peptides, which can bind to
 CC the human leukocyte antigens (HLA) DR4w4, DR1 and DR7. The peptides are
 CC used in the course of the invention. The specification describes peptides
 CC that that induce a cytotoxic T lymphocyte (CTL) response, and T-helper
 CC peptides, that are used together to generate a CTL response or the
 CC treatment or prevention of viral, fungal, bacterial or parasitic
 CC infections (e.g. hepatitis, acquired immune deficiency syndrome or
 CC malaria) or cancer (e.g. renal or cervical carcinoma, lymphoma, prostate
 CC cancer or condyloma acuminatum). Helper T-cell peptides may be used alone
 CC to induce a helper T cell response, e.g. in cases of autoimmune disease,
 CC allograft rejection, allergy, Lyme disease, hepatitis, post-streptococcal
 CC endocarditis, glomerulonephritis and food hypersensitivity

XX Sequence 15 AA;

Query Match 40.8%; Score 29; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. NO. 2.3e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 FKIVSOEPA 15
||| |:
Db 4 FKIGSDPA 12

Search completed: February 22, 2005, 09:24:35
Job time : 67.6667 secs

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OM protein - protein search, using sw model

Run on: February 22, 2005, 09:08:09 ; Search time 11.1333 Seconds
(without alignments)
129.633 Million cell updates/sec

Title: US-08-991-628-4
Perfect score: 76
Sequence: 1 TPMFLLSRNTGEVRT 15
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 2523

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	31.6	11	PH0919	T-cell receptor be
2	23	30.3	14	S22236	lipoxigenase (EC 1
3	23	30.3	14	PH1705	Ig heavy chain V r
4	23	30.3	15	C43334	orf3 3' to aadr -
5	23	30.3	15	PA0075	fructose-bisphosph
6	22	28.9	15	PA0102	fructose-bisphosph
7	21	27.6	11	S33782	acetolactate synth
8	21	27.6	14	PH0915	T-cell receptor be
9	20	26.3	6	A27696	contraction-inhibi
10	20	26.3	8	PT0691	T-cell receptor be
11	20	26.3	11	B41835	translation elonga
12	20	26.3	12	G49410	t-complex polypept
13	20	26.3	15	PH0750	T-cell receptor be
14	20	26.3	15	PC4213	bphB protein - Com
15	19	25.0	6	B27696	contraction-inhibi
16	19	25.0	10	A49581	siatokinin I - yel
17	19	25.0	11	S51732	T-cell receptor al
18	19	25.0	12	PT0216	T-cell receptor be
19	19	25.0	12	PH0920	T-cell receptor be
20	19	25.0	13	S47390	T-cell antigen rec
21	19	25.0	13	PH0796	T-cell receptor al
22	19	25.0	13	PH0799	T-cell receptor al
23	19	25.0	13	PH0783	T-cell receptor al
24	19	25.0	15	S47367	T-cell antigen rec
25	18	23.7	6	PT0518	T-cell receptor be
26	18	23.7	10	PH0926	T-cell receptor be
27	18	23.7	12	S49547	hypothetical prote
28	18	23.7	13	B36042	oxf protein - Esc
29	18	23.7	13	A26999	carboxylesterase (

30	18	23.7	13	2	I77387	AMP deaminase - ra
31	18	23.7	14	2	S58426	spermadhesin AWN h
32	18	23.7	14	2	B56819	PS I complex subun
33	18	23.7	15	2	I58116	Dp116 - human
34	18	23.7	15	2	E91061	hypothetical prote
35	18	23.7	15	2	A26228	spot 42 protein -
36	18	23.7	15	2	A40634	orf19 3' of eryK -
37	18	23.7	15	2	S03955	acidic fibroblast
38	18	23.7	15	4	I52698	hypothetical THR1
39	17.5	23.0	14	2	D45474	thrombospondin 2 -
40	17	22.4	9	2	A31576	xylose isomerase (
41	17	22.4	9	2	G85802	hypothetical prote
42	17	22.4	10	2	S63387	cytochrome-c oxida
43	17	22.4	11	2	A54348	N-acetylglucosamin
44	17	22.4	11	2	S60354	retinal oxidase -
45	17	22.4	11	2	PT0211	T-cell receptor al

ALIGNMENTS

RESULT 1

PH0919
T-cell receptor beta chain V-D-J region (isolate 5) - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C:Accession: PH0919
R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J: Exp. Med. 174, 1467-1476, 1991
A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic
A:Reference number: PH0891; MUID:92078857; PMID:1836012
A:Accession: PH0919
A:Molecule type: mRNA
A:Residues: 1-11 <GOL>
A:Experimental source: concanavalin A-activated lymphoblast
A:Note: the authors translated the codon CAG for residue 11 as Glu
C:Keywords: T-cell receptor

Query Match 31.6%; Score 24; DB 2; Length 11;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 RNTGE 12

DB 7 RNTQG 11

RESULT 2

S22236
lipoxigenase (EC 1.13.11.12) 1 - barley (fragment)
C:Species: Hordeum vulgare (barley)
C:Date: 19-Mar-1997 #sequence_revision 24-Mar-1999 #text_change 24-Mar-1999
C:Accession: S22236
R:Doderer, A.; Kokkelink, I.; van der Veen, S.; Valk, B.E.; Schram, A.W.; Douma, A.C.
Biochim. Biophys. Acta 1120, 97-104, 1992
A:Title: Purification and characterization of two lipoxigenase isoenzymes from germinatin
A:Reference number: S21772; MUID:92207997; PMID:1554746
A:Accession: S22236
A:Molecule type: protein
A:Residues: 1-14 <DOD>
A:Experimental source: var. Triumph, seed
C:Function:
A:Description: catalyzes the peroxidation of polyunsaturated fatty acids to their corres
C:Superfamily: lipoxigenase
C:Keywords: monomer; oxidoreductase; seed

Query Match 30.3%; Score 23; DB 2; Length 14;
Best Local Similarity 45.5%; Pred. No. 7.5e+02;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 PMFLLSRNTGE 12

DB 2 PYMLLYPNTSD 12

```

RESULT 3
PH1705
ig heavy chain V region (clone ASC-1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999
C:Accession: PH1705
R:McHeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.
J. Exp. Med. 178, 295-307, 1993
A:Title: Antigen-driven B cell differentiation in vivo.
A:Reference number: PH1675; MUID:93301607; PMID:8315385
A:Accession: PH1705
A:Molecule type: mRNA
A:Residues: 1-14 <MCH>
A:Experimental source: B cell
A:Note: the authors translated the codon GTA for residue 11 as Thr and ACA for residue 1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match      30.3%; Score 23; DB 2; Length 14;
Best Local Similarity 62.5%; Pred. No. 7.5e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      8 RNTGEVRT 15
      |||||
DB      6 RNTKSDET 13

RESULT 4
C43334
orf3 3' to aadR - Rhodopseudomonas palustris (fragment)
C:Species: Rhodopseudomonas palustris
C>Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: C43334
R:Dispenza, M.; Thomas, C.T.; Kim, M.K.; Perrotta, J.A.; Gibson, J.; Hatwood, C.S.
J. Bacteriol. 174, 5803-5813, 1992
A:Title: Anaerobic growth of Rhodopseudomonas palustris on 4-hydroxybenzoate is dependent
A:Reference number: A43334; MUID:92394882; PMID:1522059
A:Accession: C43334
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-15 <DIS>
A:Cross-references: UNIPROT:Q02006; GB:M92426; NID:G151870; PIDN:AAA26091.1; PID:G551951
A:Note: sequence extracted from NCBI backbone (NCBIN:112964, NCBI:P:112967)

Query Match      30.3%; Score 23; DB 2; Length 15;
Best Local Similarity 44.4%; Pred. No. 8.1e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      1 TPEMLLSRN 9
      |||||
DB      5 TPAYLRARH 13

RESULT 5
PA0075
fructose-bisphosphate aldolase (EC 4.1.2.13) I - fungus (Fusarium sporotrichioides) (fra
N:Alternate names: aldolase; fructose-1,6,-bisphosphate triosephosphate-lase
C:Species: Fusarium sporotrichioides
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: PA0075; PA0077
R:Chow, L.P.; Fukaya, N.; Sugiyura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JPID, October 1994
A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich
A:Reference number: PA0051
A:Accession: PA0075
A:Molecule type: protein
A:Residues: 1-15 <CHO>
A:Cross-references: UNIPROT:Q7M425
A:Note: this form (I) had a molecular weight of 30.6K and an isoelectric point of 5.3
A:Accession: PA0077
A:Molecule type: protein

Query Match      30.3%; Score 23; DB 2; Length 15;
Best Local Similarity 44.4%; Pred. No. 8.1e+02;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      5 LLSRNTGEV 13
      :|||::||:
DB      5 VLRSDSGVI 13

RESULT 6
PA0102
fructose-bisphosphate aldolase (EC 4.1.2.13) III - fungus (Fusarium sporotrichioides) (fr
C:Species: Fusarium sporotrichioides
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: PA0102
R:Chow, L.P.; Fukaya, N.; Sugiyura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JPID, October 1994
A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichi
A:Reference number: PA0051
A:Accession: PA0102
A:Molecule type: protein
A:Residues: 1-15 <CHO>
A:Cross-references: UNIPROT:Q7M424
C:Keywords: aldehyde-lyase; carbon-carbon lyase

Query Match      28.9%; Score 22; DB 2; Length 15;
Best Local Similarity 44.4%; Pred. No. 1.2e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      5 LLSRNTGEV 13
      :|||::||:
DB      5 VLRSKSGVI 13

RESULT 7
S33782
acetolactate synthase (EC 4.1.3.18) small chain, valine-sensitive - Serratia marcescens
C:Species: Serratia marcescens
C>Date: 19-Mar-1997 #sequence_revision 24-Mar-1999 #text_change 24-Mar-1999
C:Accession: S33782
R:Yang, J.H.; Kim, S.S.
Biochim. Biophys. Acta 1157, 178-184, 1993
A:Title: Purification and characterization of the valine sensitive acetolactate synthase
A:Reference number: S33781; MUID:93283409; PMID:8507653
A:Accession: S33782
A:Molecule type: protein
A:Residues: 1-11 <VAN>
A:Experimental source: ATCC 25419
A:Complex: heterotetramer; two small and two large chains
C:Function:
A:Description: catalyzes the condensation of pyruvate and alpha-ketobutyrate to form alpi
A:Pathway: valine, leucine, and isoleucine biosynthesis
A:Note: this isoenzyme exhibits homotropic allosterism with pyruvate
C:Keywords: branched-chain amino acid biosynthesis; carbon-carbon lyase; flavoprotein; he

Query Match      27.6%; Score 21; DB 2; Length 11;
Best Local Similarity 57.1%; Pred. No. 1.4e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      3 MFLLSRN 9
      |||::||
DB      1 MILVGRN 7

RESULT 8
PH0915
T-cell receptor beta chain V-D-J region (isolate 1) - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
A:Molecule type: protein
```

C:Accession: PH0915
R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic
A:Reference number: PH0891; MUID:92078857; PMID:1836012
A:Accession: PH0915
A:Molecule type: mRNA
A:Residues: 1-14 <GL>
A:Experimental source: concanavalin A-activated lymphoblast
A:Note: the authors translated the codon GGG for residue 8 as Glu and GAG for residue 9
C:Keywords: T-cell receptor

Query Match 27.6%; Score 21; DB 2; Length 14;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 RNTGE 12
|||
Db 5 RGTGE 9

RESULT 9
A27696
contraction-inhibiting peptide I - blue mussel
C:Species: Mytilus edulis (blue mussel)
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C:Accession: A27696
R:Hirata, T.; Kubota, I.; Iwasawa, N.; Takabatake, I.; Ikeda, T.; Muneoka, Y.
Biochem. Biophys. Res. Commun. 152, 1376-1382, 1988
A:Title: Structures and actions of Mytilus inhibitory peptides.
A:Reference number: A90142; MUID:88240357; PMID:3377776
A:Accession: A27696
A:Molecule type: protein
A:Residues: 1-6 <HR>
A:Cross-references: UNIPROT:P13736
A:Keywords: amidated carboxyl end
P:6/Modified site: amidated carboxyl end (Val) #status experimental

Query Match 26.3%; Score 20; DB 2; Length 6;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPMFL 5
:|:
Db 2 SPMFV 6

RESULT 10
PT0691
T-cell receptor beta chain V-D-J region (154-2K) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0691
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:9127601; PMID:1711558
A:Accession: PT0691
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-8 <FE>
A:Experimental source: day 18 fetal thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 26.3%; Score 20; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 TGEVRT 15
:|:
Db 2 SGEPT 7

RESULT 11
B41835
translational elongation factor EF-G homolog - Bacillus subtilis (fragment)
C:Species: Bacillus subtilis
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Dec-1997
C:Accession: B41835
R:Mitchell, C.; Morris, P.W.; Vary, J.C.
J. Bacteriol. 174, 2474-2477, 1992
A:Title: Identification of proteins phosphorylated by ATP during sporulation of Bacillus
A:Reference number: A41835; MUID:92210489; PMID:1556067
A:Accession: B41835
A:Molecule type: protein
A:Residues: 1-11 <MT>
A:Note: this protein is phosphorylated during stationary phase but not during exponential
C:Keywords: phosphoprotein

Query Match 26.3%; Score 20; DB 2; Length 11;
Best Local Similarity 60.0%; Pred. No. 2.1e+03;
Matches 6; Conservative 1; Mismatches 1; Indels 2; Gaps 1;

QY 4 FLL--SRNTG 11
|||:|
Db 1 FLEKTRNIG 10

RESULT 12
G49410
t-complex polypeptide 1 homolog (peak 6b fraction) - rabbit (fragment)
N:Alternate names: chaperonin homolog (peak 6b)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 04-Sep-1998
C:Accession: G49410
R:Rommelaere, H.; Van Troys, M.; Gao, Y.; Melki, R.; Cowan, N.J.; Vandekerckhove, J.; Am
Proc. Natl. Acad. Sci. U.S.A. 90, 11975-11979, 1993
A:Title: Eukaryotic cytosolic chaperonin contains t-complex polypeptide 1 and seven relat
A:Reference number: A49410; MUID:94089752; PMID:7903455
A:Accession: G49410
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-12 <ROM>
A:Experimental source: reticulocyte
C:Superfamily: molecular chaperone t-complex-type

Query Match 26.3%; Score 20; DB 2; Length 12;
Best Local Similarity 57.1%; Pred. No. 2.3e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 LLSRNTG 11
:|:
Db 1 ILIANTG 7

RESULT 13
PH0750
T-cell receptor beta chain (C11) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PH0750
R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilek, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A:Title: T cell receptor genes in a series of class I major histocompatibility complex-re
allelic exclusion and antigen-specific repertoire.
A:Reference number: PH0746; MUID:92078846; PMID:1836010
A:Accession: PH0750
A:Molecule type: mRNA
A:Residues: 1-15 <CAS>
A:Cross-references: EMBL:X06841
A:Experimental source: T lymphocyte
C:Keywords: T-cell receptor

Query Match 26.3%; Score 20; DB 2; Length 15;
Best Local Similarity 60.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 9 NTGEV 13
|||:
Db 8 NTGQL 12

RESULT 14

PC4213
bphB protein - Comamonas testosteroni (fragment)
C:Species: Comamonas testosteroni
C:Date: 17-Dec-1996 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004
C:Accession: PC4213
R:Sylvestre, M.; Sirois, M.; Hurtubise, Y.; Bergeron, J.; Ahmad, D.; Shareck, F.; Barria
Gene 174, 195-202, 1996
A:Title: Sequencing of Comamonas testosteroni strain B-356-biphenyl/chlorobiphenyl dioxy
A:Reference number: JC4993, MUID:97045812; PMID:8890734
A:Accession: PC4213
A:Molecule type: DNA
A:Residues: 1-15 <SYL>
A:Cross-references: UNIPROT:Q46381; GB:U47637; NID:gl245151; PIDN:AAC44530.1; PID:gl2451
A:Experimental source: strain B-356
C:Genetics:
A:Gene: bphB

Query Match 26.3%; Score 20; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 TGEV 13
|||:
Db 4 TGEV 7

RESULT 15

B27696
contraction-inhibiting peptide II - blue mussel
C:Species: Mytilus edulis (blue mussel)
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C:Accession: B27696
R:Hirata, T.; Kubota, I.; Iwasawa, N.; Takabatake, I.; Ikeda, T.; Muneoka, Y.
Biochem. Biophys. Res. Commun. 152, 1376-1382, 1988
A:Title: Structures and actions of Mytilus inhibitory peptides.
A:Reference number: A90142; MUID:88240357; PMID:3377776
A:Accession: B27696
A:Molecule type: protein
A:Residues: 1-6 <HIR>
A:Cross-references: UNIPROT:P13737
C:Keywords: amidated carboxyl end
F:6/Modified site: amidated carboxyl end (Val) #status experimental

Query Match 25.0%; Score 19; DB 2; Length 6;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PMFL 5
|||:
Db 3 PMFV 6

Search completed: February 22, 2005, 09:46:25
Job time : 12.1333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 22, 2005, 08:53:13 ; Search time 52.6 Seconds
(without alignments)
146.030 Million cell updates/sec

Title: US-08-991-628-4
Perfect score: 76
Sequence: 1 TPFLLSRNTGEVRT 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 6622

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03: +
1: uniprot_sprot: +
2: uniprot_trembl: +

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	26	34.2	13	Q9X3E1	Q9x3e1 prochloroc
2	24	31.6	10	Q8SHB1	Q8shb1 rhampheoleon
3	23	30.3	15	Q7M4Z5	Q7m4z5 fusarium sp
4	23	30.3	15	Q7RCA8	Q7rca8 plasmodium
5	22	28.9	14	Q6LCR2	Q6lcr2 mus musculus
6	22	28.9	15	Q7M4Z4	Q7m4z4 fusarium sp
7	22	28.9	15	Q842L7	Q842l7 salmonella
8	21	27.6	8	Q659Q3	Q659q3 silene oste
9	21	27.6	8	Q659Q5	Q659q5 silene invo
10	21	27.6	9	UPA6 HUMAN	P30092 homo sapien
11	20	26.3	6	CIP1_MYTED	P13736 mytilus edu
12	20	26.3	8	Q9RQ57	Q9rq57 buchnera ap
13	20	26.3	9	Q9S8J8	Q9s8j8 oryza sativ
14	20	26.3	10	Q6UJ18	Q6uj18 nephurus l
15	20	26.3	10	Q6UJ11	Q6uj11 nephurus v
16	20	26.3	13	Q13377	Q13377 homo sapien
17	20	26.3	13	Q8RSG9	Q8rsg9 uncultured
18	20	26.3	13	Q9X3J6	Q9x3j6 prochloroc
19	20	26.3	13	Q7Z2I8	Q7zz18 motacilla f
20	20	26.3	15	MILT ONCKE	P81037 oncorhynch
21	19.5	25.7	15	Q9TNP0	Q9tnp0 mus sp. m
22	19	25.0	6	CIP2_MYTED	P13737 mytilus edu
23	19	25.0	6	UN06_CLOPA	P81351 clostridium
24	19	25.0	10	TKS1_AEDAE	P42834 aedes aegypt
25	19	25.0	10	Q7RK54	Q7rks4 plasmodium
26	19	25.0	10	Q7TRU6	Q7tru6 bos taurus
27	19	25.0	10	Q8SH99	Q8sh99 brookesia n
28	19	25.0	10	Q8SHK1	Q8shk1 calumma gas
29	19	25.0	10	Q8SHL0	Q8shl0 calumma gas
30	19	25.0	10	Q8SHL3	Q8shl3 calumma fur
31	19	25.0	10	Q8SHM2	Q8shm2 calumma boe

32	19	25.0	10	2	Q8SHP0	Q8shp0 bradypodion
33	19	25.0	11	2	Q44237	Q44237 anabaena sp
34	19	25.0	12	2	Q9XNR6	Q9xnr6 pyralaella l
35	19	25.0	14	2	Q6I7N3	Q6i7n3 haemaphysal
36	19	25.0	15	1	UE15 HORVU	P34938 hordeum vul
37	18	23.7	10	2	Q7YOR0	Q7yor0 brassica ju
38	18	23.7	11	2	Q8IVG8	Q8ivg8 homo sapien
39	18	23.7	11	2	Q6SB14	Q6sb14 drosophila
40	18	23.7	11	2	Q997C1	Q997c1 east africa
41	18	23.7	12	2	Q8JIG6	Q8jig6 ashbya goss
42	18	23.7	12	2	Q9P116	Q9p116 homo sapien
43	18	23.7	12	2	Q41856	Q41856 zea mays (m
44	18	23.7	12	2	Q83U71	Q83u71 salmonella
45	18	23.7	13	2	O75905	O75905 homo sapien

ALIGNMENTS

RESULT 1
Q9X3E1 PRELIMINARY; PRT; 13 AA.
ID Q9X3E1
AC Q9X3E1;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DE 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE Cytochrome b (Fragment).
GN Name=petB;
OS Prochlorococcus sp.
OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=1220;
RN [1]
RP SEQUENCE FROM N.A.
RA Urbach E., Chisholm S.W.;
RT "Genetic diversity in Prochlorococcus populations flow cytometrically
sorted from the Sargasso Sea and Gulf Stream.";
RL Limnol. Oceanog. 43:1615-1630(1998).
DR EMBL; AF070141; MAD20755.1; -.
FT NON TER 1
SQ SEQUENCE 13 AA; 1434 MW; 57EBE8029A8666D3 CRC64;

Query Match 34.2%; Score 26; DB 2; Length 13;
Best Local Similarity 62.5%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 FLLSRNTG 11
||:||||
Db 1 FLMSRRQG 8

RESULT 2
Q8SHB1 PRELIMINARY; PRT; 10 AA.
ID Q8SHB1
AC Q8SHB1;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Rhampholeon breviceaudatus (Bearded pygmy chameleon).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Iguania; Acrodonta; Chamaeleonidae;
OC Rhampholeon.
OX NCBI_TaxID=91912;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22169767; PubMed=12182400; DOI=10.1006/mpev.2001.1076;
RA Townsend T., Larson A.;
RT "Molecular phylogenetics and mitochondrial genomic evolution in the
Chamaeleonidae (Reptilia, Squamata).";
RL Mol. Phylogenet. Evol. 23:22-36(2002).

```

RN [2]
RP SEQUENCE FROM N.A.
RA Townsend T.M., Larson A.L.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF448771; AAL90595.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER
SQ SEQUENCE 10 AA; 1291 MW; 86218B2733641771 CRC64;

Query Match 31.6%; Score 24; DB 2; Length 10;
Best Local Similarity 71.4%; Pred. No. 1.9e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TPMFLLS 7
DB 3 TPRWLLS 9

RESULT 3
Q7M4Z5 PRELIMINARY; PRT; 15 AA.
AC Q7M4Z5;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DE Fructose-bisphosphate aldolase (EC 4.1.2.13) I (Fragment).
OS Fusarium sporotrichioides.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
OX NCBI_TaxID=5514;
RN [1]
RP SEQUENCE.
RA Chow L.P., Fukaya N., Sugiura Y., Ueno Y., Tabuchi K., Tsugita A.;
RL Submitted (OCT-1994) to the PIR data bank.
DR PIR; PA0075; PA0075.
DR GO; GO:0004332; F:fructose-bisphosphate aldolase activity; IEA.
FT NON TER 1
FT NON TER 15
SQ SEQUENCE 15 AA; 1515 MW; 74E3FE99D972632F CRC64;

Query Match 30.3%; Score 23; DB 2; Length 15;
Best Local Similarity 44.4%; Pred. No. 4.6e+03;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 5 LLSRNTGEV 13
DB 5 VLSDSGVI 13

RESULT 4
Q7RCAB PRELIMINARY; PRT; 15 AA.
AC Q7RCAB;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DE Hypothetical protein (Fragment).
GN Name=PY05876;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17XNL;
RX PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angluu S.V., Suh B.B., Kooij T.W., Pettea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selenkut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoaibi A., Cummings L.M.,
RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,

van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
DR EMBL; AABL01001927; EAA17977.1; -.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 15 AA; 1730 MW; 9CF62D019481ACF8 CRC64;

Query Match 30.3%; Score 23; DB 2; Length 15;
Best Local Similarity 57.1%; Pred. No. 4.6e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 TPMFLLS 7
DB 2 SPLFYLS 8

RESULT 5
Q6LCR2 PRELIMINARY; PRT; 14 AA.
AC Q6LCR2;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Short-chain acyl-CoA dehydrogenase (Fragment).
GN Name=Acads;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RX MEDLINE=96325094; PubMed=8661694;
RA Kelly C.L., Wood P.A.;
RT "Cloning and characterization of the mouse short-chain acyl-CoA
dehydrogenase gene.";
RL Mamm. Genome 7:262-264(1996).
DR EMBL; U36274; AAB99744.1; -.
FT NON TER 14
FT NON TER 14
SQ SEQUENCE 14 AA; 1467 MW; DF251B3D3157FD0D CRC64;

Query Match 28.9%; Score 22; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 6.4e+03;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 LLSRNTGEVR 14
DB 5 LLARARGPLR 14

RESULT 6
Q7M4Z4 PRELIMINARY; PRT; 15 AA.
AC Q7M4Z4;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Fructose-bisphosphate aldolase (EC 4.1.2.13) III (Fragment).
OS Fusarium sporotrichioides.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
OX NCBI_TaxID=5514;
RN [1]
RP SEQUENCE.
RA Chow L.P., Fukaya N., Sugiura Y., Ueno Y., Tabuchi K., Tsugita A.;
RL Submitted (OCT-1994) to the PIR data bank.

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DR PIR; PA0102; PA0102.
 DR GO; GO:0004332; F:fructose-bisphosphate aldolase activity; IEA.
 FT NON_TER 1
 FT NON_TER 15
 SQ SEQUENCE 15 AA; 1528 MW; 74B3FE999D726ABF CRC64;
 Query Match 28.9%; Score 22; DB 2; Length 15;
 Best Local Similarity 44.4%; Pred. No. 6.9e+03;
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 5 LLSRNTGEV 13 :|||:|
 Db 5 VLSRKSGVI 13 :|||:|
 RESULT 7
 Q842L7 PRELIMINARY; PRT; 15 AA.
 AC Q842L7;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE QacEdelta1 (Fragment).
 GN Name=qacEdelta1;
 OS Salmonella enterica subsp. enterica serovar Typhi.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmonella.
 OX NCBI_TaxID=90370;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=YMC95/6/4405;
 RA Yum J.H., Yong D., Lee K., Chong Y.;
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY245101; AAO89217.1; -.
 FT NON_TER 15
 SQ SEQUENCE 15 AA; 1675 MW; C2E1985D5C9E287B CRC64;
 Query Match 28.9%; Score 22; DB 2; Length 15;
 Best Local Similarity 45.5%; Pred. No. 6.9e+03;
 Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 3 MFLLSRNTGEV 13 :|||:|
 Db 5 LFLVIAIVGEV 15 :|||:|
 RESULT 8
 Q659Q3 PRELIMINARY; PRT; 8 AA.
 AC Q659Q3;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Photo system II reaction centre subunit V (Fragment).
 GN Name-psbE;
 OS Silene ostenfeldii.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllales; Caryophyllaceae; Silene.
 OX NCBI_TaxID=269081;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leaf;
 RA Popp M., Erixon P., Eggens F., Oxelman B.;
 RT "Origin and Evolution of a Circumpolar Polyploid Species Complex in
 RT Silene (Caryophyllaceae) Inferred from Low Copy Nuclear RNA Polymerase
 RT Introns, rDNA, and Chloroplast DNA.";
 RL Syst. Bot. 0:0-0(0).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leaf;
 RA Popp M.;
 RT "Disentangling the reticulate history of polyploids in Silene
 RT (Caryophyllaceae).";
 RL Thesis (2004), Department of Evolutionary Biology, Systematic Botany,
 RL Uppsala University, Uppsala, Sweden.
 DR EMBL; AJ831755; CAH41963.1; -.
 KW Chloroplast.
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 824 MW; ED0B1861B5B865B6 CRC64;
 Query Match 27.6%; Score 21; DB 2; Length 8;
 Best Local Similarity 57.1%; Pred. No. 1.6e+06;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 6 LSRNTGE 12 :|||:|
 Db 1 MSGSTGE 7 :|||:|
 RESULT 10
 UPAG6 HUMAN
 ID UPAG6 HUMAN STANDARD; PRT; 9 AA.
 AC P30092;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Unknown protein from 2D-PAGE of plasma (Spot 14) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

RT "Disentangling the reticulate history of polyploids in Silene
 RT (Caryophyllaceae).";
 RL Thesis (2004), Department of Evolutionary Biology, Systematic Botany,
 RL Uppsala University, Uppsala, Sweden.
 DR EMBL; AJ831757; CAH41967.1; -.
 KW Chloroplast.
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 824 MW; ED0B1861B5B865B6 CRC64;
 Query Match 27.6%; Score 21; DB 2; Length 8;
 Best Local Similarity 57.1%; Pred. No. 1.6e+06;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 6 LSRNTGE 12 :|||:|
 Db 1 MSGSTGE 7 :|||:|
 RESULT 9
 Q659Q5 PRELIMINARY; PRT; 8 AA.
 AC Q659Q5;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Photo system II reaction centre subunit V (Fragment).
 GN Name-psbE;
 OS Silene involucreata.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllales; Caryophyllaceae; Silene.
 OX NCBI_TaxID=39884;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leaf;
 RA Popp M., Erixon P., Eggens F., Oxelman B.;
 RT "Origin and Evolution of a Circumpolar Polyploid Species Complex in
 RT Silene (Caryophyllaceae) Inferred from Low Copy Nuclear RNA Polymerase
 RT Introns, rDNA, and Chloroplast DNA.";
 RL Syst. Bot. 0:0-0(0).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leaf;
 RA Popp M.;
 RT "Disentangling the reticulate history of polyploids in Silene
 RT (Caryophyllaceae).";
 RL Thesis (2004), Department of Evolutionary Biology, Systematic Botany,
 RL Uppsala University, Uppsala, Sweden.
 DR EMBL; AJ831755; CAH41963.1; -.
 KW Chloroplast.
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 824 MW; ED0B1861B5B865B6 CRC64;
 Query Match 27.6%; Score 21; DB 2; Length 8;
 Best Local Similarity 57.1%; Pred. No. 1.6e+06;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 6 LSRNTGE 12 :|||:|
 Db 1 MSGSTGE 7 :|||:|
 RESULT 10
 UPAG6 HUMAN
 ID UPAG6 HUMAN STANDARD; PRT; 9 AA.
 AC P30092;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Unknown protein from 2D-PAGE of plasma (Spot 14) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
RA Hochetasser D.F.;
RT "Plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -I- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
protein is: 5, its MW is: 48 kDa.
KW SWISS-2DPAGE; P30092; HUMAN.
DR Direct protein sequencing.
FT NON_TER 1
FT NON_TER 9
SQ SEQUENCE 9 AA; 935 MW; 528F2CAA8676447 CRC64;

Query Match 27.6%; Score 21; DB 1; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.6e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 NTGEVVT 15
DB 3 NPGDVXT 9

RESULT 11
CIP1_MYTD STANDARD; PRT; 6 AA.
AC P13736;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Contraction-inhibiting peptide I (MIP I).
OS Mytilus edulis (Blue mussel).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
OC Mytiloidea; Mytilidae; Mytilus.
OX NCBI_TaxID=6550;
RN [1]
RP SEQUENCE.
RC TISSUE=Pedal ganglion;
RX MEDLINE=88240357; PubMed=3377776;
RA Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.;
RT "Structures and actions of Mytilus inhibitory peptides.";
RL Biochem. Biophys. Res. Commun. 152:1376-1382(1988).
CC -I- FUNCTION: Inhibitory action on contractions in several molluscan
muscles.
CC -I- SIMILARITY: To MIP II.
DR PIR; A27696; A27696.
KW Amidation; Direct protein sequencing; Hormone.
FT MOD_RES 6
FT MOD_RES 6 Valine amide.
SQ SEQUENCE 6 AA; 637 MW; 72C9C6877581000 CRC64;

Query Match 26.3%; Score 20; DB 1; Length 6;
Best Local Similarity 60.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPMFL 5
DB 2 SPMFV 6

RESULT 12
Q9RQ57
ID Q9RQ57 PRELIMINARY; PRT; 8 AA.
AC Q9RQ57;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Nifs protein homolog (Fragment).
GN Name=nifs;

OS Buchnera aphidicola.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
OX NCBI_TaxID=9;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20022990; PubMed=10555290;
RA Clark M.A., Moran N.A., Baumann P.;
RT "Sequence evolution in bacterial endosymbionts having extreme base
compositions.";
RL Mol. Biol. Evol. 16:1586-1598(1999).
DR EMBL; AF130812; AAF13797.1; -.
FT NON_TER 8
FT NON_TER 8
SQ SEQUENCE 8 AA; 980 MW; F3A73B504771A336 CRC64;

Query Match 26.3%; Score 20; DB 2; Length 8;
Best Local Similarity 60.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPMFL 5
DB 3 TPILY 7

RESULT 13
Q9S8J8 PRELIMINARY; PRT; 9 AA.
AC Q9S8J8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE ORYZATENSIN=BIOACTIVE peptide.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE.
RX MEDLINE=95102521; PubMed=7804141;
RA Takahashi M., Moriguchi S., Yoshikawa M., Sasaki R.;
RT "Isolation and characterization of oryzatensin: a novel bioactive
RT peptide with ileum-contracting and immunomodulating activities derived
RT from rice albumin.";
RL Biochem. Mol. Biol. Int. 33:1151-1158(1994).
DR Granene; Q9S8J8; -.
SQ SEQUENCE 9 AA; 1093 MW; 0E8C67377B56877B CRC64;

Query Match 26.3%; Score 20; DB 2; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.6e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PMFLLSR 8
DB 3 PMYPLPR 9

RESULT 14
Q6UJ18 PRELIMINARY; PRT; 10 AA.
AC Q6UJ18;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Nephurus laevisimilis.
OS Nephurus laevisimilis.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scieroglossa; Gekkota; Gekkonidae; Nephurus.
OX NCBI_TaxID=255191;
RN [1]
RP SEQUENCE FROM N.A.

```


RA Melville J., Schulte J.A. II, Larson A.;
 RT "A Molecular Study of Phylogenetic Relationships and Evolution of
 RT Antipredator Strategies in Australian Dipodactylus Geckos, Subgenus
 RT Strophurus";
 RL Biol. J. Linn. Soc. Lond. 82:123-138(2004).
 DR EMBL; AY369020; AAR18892.1; -;
 DR GO; GO:0005739; C.mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1270 MW; 9AD380C733641771 CRC64;

Query Match 26.3%; Score 20; DB 2; Length 10;
 Best Local Similarity 57.1%; Pred. No. 1e+04;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TPMFLLS 7
 || : ||
 Db 3 TPRWLF 9

RESULT 15

Q6UJJ1
 ID Q6UJJ1 PRELIMINARY; PRT; 10 AA.
 AC Q6UJJ1
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN Name=COI;
 OS Nephurus vertebralis.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Gekkota; Gekkonidae; Nephurus.
 OX NCBI_TaxID=255190;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Melville J., Schulte J.A. II, Larson A.;
 RT "A Molecular Study of Phylogenetic Relationships and Evolution of
 RT Antipredator Strategies in Australian Dipodactylus Geckos, Subgenus
 RT Strophurus";
 RL Biol. J. Linn. Soc. Lond. 82:123-138(2004).
 DR EMBL; AY369019; AAR18889.1; -;
 DR GO; GO:0005739; C.mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1270 MW; 9AD380C733641771 CRC64;

Query Match 26.3%; Score 20; DB 2; Length 10;
 Best Local Similarity 57.1%; Pred. No. 1e+04;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TPMFLLS 7
 || : ||
 Db 3 TPRWLF 9

Search completed: February 22, 2005, 09:37:51
 Job time : 54.6667 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 22, 2005, 09:08:09 ; Search time 11.1333 Seconds
(without alignments)
129.633 Million cell updates/sec

Title: US-08-991-628-5
Perfect score: 88
Sequence: 1 CECNTKVKVDNDNFP 15
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 2523

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	31.8	12	2 S71034	potB protein - sal
2	24	27.3	15	2 PC2215	fibrinogenolytic p
3	23.5	26.7	14	2 S41601	interferon alpha r
4	23	26.1	5	2 A33882	cadmium-binding pe
5	23	26.1	7	2 B33882	very late antigen
6	23	26.1	14	2 A28018	T-cell antigen rec
7	22	25.0	13	2 S47362	antibiotic GE2270
8	22	25.0	13	2 A61210	tubulin beta chain
9	21	23.9	11	2 S54347	topoisomerase I -
10	21	23.9	15	2 A47146	29K protein 4228 -
11	21	23.9	15	2 PS0212	T cell receptor V-
12	20	22.7	15	2 S57584	capsid protein VP-
13	19	21.6	8	2 PL0184	caldesquestrin, car
14	19	21.6	9	2 A61230	alpha-2-macroglobu
15	19	21.6	9	2 S66635	hemagglutinin - in
16	19	21.6	10	2 S51912	T antigen variant
17	19	21.6	11	2 PH1376	ribosomal protein
18	19	21.6	12	2 PN0160	ubiquitin-carrier
19	19	21.6	15	2 A54397	major fat-globule
20	19	21.6	15	2 D48394	milk band B protei
21	19	21.6	15	2 C61511	T-cell receptor be
22	19	21.6	15	2 C49455	callifMRamide 11
23	18	20.5	7	2 B44787	metallothionein is
24	18	20.5	8	2 S59622	T-cell receptor be
25	18	20.5	10	2 PH0933	callifMRamide 12
26	18	20.5	10	2 C47877	sialokin II - ye
27	18	20.5	10	2 B49581	hypothetical prote
28	18	20.5	11	2 T06383	T antigen variant
29	18	20.5	11	2 PH1375	

30	18	20.5	12	2 A49033	T-cell receptor de
31	18	20.5	12	2 B49033	hypothetical 1.4K
32	18	20.5	12	2 JQ2308	hypothetical 1.4K
33	18	20.5	12	2 JQ2318	hypothetical 1.4K
34	18	20.5	13	2 S47392	T-cell antigen rec
35	18	20.5	13	2 B25448	Ig kappa-1 chain,
36	18	20.5	13	2 JH0460	corticostatic pept
37	18	20.5	14	2 S29486	GTP-binding protei
38	18	20.5	15	2 A49252	T-cell receptor be
39	18	20.5	15	2 PN0118	hemoglobin beta ch
40	17.5	19.9	13	2 S29488	GTP-binding protei
41	17	19.3	8	2 S19288	acylase - Kluysera
42	17	19.3	10	1 SPPGNK	neuromedin K - pig
43	17	19.3	10	2 S27873	hypothetical prote
44	17	19.3	11	2 B49164	chromogranin-B - r
45	17	19.3	11	2 D58502	27K bile and gallb

ALIGNMENTS

RESULT 1

S71034
potB protein - Salmonella typhimurium (fragment)
C;Species: Salmonella typhimurium
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S71034
R;Stein, M.A.; Leung, K.Y.; Zwick, M.; Garcia-del Portillo, F.; Finlay, B.B.
Mol. Microbiol. 20: 151-164, 1996
A;Title: Identification of a Salmonella virulence gene required for formation of filament
A;Reference number: S71033; MUID:97014378; PMID:8861213
A;Accession: S71034
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-12 <SPE>
A;Cross-references: UNIPROT:Q56060; EMBL:U51867; NID:g1272322; PIDN:AAA97466.1; PID:g1272322
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1996
C;Genetics:
A;Gene: potB

Query Match 31.8%; Score 28; DB 2; Length 12;
Best Local Similarity 55.6%; Pred. No. 2.7e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 NIKVKDND 12

DB 4 NKKVSDISD 12

RESULT 2

PC2215
fibrinogenolytic proteinase A2 (EC 3.4.21.-) - western diamondback rattlesnake (fragment)
N;Alternate names: alpha-fibrinogenase A2
C;Species: Crotalus atrox (western diamondback rattlesnake)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: PC2215
R;Hung, C.C.; Chiou, S.H.
Biochem. Biophys. Res. Commun. 201, 1414-1423, 1994
A;Title: Isolation of multiple isoforms of alpha-fibrinogenase from the western diamondback rattlesnake
A;Reference number: PC2214; MUID:94296418; PMID:8024586
A;Accession: PC2215
A;Molecule type: protein
A;Residues: 1-15 <HUN>
A;Cross-references: UNIPROT:Q9PRW3
C;Superfamily: trypsin; trypsin homology
C;Keywords: hydrolase; serine proteinase

Query Match 27.3%; Score 24; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ECNI 5

```
Db          6 ECNI 9
|||||
RESULT 3
S41601
interferon alpha receptor 1 - human (fragments)
C:Species: Homo sapiens (man)
C:Date: 25-Dec-1994 #sequence_revision 01-Dec-1995 #text_change 30-May-1997
C:Accession: S41601
R:Abrahamovich, C.; Ratovitski, E.; Lundgren, E.; Revel, M.
Proc. Natl. Acad. Sci. U.S.A. 84, 6619-6623, 1987
F:EBL Lett. 338, 295-300, 1994
A:Title: Identification of mRNAs encoding two different soluble forms of the human inter
A:Reference number: S41601; MUID:94139943; PMID:8307198
A:Accession: S41601
A:Molecule type: mRNA
A:Residues: 1-14 <ABR>
C:Keywords: cytokine receptor

Query Match          26.7%; Score 23.5; DB 2; Length 14;
Best Local Similarity 62.5%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 CEC-NIKV 7
|||
Db 4 CECENISL 11

RESULT 4
A33882
cadmium-binding pentapeptide - downy thornapple
C:Species: Datura innoxia (downy thornapple)
C:Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 18-Jun-1993
C:Accession: A33882
R:Jackson, P.J.; Unkefer, C.J.; Doolen, J.A.; Watt, K.; Robinson, N.J.
Proc. Natl. Acad. Sci. U.S.A. 84, 6619-6623, 1987
A:Title: Poly(gamma-glutamylcysteinyl)glycine: its role in cadmium resistance in plant
A:Reference number: A94182; MUID:88016144; PMID:3477793
A:Accession: A33882
A:Molecule type: protein
A:Residues: 1-5 <JAC>

Query Match          26.1%; Score 23; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEC 3
|||
Db 2 CEC 4

RESULT 5
B33882
cadmium-binding heptapeptide - downy thornapple
C:Species: Datura innoxia (downy thornapple)
C:Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 18-Jun-1993
C:Accession: B33882
R:Jackson, P.J.; Unkefer, C.J.; Doolen, J.A.; Watt, K.; Robinson, N.J.
Proc. Natl. Acad. Sci. U.S.A. 84, 6619-6623, 1987
A:Title: Poly(gamma-glutamylcysteinyl)glycine: its role in cadmium resistance in plant
A:Reference number: A94182; MUID:88016144; PMID:3477793
A:Accession: B33882
A:Molecule type: protein
A:Residues: 1-7 <JAZ>

Query Match          26.1%; Score 23; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CEC 3
|||
Db 2 CEC 4
```

```
RESULT 6
A28018
very late antigen-1 alpha chain - human (fragment)
N:Alternate names: VLA-1 alpha chain
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 12-May-1994
C:Accession: A28018
R:Takada, Y.; Strominger, J.L.; Hemler, M.E.
Proc. Natl. Acad. Sci. U.S.A. 84, 3239-3243, 1987
A:Title: The very late antigen family of heterodimers is part of a superfamily of molecu
A:Reference number: A94151; MUID:87204112; PMID:3033641
A:Accession: A28018
A:Molecule type: protein
A:Residues: 1-14 <TAK>
C:Keywords: duplication; heterodimer; membrane protein

Query Match          26.1%; Score 23; DB 2; Length 14;
Best Local Similarity 66.7%; Pred. No. 1.9e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 NIKVKD 9
|: |||
Db 2 NVDVKD 7

RESULT 7
S47362
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47362
R:Lehner, P.J.
Submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T ce
A:Reference number: S47355
A:Accession: S47362
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-references: EMBL:235688; NID:G527465; PIDN:CAA84757.1; PID:G527466
C:Keywords: T-cell receptor

Query Match          25.0%; Score 22; DB 2; Length 13;
Best Local Similarity 33.3%; Pred. No. 2.6e+03;
Matches 4; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 3 CNIKVKVDNDF 14
|: |||
Db 1 CASSVSSYNEQF 12

RESULT 8
A61210
antibiotic GE2270 - Planobispora rosea (ATCC 53773)
C:Species: Planobispora rosea
C:Date: 13-May-1994 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004
C:Accession: A61210
R:Kettnering, J.; Colombo, L.; Ferrari, P.; Tavecchia, P.; Nebuloni, M.; Vekey, K.; Gall
J. Antibiot. 44, 702-715, 1991
A:Title: Antibiotic GE2270 A: a novel inhibitor of bacterial protein synthesis. II. Stru
A:Reference number: A61210; MUID:91349090; PMID:1880060
A:Accession: A61210
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-13 <KET>
A:Cross-references: UNIPROT:Q7M0J8
C:Keywords: amidated carboxyl end; methylated amino acid; oxazole/thiazole ring
F:1-10/Cross-link: thiazole amino end (Cys-Lys) (by 10-C6) #status experimental
F:2-3/Cross-link: 5-methoxythiazole (Val-Cys) #status experimental
F:4-5/Cross-link: 5-methylthiazole (Asn-Cys) #status experimental
F:4/Modified site: N4-methylasparagine (Asn) #status experimental
F:7-8/Cross-link: thiazole (Phe-Cys) #status experimental
```

F;7/Modified site: 3-hydroxyphenylalanine (Phe) #status experimental
F;8-9/Cross-link: thiazole (Cys-Cys) #status experimental
F;9-10/Cross-link: pyridine (Cys-Lys) #status experimental
F;10-11/Cross-link: thiazole (Lys-Cys) #status experimental
F;11-12/Cross-link: 2-oxazoline (Cys-Ser) #status experimental
F;13/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 25.0%; Score 22; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CECN 4
| | |
Db 1 CVCN 4

RESULT 9

S54347

tubulin beta chain - bovine (fragment)

C;Species: Bos primigenius taurus (cattle)
C;Date: 27-Oct-1995 #sequence_revision 30-Jan-1998 #text_change 09-Jul-2004
C;Accession: S54347

R;Okazaki, K.; Obata, N.H.; Inoue, S.; Hidaka, H.

Biochem. J. 306, 551-555, 1995

A;Title: S100-beta is a target protein of neurocalcin delta, an abundant isoform in glia

A;Reference number: S54347; PMID:7887910

A;Accession: S54347

A;Molecule type: protein

A;Residues: 1-11 <OKA>

A;Cross-references: UNIPROT:Q7M372

Query Match 23.9%; Score 21; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KQVN 11
| | | |
Db 1 KQVN 4

RESULT 10

A47146

topoisomerase I - vaccinia virus (fragment)

C;Species: vaccinia virus
C;Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 09-Jul-2004
C;Accession: A47146

R;Klemperer, N.; Traktman, P.

J. Biol. Chem. 268, 15887-15899, 1993

A;Title: Biochemical analysis of mutant alleles of the vaccinia virus topoisomerase I ca

A;Reference number: A47146; PMID:8393454

A;Accession: A47146

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-15 <KLE>

A;Cross-references: UNIPROT:Q9UFB0; GB:L13447

C;Superfamily: vaccinia virus DNA topoisomerase

Query Match 23.9%; Score 21; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 4.3e+03;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 5 IKVKDV 10
| : | | |
Db 2 IRIKDL 7

RESULT 11

PS0212

29K protein 4228 - rice (strain Nihonbare) (fragment)

C;Species: Oryza sativa (rice)

C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004

C;Accession: PS0212

R;Tsugita, A.; Miyatake, N.

submitted to JIPID, April 1993
A;Reference number: PS0208
A;Accession: PS0212
A;Molecule type: protein
A;Residues: 1-15 <TSU>
A;Cross-references: UNIPROT:Q7M279
A;Experimental source: germ
C;Comment: molecular weight 29K, pI 6.1.

Query Match 23.9%; Score 21; DB 2; Length 15;
Best Local Similarity 42.9%; Pred. No. 4.3e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 8 KDVDNDF 14
: | | | :
Db 7 RDVGDRY 13

RESULT 12

S57584

T cell receptor V-D-J junctional alpha chain region - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 19-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 05-Nov-1999

C;Accession: S57584

R;Burrows, S.R.; Silins, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Argaeet, V.P.

submitted to the EMBL Data Library, June 1995

A;Description: T cell receptor repertoire for a viral epitope in humans is diversified by

A;Reference number: S57494

A;Accession: S57584

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-15 <BUR>

A;Cross-references: EMBL:Z49956; NID:g887466; PIDN:CRA90227.1; PID:g887467

C;Keywords: T-cell receptor

Query Match 22.7%; Score 20; DB 2; Length 15;
Best Local Similarity 33.3%; Pred. No. 6.2e+03;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 CECNIKVKD 9
| | | | :
Db 1 CAVNARERD 9

RESULT 13

PL0184

capsid protein VP-1 - murine poliovirus (fragment)

C;Species: murine poliovirus, Theiler's encephalomyelitis virus

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Feb-1995

C;Accession: PL0184

R;Zurbriggen, A.; Hogle, J.M.; Fujinami, R.S.

J. Exp. Med. 170, 2037-2049, 1989

A;Title: Alteration of amino acid 101 within capsid protein VP-1 changes the pathogenicit

A;Reference number: PL0184; PMID:90063468; PMID:2479706

A;Accession: PL0184

A;Molecule type: genomic RNA

A;Residues: 1-8 <ZUR>

C;Keywords: capsid protein

Query Match 21.6%; Score 19; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 NFP 15
| | | |
Db 6 NFP 8

RESULT 14

A61230

calsequestrin, cardiac and slow skeletal muscle - northern leopard frog (fragment)

C;Species: Rana pipiens (northern leopard frog)

C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C;Accession: A61230
R;McLeod, A.G.; Shen, A.C.Y.; Campbell, K.P.; Michalak, M.; Jorgensen, A.O.
Circ. Res. 69, 344-359, 1991
A;Title: Frog cardiac calsequestrin. Identification, characterization, and subcellular
distribution.
A;Reference number: A61230; MUID:91316784; PMID:1860177
A;Accession: A61230
A;Molecule type: protein
A;Residues: 1-9 <MCL>
A;Cross-references: UNIPROT:Q7LZ81
C;Comment: Calsequestrin is a high-capacity and moderate-affinity calcium binding protein
C;Comment: Calsequestrin acts as a calcium buffer, and the release of calcium bound to
C;Comment: The fast skeletal muscle isoform of calsequestrin can be phosphorylated in vi
C;Superfamily: calsequestrin
C;Keywords: calcium binding; cardiac muscle; glycoprotein; heart; phosphoprotein; skelet

Query Match 21.6%; Score 19; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 NFP 15
Db 5 NFP 7

RESULT 15
S66635
alpha-2-macroglobulin isoform 1 - bovine (fragment)
C;Species: Bos primigenius indicus (zebu cattle)
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S66635
R;Dolmer, K.; Jenner, L.B.; Jacobsen, L.; Andersen, G.R.; Koch, T.J.; Thirup, S.; Sottr
FEBS Lett. 372, 93-95, 1995
A;Title: Crystallisation and preliminary X-ray analysis of the receptor-binding domain c
A;Reference number: S66634; MUID:96032553; PMID:7556651
A;Accession: S66635
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <DOL>
A;Cross-references: UNIPROT:Q7M2N8

Query Match 21.6%; Score 19; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 DNFP 15
Db 2 DEFP 5

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 22, 2005, 08:52:23 ; Search time 65.6667 Seconds
(without alignments)
88.346 Million cell updates/sec

Title: US-08-991-628-4

Perfect score: 76

Sequence: 1 TFMFLSRNTGVRT 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 632537

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp19808:*

2: Geneseqp19908:*

3: Geneseqp20008:*

4: Geneseqp20018:*

5: Geneseqp20028:*

6: Geneseqp20038a:*

7: Geneseqp20038b:*

8: Geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	76	100.0	15	2 AAW04844	Aaw04844 Self epit
2	76	100.0	15	2 AAW64816	Aaw64816 Desmoglei
3	76	100.0	15	2 AAW78815	Aaw78815 Desmoglei
4	76	100.0	15	3 AAB33626	Aab33626 MHC class
5	76	100.0	15	4 AAG93722	Aag93722 Human des
6	76	100.0	15	5 AAO17034	Aao17034 Desmoglei
7	76	100.0	15	8 ABU96578	Abu96578 MHC class
8	76	100.0	15	8 ADQ14319	Adq14319 Human des
9	76	100.0	15	8 ADR41701	Adr41701 Desmoglei
10	76	100.0	15	8 ADS14311	Ads14311 Desmoglei
11	43	56.6	11	3 AAY63823	Aay63823 Desmoglei
12	43	56.6	11	5 ABA45875	Ab45875 Desmoglei
13	40	52.6	11	3 AAY63733	Aay63733 Desmoglei
14	40	52.6	11	5 ABB45785	Abb45785 Desmoglei
15	39	51.3	11	3 AAY63778	Aay63778 Desmoglei
16	39	51.3	11	5 AAY63688	Aay63688 Desmoglei
17	39	51.3	11	5 ABB45830	Abb45830 Desmoglei
18	39	51.3	11	5 ABB45740	Abb45740 Desmoglei
19	38	50.0	9	3 AAY63862	Aay63862 Desmoglei
20	38	50.0	9	3 AAY63599	Aay63599 Desmoglei
21	38	50.0	9	5 ABB45654	Abb45654 Non-class
22	38	50.0	9	5 ABB45371	Abb45371 Desmoglei
23	38	50.0	9	5 ABB45387	Abb45387 Desmoglei
24	38	50.0	9	5 ABB45914	Abb45914 Desmoglei
25	38	50.0	10	3 AAY63820	Aay63820 Desmoglei

26	38	50.0	10	5 ABB45872	Abb45872 Desmoglei
27	38	50.0	11	3 AAY63643	Aay63643 Desmoglei
28	38	50.0	11	5 ABB45695	Abb45695 Desmoglei
29	35	46.1	10	3 AAY63730	Aay63730 Desmoglei
30	35	46.1	10	5 ABB45782	Abb45782 Desmoglei
31	35	46.1	11	3 AAY61096	Aay61096 Cadherin-
32	34	44.7	10	3 AAY63685	Aay63685 Desmoglei
33	34	44.7	10	3 AAY63775	Aay63775 Desmoglei
34	34	44.7	10	5 ABB45827	Abb45827 Desmoglei
35	34	44.7	10	5 ABB45737	Abb45737 Desmoglei
36	33	43.4	8	3 AAY63596	Aay63596 Desmoglei
37	33	43.4	8	3 AAY63859	Aay63859 Desmoglei
38	33	43.4	8	5 ABB45368	Abb45368 Desmoglei
39	33	43.4	8	5 ABB45911	Abb45911 Desmoglei
40	33	43.4	10	3 AAY61093	Aay61093 Cadherin-
41	33	43.4	10	3 AAY63640	Aay63640 Desmoglei
42	33	43.4	10	5 ABB45692	Abb45692 Desmoglei
43	33	43.4	11	3 AAY61477	Aay61477 Cadherin-
44	33	43.4	11	3 AAY61636	Aay61636 Cadherin-
45	33	43.4	15	2 AAW04842	Aaw04842 Self epit

ALIGNMENTS

RESULT 1

AAW04844

ID AAW04844 standard; peptide; 15 AA.

AC AAW04844;

DT 18-FEB-1997 (first entry)

DE Self epitope of desmoglein 3, implicated in autoimmune disease.

XX Tolerisation; self-epitope; antigen; autoimmune disease; autoantigen;
KW HLA; human leukocyte antigen; T-cell; thymocyte; pemphigus vulgaris;
KW desmoglein; multiple sclerosis; herpes simplex virus; adenovirus;
KW phosphomannomutase; human papillomavirus; Epstein-Barr virus;
KW DNA polymerase; influenza; haemagglutinin; reovirus; sigma protein.

XX Homo sapiens.

XX WO9627387-A1.

XX 12-SEP-1996.

XX 07-MAR-1996; 96WO-US003182.

XX 07-MAR-1995; 95US-00400796.

(HARD) HARVARD COLLEGE.

PI Strominger JL, Wuchterfennig KW;

XX WPI; 1996-425218/42.

XX Pemphigus vulgaris auto-antigens and multiple sclerosis non-self antigens
PT - useful in disease treatment, and method for identification of other
XX self and non-self antigens implicated in auto-immune disease.

Claim 1; Page 40; 58pp; English.

XX Pharmaceutical preparations for tolerisation to antigens comprise either
CC an isolated human non-collagen or non-mysin basic protein (MBP)
CC polypeptide which is capable of tolerising an individual to an
CC autoantigen; or an isolated human pathogen polypeptide capable of
CC tolerising an individual to that polypeptide. In both cases, the
CC polypeptide (whether self or non-self) includes an amino acid sequence
CC corresponding to a sequence motif for a MHC class II protein, such as HLA
CC -DR, which is associated with a human autoimmune disease and which binds
CC to the polypeptide to activate autoreactive T-cells in individuals with
CC the autoimmune disease. This peptide is derived from the human desmoglein

CC 3 protein (amino acids 206-220) and is implicated as a self epitope in
CC pemphigus vulgaris. Peptides derived from the human desmoglein protein
CC are described in AAW04841-47
XX
SQ Sequence 15 AA;
Query Match 100.0%; Score 76; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TPMFLLSRNTGEVRT 15
| | | | | | | | | | | | | | | |
Db 1 TPMFLLSRNTGEVRT 15
| | | | | | | | | | | | | | | |
RESULT 2
AAW64816
ID AAW64816 standard; peptide; 15 AA.
XX
AC AAW64816;
XX
DT 29-SEP-1998 (first entry)
XX
DE Desmoglein-3 206-220.
XX
KW Desmoglein; DG; gene therapy; pemphigus vulgaris; microparticle;
KW autoantigen; autoimmune disease; MHC.
OS Homo sapiens.
XX
PN US5783567-A.
XX
PD 21-JUL-1998.
XX
PF 22-JAN-1997; 97US-00787547.
XX
PR 22-JAN-1997; 97US-00787547.
XX
PA (PANG-) PANGAEA PHARM INC.
XX
PI Langer RS, Hedley ML, Curley JM;
XX WPI; 1998-427077/36.
XX
DR Microparticle encapsulated nucleic acids - for recombinant expression of
XX proteins e.g. in gene therapy.
XX
PS Disclosure; Col 4; 42pp; English.
XX
CC The patent describes a new preparation of microparticles each comprising
CC a polymeric matrix and a nucleic acid. The polymeric matrix consists of
CC one or more synthetic polymers having a solubility in water of less than
CC 1 mg/l (e.g. poly-lactic-co-glycolic acid); and at least 90% of the
CC microparticles have a diameter of less than 100 microns. The
CC microparticles are useful for the delivery of nucleic acids to phagocytic
CC cells. In one embodiment the microparticles are less than 20 microns in
CC diameter and the nucleic acid (preferably in closed circular form)
CC includes an expression control sequence operatively linked to a coding
CC sequence, where the expression product of the coding sequence is a
CC polypeptide having a length and a sequence which permits it to bind to an
CC MHC class I or II molecule. The expression product is thus an effective
CC stimulator of an immune response in mammals. The present sequence, an
CC antigenic portion of desmoglein 3, is an example of an MHC class II
CC peptide which can be expressed by the nucleic acid. It is associated with
CC pemphigus vulgaris
XX
SQ Sequence 15 AA;
Query Match 100.0%; Score 76; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TPMFLLSRNTGEVRT 15
| | | | | | | | | | | | | | | |

Db 1 TPMFLLSRNTGEVRT 15
| | | | | | | | | | | | | | | |
RESULT 3
AAW78815
ID AAW78815 standard; peptide; 15 AA.
XX
AC AAW78815;
XX
DT 17-NOV-1998 (first entry)
XX
DE Desmoglein 3 protein fragment 206-220.
XX
KW Microparticle; delivery; polymeric matrix; autoantigen; tumour antigen;
KW class II associated peptide; pathogen; gene therapy; genetic disease;
KW infection; downregulation; immune response.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO9831398-A1.
XX
PD 23-JUL-1998.
XX
PF 22-JAN-1998; 98WO-US001499.
XX
PR 22-JAN-1997; 97US-00787547.
PR 06-JAN-1998; 98US-00003253.
XX
PA (PANG-) PANGAEA PHARM INC.
XX
PI Hedley ML, Curley JM, Langer RS, Lunsford LB;
XX WPI; 1998-427556/36.
XX
DR New preparations of microparticles - comprising a synthetic polymer
XX matrix and nucleic acid comprising an expression vector for use in gene
XX therapy.
XX
PS Disclosure; Page 8; 101pp; English.
XX
CC A microparticle preparation (MP) has been developed, consisting of
CC microparticles having a diameter of less than 100 mu m. The MP comprises:
CC (a) a polymeric matrix (PM) consisting of one or more synthetic polymers
CC having a solubility in water of less than 1 mg/l; and (b) an expression
CC vector selected from RNA molecules (at least 50% of which are closed
CC circles) or circular plasmid DNA (at least 50% of which are supercoiled).
CC Also described is a MP of at most 20 microns in diameter, comprising: (a)
CC a PM; and (b) a NAM comprising an expression control sequence operatively
CC linked to a coding sequence, where the coding sequence encodes an
CC expression product selected from: (i) a polypeptide at least 7 amino
CC acids in length, having a sequence identical to the sequence of: (i) a
CC fragment of a naturally-occurring mammalian protein; or (ii) a fragment
CC of a naturally-occurring protein from an infectious agent which infects a
CC mammal; (2) a peptide having a length and sequence which permits it to
CC bind to an MHC class I or II molecule; and (3) the polypeptide or the
CC peptide linked to a trafficking sequence. AAW69763 to AAW69765, and
CC AAW78793 to AAW78897 are peptide fragments for use in the present
CC invention. The MPs are highly effective vehicles for the delivery of
CC polynucleotides into phagocytic cells. They can be used for gene therapy,
CC e.g. for treating genetic diseases, infections or tumours or for
CC downregulating an immune response
XX
SQ Sequence 15 AA;
Query Match 100.0%; Score 76; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TPMFLLSRNTGEVRT 15
| | | | | | | | | | | | | | | |
Db 1 TPMFLLSRNTGEVRT 15
| | | | | | | | | | | | | | | |

RESULT 4
AAB33626
ID AAB33626 standard; peptide; 15 AA.
XX
AC AAB33626;
XX
DT 26-JAN-2001 (first entry)
XX
DE MHC class II associated immunogenic peptide SEQ ID 25.
XX
KW Microparticle; nucleic acid delivery; immunogenic peptide; MHC I; MHC II;
KW major histocompatibility complex; vaginal tissue; mucosal tissue.
XX
OS Unidentified.
XX WO200053161-A2.
XX
PD 14-SEP-2000.
XX
PF 10-MAR-2000; 2000WO-US006578.
XX
PR 11-MAR-1999; 99US-00266463.
PR 27-MAY-1999; 99US-00321346.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Lunsford LB, Putnam D, Hedley ML;
XX
DR WPI; 2000-638130/61.
XX
PT Microparticles useful for administering a nucleic acid into the mucosal
PT tissue preferably vaginal tissue of an animal, comprises a polymeric
PT matrix, a lipid and a nucleic acid molecule.
XX
PS Claim 25; Page 11; 96pp; English.
XX
CC The present invention relates to microparticles which are less than 20
CC microns in diameter, which comprise a polymeric matrix, a lipid and a
CC nucleic acid molecule. The microparticle is specifically not encapsulated
CC in a liposome and does not comprise a cell. The nucleotide sequence
CC encodes an expression product that binds to major histocompatibility
CC complex (MHC) type I or II molecules. Peptides AAB33602-B33647 represent
CC MHC class II associated immunogenic peptides, and AAB33648-B33710
CC represent MHC class I associated immunogenic peptides. The peptides are
CC examples of the expression products of the nucleotide sequences which can
CC be included in the microparticles of the invention. Sequences AAB33711-
CC B33716 represent alternative expression products and nuclear localisation
CC signals also used in the invention. The microparticles are useful for
CC administering a nucleic acid into the mucosal tissue preferably vaginal
CC tissue of an animal
XX
SQ Sequence 15 AA;
Query Match 100.0%; Score 76; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TPMFLLSRNTGVRT 15
DB 1 TPMFLLSRNTGVRT 15
RESULT 5
AAG93722
ID AAG93722 standard; peptide; 15 AA.
XX
AC AAG93722;
XX
DT 17-SEP-2001 (first entry)
XX
DE Human desmoglein 3 peptide 2.

XX Continuous flow production; microparticle; gene therapy;
KW antisense therapy; vaccination; treatment; autoimmune disease;
KW immune response modulation.
XX
OS Homo sapiens.
XX
XX WO200136583-A1.
XX
PD 25-MAY-2001.
XX
PF 17-NOV-2000; 2000WO-US031770.
XX
PR 19-NOV-1999; 99US-00443654.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Hedley ML, Hsu Y, Tyo M;
XX
DR WPI; 2001-425203/45.
XX
CC Continuous production of microparticles containing nucleic acid for e.g.
CC gene therapy, comprises mixing a solution of polymeric material and
CC nucleic acid with a surfactant solution, removing solvent and drying.
XX
PS Disclosure; Page 9; 47pp; English.
XX
CC The present sequence is that of a peptide of the invention. The invention
CC relates to a method for scalable, continuous flow production of a nucleic
CC acid containing microparticle that maintains the structural integrity of
CC the associated nucleic acid and results in a microparticle having purity
CC suitable for introduction into an animal host. Microparticles prepared
CC according to the method can be used for delivery of a nucleic acid for
CC gene therapy, antisense therapy, vaccination, treatment of autoimmune
CC disease and either specific or non-specific modulation of an immune
CC response. The microparticles may also be used to deliver nucleic acid
CC encoding a protein or peptide useful in any kind of therapy. The method
CC is economical, aseptic and scalable. The method also enables control over
CC the size of microparticles. The microparticles produced are free of
CC impurities such as organic solvents and are readily dispersed in a wide
CC range of dispersing agents
XX
SQ Sequence 15 AA;
Query Match 100.0%; Score 76; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 TPMFLLSRNTGVRT 15
DB 1 TPMFLLSRNTGVRT 15
RESULT 6
AAO17034
ID AAO17034 standard; peptide; 15 AA.
XX
AC AAO17034;
XX
DT 29-MAY-2002 (first entry)
XX
DE Desmoglein 3 residues 206-220 SEQ ID NO: 31.
XX
KW Alpha-MSH; inflammation; autoimmune disease; gene therapy; sepsis;
KW alpha-melanocyte stimulating hormone; rheumatoid arthritis; asthma;
KW cirrhosis; dermatitis; psoriasis; inflammatory bowel disease;
KW immunosuppressive; antinflammatory; antirheumatic; antiarthritic;
KW antiasthmatic; antibacterial; dermatological; antipsoriatic;
KW antidiabetic; ophthalmological; neuroprotective; multiple sclerosis;
KW diabetes; uveitis; coeliac disease.
XX
OS Unidentified.

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PN WO200206316-A2.
XX
PD 24-JAN-2002.
XX
PF 16-JUL-2001; 2001WO-US022263.
XX
PR 14-JUL-2000; 2000US-0218381P.
PR 18-AUG-2000; 2000US-0226382P.
PR 06-OCT-2000; 2000US-0238380P.
PR 29-DEC-2000; 2000US-0258764P.
PR 14-JUN-2001; 2001US-0298317P.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Hedley ML, Urban R, Aziz N, Chen H, Etemad-Moghadam B, Yin P;
XX WPI; 2002-195801/25.
XX
PT Novel nucleic acid encoding fusion protein comprising alpha-melanocyte
PT stimulating hormone concatamer or its analog, for treating inflammatory
PT or autoimmune disorders.
XX
PS Disclosure; Page 26; 89pp; English.
XX
CC The present invention relates to a nucleic acid comprising a sequence
CC encoding a fusion polypeptide having an alpha-melanocyte stimulating
CC hormone (MSH) concatamer. The sequences are useful for treating an
CC individual suffering from, or at risk of, a disorder of the immune system
CC e.g. inflammatory disorder or autoimmune disorder, including rheumatoid
CC arthritis, asthma, sepsis, cirrhosis, dermatitis, psoriasis, contact
CC hypersensitivity, inflammatory bowel disease, autoimmune encephalitis,
CC multiple sclerosis, diabetes, lupus, uveitis and coeliac disease. The
CC present sequence is a peptide described in the exemplification of the
CC invention
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 76; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TPMFLLSRNTGEVRT 15
Db |||||
1 TPMFLLSRNTGEVRT 15

RESULT 7
ABU96578
ID ABU96578 standard; peptide; 15 AA.
XX
AC ABU96578;
XX
DT 12-AUG-2003 (first entry)
XX
DE MHC class II associated desmoglein 3 peptide 206-220.
XX
KW Microparticle; microsphere; polynucleotide delivery; phagocytic cell;
KW tumour; viral infection; bacterial infection; fungal infection;
KW protozoan infection; gene therapy; major histocompatibility complex;
KW MHC class II.
XX
OS Unidentified.
XX
PN US2002182258-A1.
XX
PD 05-DEC-2002.
XX
PF 18-JUL-2001; 2001US-00909460.
XX
PR 22-JAN-1997; 97US-0035983P.
PR 06-JAN-1998; 98US-00003253.
PR 22-JAN-1998; 98WO-US001499.
PR 11-MAR-1999; 99US-00266463.

PR 27-MAY-1999; 99US-00321346.
XX
PA (ZYCO-) ZYCOS INC.
XX
PI Lunsford LB, Putnam D, Hedley ML;
XX WPI; 2003-438782/41.
XX
PT Microparticles, useful as vehicles for delivery of polynucleotides to
PT phagocytic cells, comprises polymeric matrix, lipid, and nucleic acid
PT molecule.
XX
PS Disclosure; Page 3; 37pp; English.
XX
CC The invention relates to a microparticle (microsphere) less than 20
CC microns in diameter that comprises: (1) a polymeric matrix; (2) a lipid;
CC and (3) a nucleic acid molecule. The microparticle is not encapsulated in
CC a liposome and the microparticle does not comprise a cell. The
CC microparticles are used as vehicles for the delivery of polynucleotides
CC into phagocytic cells. The microparticles can be used to express antigens
CC to treat tumour cells or viral, bacterial, fungal or protozoan
CC infections. The microparticles can be made without adversely affecting
CC nucleic acid integrity. The present sequence represents the amino acid
CC sequence of a major histocompatibility complex, MHC, class II associated
CC peptide
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 76; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TPMFLLSRNTGEVRT 15
Db |||||
1 TPMFLLSRNTGEVRT 15

RESULT 8
ADQ14319
ID ADQ14319 standard; peptide; 15 AA.
XX
AC ADQ14319;
XX
DT 07-OCT-2004 (first entry)
XX
DE Human desmoglein 3 (DSG3) antigenic determinant (residues 206-220).
XX
KW Notch signalling; modulator; antigen; antigenic determinant;
KW immunomodulator; immune disorder; immune response; immune tolerance;
KW peripheral T-cell activation; regulatory T-cell; T reg; tumour; cancer;
KW autoimmune disorder; allergy; transplant rejection; immunosuppressive;
KW cytostatic; antiallergic; vaccine; human; autoantigen; desmoglein 3;
KW DSG3; pemphigus; MHC class II peptide; major histocompatibility complex;
KW antigenic determinant; epitope.
XX
OS Homo sapiens.
XX
PN WO2004060262-A2.
XX
PD 22-JUL-2004.
XX
PF 07-JAN-2004; 2004WO-GB0000046.
XX
PR 07-JAN-2003; 2003GB-00000234.
PR 23-JAN-2003; 2003GB-00001510.
PR 23-JAN-2003; 2003GB-00001512.
PR 23-JAN-2003; 2003GB-00001513.
PR 23-JAN-2003; 2003GB-00001515.
PR 23-JAN-2003; 2003GB-00001518.
PR 23-JAN-2003; 2003GB-00001519.
PR 23-JAN-2003; 2003GB-00001521.
PR 23-JAN-2003; 2003GB-00001522.
PR 23-JAN-2003; 2003GB-00001524.

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PR 23-JAN-2003; 2003GB-00001526.
 PR 23-JAN-2003; 2003GB-00001527.
 PR 23-JAN-2003; 2003GB-00001529.
 PR 22-MAR-2003; 2003GB-00006621.
 PR 04-APR-2003; 2003WO-GB0001525.
 PR 24-MAY-2003; 2003GB-00012062.
 PR 01-AUG-2003; 2003GB-GB003285.
 PR 03-OCT-2003; 2003GB-00023130.
 XX
 PA (LORA-) LORANTIS LTD.
 XX
 PI Bodner MW, Briend ECP, Champion BR, Lennard AC, McKenzie GJ;
 PI Tugal T, Ward GA, Young LL;
 XX
 XX WPI; 2004-534298/51.
 XX
 XX New product for modulating the immune system, comprises a pharmaceutical
 PT support matrix bearing modulators of Notch signaling, and an antigen or
 PT antigenic determinant, or a polynucleotide coding for the antigen or
 PT determinant.
 XX
 PS Disclosure; Page 126; 294pp; English.
 XX
 CC The invention relates to a product comprising (1) a pharmaceutical
 CC support matrix for in vivo administration bearing modulators of Notch
 CC signalling (especially a Delta or Serrate/Jagged protein or fragment or
 CC homologue thereof); and (2) an antigen or antigenic determinant, or
 CC polynucleotide encoding an antigen or antigenic determinant. The product
 CC acts as a combined preparation for modulation of the immune system or for
 CC modulation of an immune response to the antigen or antigenic determinant.
 CC The invention also relates to a pharmaceutical composition comprising the
 CC product; a particle with a maximum linear dimension of less than 500
 CC (preferably 30-70) nm having several bound modulators of Notch signalling
 CC; a method of modulating Notch signalling; methods of treating an immune
 CC disorder, for reducing an immune response, for promoting immune tolerance
 CC in a mammal; and a method for increasing an immune response to a tumour
 CC or pathogen antigen or its antigenic determinant in a mammal. The
 CC composition and methods are useful for modulating peripheral T-cell
 CC activation, for generating regulatory T-cells (T reg), for reducing an
 CC immune response to an antigen or antigenic determinant, for promoting
 CC immune tolerance to an antigen or antigenic determinant, or for treating
 CC tumours, autoimmune disease, allergies or transplant rejection. The
 CC present sequence represents an antigenic determinant derived from a human
 CC autoantigen which may be used in a product of the invention.
 XX
 SQ Sequence 15 AA;
 Query Match 100.0%; Score 76; DB 8; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.5e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TPFLLSRNTGVRT 15
 Db 1 TPFLLSRNTGVRT 15
 RESULT 9
 ADR41701
 ID ADR41701 standard; peptide; 15 AA.
 AC ADR41701;
 XX
 XX 21-OCT-2004 (first entry)
 DT
 XX Desmoglein 3 (DSG3) (aa 206-220), class II MHC associated autoantigen.
 DE
 XX DSG3; Desmoglein 3; autoantigen; notch signalling pathway;
 KW autoimmune disorder; bystander effect; suppression; DSL domain;
 KW EGF domain; Goodpasture's disease; Wegener's granulomatosis; anaemia;
 KW thrombocytopenia; gastritis; hepatitis; vasculitis; scleroderma;
 KW myositis; arthritis; systemic lupus erythematosus; SLE;
 KW Sjogren's syndrome; hepatic fibrosis; liver cirrhosis; thyroiditis;
 KW dermatitis; placental dysfunction; eclampsia;

KW inflammatory related gynaecological disease; neurodegenerative disorder;
 KW Alzheimer's disease; Parkinson's disease; Huntington disease;
 KW encephalitis; psychiatric disorder; Down's syndrome; stroke; exogenous;
 KW bystander antigen; multiple sclerosis; delta serrate lag;
 KW inflammatory bowel disease; notch receptor.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX WO2004064863-A1.
 PN
 XX
 XX 05-AUG-2004.
 PD
 XX
 XX 23-JAN-2004; 2004WO-GB000263.
 PF
 XX
 PR 23-JAN-2003; 2003GB-00001510.
 PR 23-JAN-2003; 2003GB-00001512.
 PR 23-JAN-2003; 2003GB-00001513.
 PR 23-JAN-2003; 2003GB-00001515.
 PR 23-JAN-2003; 2003GB-00001518.
 PR 23-JAN-2003; 2003GB-00001519.
 PR 23-JAN-2003; 2003GB-00001521.
 PR 23-JAN-2003; 2003GB-00001522.
 PR 23-JAN-2003; 2003GB-00001524.
 PR 23-JAN-2003; 2003GB-00001526.
 PR 23-JAN-2003; 2003GB-00001527.
 PR 23-JAN-2003; 2003GB-00001529.
 PR 04-APR-2003; 2003WO-GB0001525.
 PR 24-MAY-2003; 2003GB-00012062.
 PR 01-AUG-2003; 2003WO-GB003285.
 PR 03-OCT-2003; 2003GB-00023130.
 PR 07-JAN-2004; 2004WO-GB000046.
 XX
 PA (LORA-) LORANTIS LTD.
 XX
 XX Champion BR, Ragno S, Young LL;
 PI WPI; 2004-562091/54.
 XX
 XX New product having a modulator of the Notch signaling pathway, useful for
 PT modulating an immune response in autoimmune disorders, such as anemia,
 PT gastritis, hepatitis, scleroderma and myositis.
 XX
 PS Disclosure; Page 66; 244pp; English.
 XX
 CC The invention relates to the modulation of immune function through a
 CC notch signalling pathway for the prevention of autoimmune diseases. It
 CC has been found that the notch signalling pathway provides a bystander
 CC effect or bystander suppression effect, which can be used in a wide
 CC variety of ways to suppress unwanted immune responses in immune diseases
 CC and disorders. Autoimmune diseases are characterised by immune responses
 CC that are directed against self antigens. T lymphocytes are activated upon
 CC recognition of a self antigen and/or a foreign antigen as a complex with
 CC self major histocompatibility complex (MHC) gene products on the surface
 CC of antigen presenting cells (APC). The invention provides the method of
 CC modulating of an immune response, modulator information and a
 CC pharmaceutical kit for suppression of an immune response. The modulator
 CC of the notch signalling pathway is an agent which activates the notch
 CC receptor or a polynucleotide which codes for such an agent. It comprises
 CC a protein or polypeptide comprising a notch ligand DSL (delta serrate
 CC lag) domain, notch ligand EGF domain, optionally all or part of a notch
 CC ligand N terminal domain, and optionally one or more heterologous amino
 CC acid or a polynucleotide sequences. The modulator can be a fusion protein
 CC comprising a segment of a notch ligand extracellular domain and an
 CC immunoglobulin Fc segment. The disorders include Goodpasture's disease,
 CC Wegener's granulomatosis, autoimmune anaemia, thrombocytopenia,
 CC gastritis, autoimmune hepatitis, inflammatory bowel disease, autoimmune
 CC vasculitis, scleroderma, myositis, autoimmune arthritis, Systemic Lupus
 CC Erythematosus (SLE) or Sjogren's syndrome, hepatic fibrosis, liver
 CC cirrhosis, thyroiditis, dermatitis, placental dysfunction, eclampsia,
 CC inflammatory related gynaecological diseases, neurodegenerative disorders
 CC (such as Alzheimer's disease, Parkinson's disease, Huntington disease)
 CC encephalitis, psychiatric disorders, Down's syndrome, stroke, multiple

CC sclerosis, etc. The invention discloses a method for generating immune
 CC suppression at a disease locus by administering an exogenous antigen. It
 CC also provides the use of modulator or activator of notch signalling in
 CC simultaneous, separate or sequential combination with a bystander antigen
 CC or antigenic determinant for reducing an immune response to a target
 CC antigen. The presented protein sequence is the desmoglein 3 (DSG3) (aa
 CC 206-220), class II MHC associated autoantigen.

XX Sequence 15 AA;

Query Match 100.0%; Score 76; DB 8; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.5e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPMFLLSRNTGEVRT 15

DB 1 TPMFLLSRNTGEVRT 15

RESULT 10
 ADS14311
 ID ADS14311 standard; peptide; 15 AA.
 XX
 AC ADS14311;
 XX
 DT 16-DEC-2004 (first entry)
 XX
 DE Desmoglein 3 antigenic peptide residues 206-220.

XX Cytostatic; Immunosuppressive; Antidiabetic; Neuroprotective;
 KW Antiarthritic; Antirheumatic; Antiallergic; Vaccine; Notch signaling;
 KW Notch; Notch ligand; Delta protein; Serrate protein; Jagged protein;
 KW multiple sclerosis; rheumatoid arthritis; diabetes; allergy;
 KW immune disorder; autoimmune disease; graft rejection; cancer;
 KW organ transplant; desmoglein 3.

XX Unidentified.

XX WO2004083372-A2.

XX 30-SEP-2004.

XX 22-MAR-2004; 2004WO-GB001229.

XX 21-MAR-2003; 2003GB-00006582.

XX 21-MAR-2003; 2003GB-00006583.

XX 22-MAR-2003; 2003GB-00006621.

XX 22-MAR-2003; 2003GB-00006622.

XX 22-MAR-2003; 2003GB-00006624.

XX 22-MAR-2003; 2003GB-00006626.

XX 22-MAR-2003; 2003GB-00006640.

XX 22-MAR-2003; 2003GB-00006644.

XX 22-MAR-2003; 2003GB-00006650.

XX 22-MAR-2003; 2003GB-00006651.

XX 22-MAR-2003; 2003GB-00006654.

XX (LORA-) LORANTIS LTD.

XX Champion BR, Ragno S;
 XX WPI; 2004-709927/69.

XX Particle capable of being inserted into or taken up by cell useful for
 PT modulating immune response to antigen in subject, comprises
 PT polynucleotide coding for modulator of Notch signaling, and
 PT polynucleotide coding for antigen.
 XX Disclosure; Page 119; 278pp; English.

XX The present invention relates to a particle (I) capable of being inserted
 CC into or taken up by a cell comprising (i) a polynucleotide coding for a
 CC modulator of Notch signaling, and (ii) a polynucleotide coding for an
 CC antigen or antigenic determinant. The first polynucleotide sequence codes

CC for a Notch ligand such as a Delta or Serrate/Jagged protein or its
 CC fragment, derivative, homologue, analogue or allelic variant, or for a
 CC protein which comprises a Notch ligand DSL domain and at least one Notch
 CC ligand EGF-like domain and optionally a membrane binding or transmembrane
 CC domain. The first and second sequences are operably linked to one or more
 CC promoters or enhancers or polyadenylation sequences. The antigen or
 CC antigenic determinant is an allergen, autoantigen, Major
 CC histocompatibility complex (MHC) (transplant) antigen, pathogen antigen,
 CC tumour antigen or their antigenic determinant. (I) is useful for
 CC modulating an immune response to an antigen in a subject. Pharmaceutical
 CC compositions comprising (I) are useful for treating or preventing
 CC conditions mediated by T cells, such as multiple sclerosis, rheumatoid
 CC arthritis, diabetes, allergy, for treating immune disorders such as
 CC autoimmune diseases of graft rejection such as allograft rejection,
 CC treating cancer and organ transplants. The present sequence is a
 CC desmoglein 3 antigenic peptide (a class II MHC-associated autoantigen
 CC peptide), which can be used as an antigen to prepare the particle of the
 CC invention.

XX Sequence 15 AA;

Query Match 100.0%; Score 76; DB 8; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.5e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TPMFLLSRNTGEVRT 15

DB 1 TPMFLLSRNTGEVRT 15

RESULT 11
 AAY63823
 ID AAY63823 standard; peptide; 11 AA.

XX AAY63823;

XX 02-MAR-2000 (first entry)

XX Desmoglein cell adhesion recognition cyclic peptide SEQ ID NO:3275.

XX Modulation; nonclassical cadherin mediated cell adhesion; CAR;
 KW inhibition; cadherin extracellular domain; cell adhesion recognition;
 KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;
 KW cadherin-14; cadherin-15; T-cadherin; PB-cadherin;
 KW cadherin related neuronal receptor; LI-cadherin; protocadherin;
 KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
 KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
 KW neurological disease; cyclic.

OS Synthetic.

OS Homo sapiens.

XX Key Location/Qualifiers

XX Modified-site 1..11

XX /note= "the terminal residues are condensed with each
 XX other to form a cyclic peptide"

XX WO9957149-A2.

XX 11-NOV-1999.

XX 05-MAY-1999; 99WO-CA000363.

XX 05-MAY-1998; 98US-00073040.

XX 06-NOV-1998; 98US-00187859.

XX 20-JAN-1999; 99US-00234395.

XX 08-MAR-1999; 99US-00264516.

XX (ADHE-) ADHEREX TECHNOLOGIES INC.

XX Blaschuk OW, Gour BJ, Byers S;

XX WPI; 2000-038791/03.

XX New cadherin modulating agents, used for modulating nonclassical cadherin
 PT -mediated functions for treating e.g. cancers, obesity, rheumatoid
 PT arthritis, multiple sclerosis, diabetes or a neurological disease.
 XX
 XX Claim 90; Page 209; 252pp; English.

XX The present invention describes cadherin modulating agents (MA)
 CC comprising peptides which comprise a nonclassical cadherin cell adhesion
 CC recognition (CAR) sequence. The MAs can be used for modulating
 CC nonclassical cadherin-mediated functions. They can be used for e.g.
 CC inhibiting adhesion of nonclassical-cadherin expressing cells in a
 CC mammal, enhancing delivery of a drug through the skin of a mammal,
 CC enhancing delivery of a drug to a tumour in a mammal, treating cancer in
 CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting
 CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
 CC expressing cell, preventing or treating obesity in a mammal, stimulating
 CC blood vessel regression in a mammal, enhancing drug delivery to the
 CC central nervous system, treating a demyelinating neurological disease,
 CC increasing vasopermeability in a mammal, enhancing adhesion of
 CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in
 CC a mammal, or preventing pregnancy in a mammal. They can also be used for
 CC e.g. enhancing or directing neurite outgrowth, facilitating wound healing
 CC or reducing scar tissue, or enhancing adhesion of foreign tissue in a
 CC mammal. They can also be used for treating e.g. psoriasis, arthritis, age
 CC -related macular degeneration, multiple sclerosis and diabetes. The
 CC products can also be used for detection and diagnosis and in bioreactors.
 CC AAY60592 to AAY64572 represent specifically claimed peptides, and
 CC AAY64573 to AAY64643 and AAZ33183 to AAZ33186 represent sequences used in
 CC the exemplification of the present invention

XX Sequence 11 AA;

Query Match 56.6%; Score 43; DB 3; Length 11;
 Best Local Similarity 70.0%; Pred. No. 0.88;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 MFLLSRNTGGE 12
 ||:|||||
 DB 2 MFIINRNTGGE 11

RESULT 12
 ABB45875
 ID ABB45875 standard; peptide; 11 AA.

AC ABB45875;

XX 30-JAN-2002 (first entry)

DE Desmoglein CAR sequence cyclic peptide SEQ ID NO 619.

XX Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
 KW cytostatic; antiapoptotic; wound healing; reduce scar tissue; skin graft;
 KW organ implant; autoimmune blistering disorder; cancer; apoptosis; cyclic.
 XX Synthetic.

XX WO200172956-A2.

XX 04-OCT-2001.

XX 27-MAR-2001; 2001WO-IB001400.

XX 27-MAR-2000; 2000US-00535852.

XX (ADHE-) ADHEREX TECHNOLOGIES INC.

XX Blaschuk OW, Symonds JM, Gour BJ;

XX WPI; 2002-025778/03.

XX Modulating agents for inhibiting or enhancing desmosomal cadherin

PT mediated cell adhesion, useful for facilitating wound healing and/or
 PT reducing scar tissue, treating cancer and inducing apoptosis.

XX Claim 18; Page 99; 127pp; English.

XX The invention relates to modulating agents for inhibiting or enhancing
 CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
 CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
 CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
 CC sequence, a substance such as an antibody or antigen-binding fragment
 CC that specifically binds a desmosomal cadherin CAR sequence and/or a
 CC polynucleotide encoding a polypeptide that comprises a desmosomal
 CC cadherin CAR sequence or analogue. The modulating agents have
 CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
 CC facilitate wound healing and/or reduce scar tissue, for enhancing
 CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
 CC treating an autoimmune blistering disorder and to treat cancer (e.g.
 CC carcinoma, leukaemia or melanoma) and induce apoptosis

XX Sequence 11 AA;

Query Match 56.6%; Score 43; DB 5; Length 11;
 Best Local Similarity 70.0%; Pred. No. 0.88;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 MFLLSRNTGGE 12
 ||:|||||
 DB 2 MFIINRNTGGE 11

RESULT 13

AAY63733

ID AAY63733 standard; peptide; 11 AA.

AC AAY63733;

XX 02-MAR-2000 (first entry)

DE Desmoglein cell adhesion recognition cyclic peptide SEQ ID NO:3185.

XX Modulation; nonclassical cadherin mediated cell adhesion; CAR;
 KW inhibition; cadherin extracellular domain; cell adhesion recognition;
 KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;
 KW cadherin-14; cadherin-15; T-cadherin; PB-cadherin;
 KW cadherin related neuronal receptor; LI-cadherin; protocadherin;
 KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
 KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
 KW neurological disease; cyclic.

XX Synthetic.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 1..11

FT /note= "the terminal residues are condensed with each
 other to form a cyclic peptide"

XX WO9557149-A2.

XX 11-NOV-1999.

XX 05-MAY-1999; 99WO-CA000363.

XX 05-MAY-1998; 98US-00073040.

XX 06-NOV-1998; 98US-00187859.

XX 20-JAN-1999; 99US-00234395.

XX 08-MAR-1999; 99US-00264516.

XX (ADHE-) ADHEREX TECHNOLOGIES INC.

XX Blaschuk OW, Gour BJ, Byers S;

XX WPI; 2000-038791/03.

XX New cadherin modulating agents, used for modulating nonclassical cadherin
PT -mediated functions for treating e.g. cancers, obesity, rheumatoid
PT arthritis, multiple sclerosis, diabetes or a neurological disease.
XX
XX Claim 90; Page 208; 252pp; English.
XX
XX The present invention describes cadherin modulating agents (MA)
CC comprising peptides which comprise a nonclassical cadherin cell adhesion
CC recognition (CAR) sequence. The MAs can be used for modulating
CC nonclassical cadherin-mediated functions. They can be used for e.g.
CC inhibiting adhesion of nonclassical-cadherin expressing cells in a
CC mammal, enhancing delivery of a drug through the skin of a mammal,
CC enhancing delivery of a drug to a tumour in a mammal, treating cancer in
CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting
CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
CC expressing cell, preventing or treating obesity in a mammal, stimulating
CC blood vessel regression in a mammal, enhancing drug delivery to the
CC central nervous system, treating a demyelinating neurological disease,
CC increasing vasopermeability in a mammal, enhancing adhesion of
CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in
CC a mammal, or preventing pregnancy in a mammal. They can also be used for
CC e.g. enhancing or directing neurite outgrowth, facilitating wound healing
CC or reducing scar tissue, or enhancing adhesion of foreign tissue in a
CC mammal. They can also be used for treating e.g. psoriasis, arthritis, age
CC -related macular degeneration, multiple sclerosis and diabetes. The
CC products can also be used for detection and diagnosis and in bioreactors.
CC AA60592 to AA64572 represent specifically claimed peptides, and
CC AA64573 to AA64643 and AA233183 to AA233186 represent sequences used in
CC the exemplification of the present invention
XX
XX Sequence 11 AA;

Query Match 52.6%; Score 40; DB 3; Length 11;
Best Local Similarity 60.0%; Pred. NO. 3.1;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MFLLSRNTGE 12
| | | | | | | | | | | | | |
Db 2 MFIINRNTGD 11

RESULT 14
ABB45785
ID ABB45785 standard; peptide; 11 AA.

AC ABB45785;

XX 30-JAN-2002 (first entry)

DE Desmoglein CAR sequence cyclic peptide SEQ ID NO 529.

XX Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
KW cytosolic; antiapoptotic; wound healing; reduce scar tissue; skin graft;
KW organ implant; autoimmune blistering disorder; cancer; apoptosis; cyclic.
XX
XX Synthetic.

XX WO200172956-A2.

XX 04-OCT-2001.

XX 27-MAR-2001; 2001WO-IB001400.

XX 27-MAR-2000; 2000US-00535852.

XX (ADHE-) ADHEREX TECHNOLOGIES INC.

XX Blaschuk OW, Symonds JM, Gour BJ;

XX WPI; 2002-025778/03.

XX Modulating agents for inhibiting or enhancing desmosomal cadherin

PT mediated cell adhesion, useful for facilitating wound healing and/or
PT reducing scar tissue, treating cancer and inducing apoptosis.
XX
XX Claim 18; Page 98; 127pp; English.

XX The invention relates to modulating agents for inhibiting or enhancing
CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
CC sequence, a substance such as an antibody or antigen-binding fragment
CC that specifically binds a desmosomal cadherin CAR sequence and/or a
CC polynucleotide encoding a polypeptide that comprises a desmosomal
CC cadherin CAR sequence or analogue. The modulating agents have
CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
CC facilitate wound healing and/or reduce scar tissue, for enhancing
CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
CC treating an autoimmune blistering disorder and to treat cancer (e.g.
CC carcinoma, leukaemia or melanoma) and induce apoptosis
XX
XX Sequence 11 AA;

Query Match 52.6%; Score 40; DB 5; Length 11;
Best Local Similarity 60.0%; Pred. No. 3.1;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MFLLSRNTGE 12
| | | | | | | | | | | | | |
Db 2 MFIINRNTGD 11

RESULT 15

RAY63778
ID AAY63778 standard; peptide; 11 AA.

AC AAY63778;

XX 02-MAR-2000 (first entry)

XX Desmoglein cell adhesion recognition cyclic peptide SEQ ID NO:3230.

DE Modulation; nonclassical cadherin mediated cell adhesion; CAR;
KW inhibition; cadherin extracellular domain; cell adhesion recognition;
KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;
KW cadherin-14; cadherin-15; T-cadherin; PB-cadherin;
KW cadherin related neuronal receptor; Li-cadherin; protocadherin;
KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
KW neurological disease; cyclic.

OS Synthetic.
OS Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 1..11
FT /note= "the terminal residues are condensed with each
FT other to form a cyclic peptide"

XX WO9957149-A2.

XX 11-NOV-1999.

XX 05-MAY-1999; 99WO-CA000363.

XX 05-MAY-1998; 98US-00073040.

XX 06-NOV-1998; 98US-00187859.

XX 20-JAN-1999; 99US-00234395.

XX 08-MAR-1999; 99US-00264516.

XX (ADHE-) ADHEREX TECHNOLOGIES INC.

XX Blaschuk OW, Gour BJ, Byers S;

XX WPI; 2000-038791/03.

XX New cadherin modulating agents, used for modulating nonclassical cadherin
PT mediated functions for treating e.g. cancers, obesity, rheumatoid
PT arthritis, multiple sclerosis, diabetes or a neurological disease.
XX
XX Claim 90: Page 209; 252pp; English.
XX
XX The present invention describes cadherin modulating agents (MA)
CC comprising peptides which comprise a nonclassical cadherin cell adhesion
CC recognition (CAR) sequence. The MA can be used for modulating
CC nonclassical cadherin-mediated functions. They can be used for e.g.
CC inhibiting adhesion of nonclassical-cadherin expressing cells in a
CC mammal, enhancing delivery of a drug through the skin of a mammal,
CC enhancing delivery of a drug to a tumour in a mammal, treating cancer in
CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting
CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
CC expressing cell, preventing or treating obesity in a mammal, stimulating
CC blood vessel regression in a mammal, enhancing drug delivery to the
CC central nervous system, treating a demyelinating neurological disease,
CC increasing vasopermeability in a mammal, enhancing adhesion of
CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in
CC a mammal, or preventing pregnancy in a mammal. They can also be used for
CC e.g. enhancing or directing neurite outgrowth, facilitating wound healing
CC or reducing scar tissue, or enhancing adhesion of foreign tissue in a
CC mammal. They can also be used for treating e.g. psoriasis, arthritis, age
CC related macular degeneration, multiple sclerosis and diabetes. The
CC products can also be used for detection and diagnosis and in bioreactors.
CC AA160592 to AA164572 represent specifically claimed peptides, and
CC AA164573 to AA164643 and AA233183 to AA233186 represent sequences used in
CC the exemplification of the present invention
XX
XX Sequence 11 AA;
XX

Query Match 51.3%; Score 39; DB 3; Length 11;
Best Local Similarity 60.0%; Pred. NO. 4.6;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 3 MFLLSRNTGE 12
Db 2 MFIINRNTGK 11

Search completed: February 22, 2005, 09:24:36
Job time : 66.6667 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 22, 2005, 08:53:13 ; Search time 52.6 Seconds
(without alignments)
146.030 Million cell updates/sec

Title: US-08-991-628-5

Perfect score: 88

Sequence: 1 CECNIKVKDNDNFP 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 6622

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	31.8	15	2 Q9SOV1	Q9SOV1 nitrogen fi
2	26	29.5	9	2 Q48686	Q48686 lactococcus
3	25	28.4	12	2 Q9ICE5	Q9ICE5 human immun
4	25	28.4	15	2 Q7S362	Q7S362 neurospora
5	24	27.3	8	1 PLP_BRANA	P81707 brasica na
6	24	27.3	11	1 CS15_BACSU	P81095 bacillus su
7	24	27.3	13	2 Q9KHJ4	Q9KHJ4 caulobacter
8	24	27.3	14	2 Q661E1	Q661E1 borrelia ga
9	24	27.3	15	1 VSP3_AGKHP	P80899 agkistrodon
10	24	27.3	15	2 Q9PRW2	Q9PRW2 crotalus at
11	24	27.3	15	2 Q9PRW3	Q9PRW3 crotalus at
12	23	26.1	14	2 Q7X9S0	Q7X9S0 malus domes
13	23	26.1	15	2 Q7R923	Q7R923 plasmodium
14	23	26.1	15	2 Q9TRP2	Q9TRP2 sus scrofa
15	23	26.1	15	2 Q9QV01	Q9QV01 mus sp. . 1
16	22	25.0	8	2 Q9NGM5	Q9NGM5 toxoplasma
17	22	25.0	11	2 Q48933	Q48933 mycobacteri
18	22	25.0	11	2 Q79C20	Q79C20 mycobacteri
19	22	25.0	11	2 Q79C22	Q79C22 mycobacteri
20	22	25.0	11	2 Q707P1	Q707P1 rattus norv
21	22	25.0	13	2 Q7M0J8	Q7M0J8 planobispor
22	22	25.0	14	1 ANS4_ANTIS1	P83885 anisakis si
23	22	25.0	14	2 Q6JVP2	Q6JVP2 ottopappus e
24	22	25.0	14	2 Q6JVP4	Q6JVP4 jefea pring
25	22	25.0	14	2 Q6JVP6	Q6JVP6 angelphytum
26	22	25.0	15	2 Q9BXX4	Q9BXX4 homo sapien
27	22	25.0	15	2 Q19468	Q19468 mus musculu
28	22	25.0	15	2 Q6LCH6	Q6LCH6 mus musculu
29	21	23.9	10	2 Q9UMK9	Q9UMK9 homo sapien
30	21	23.9	11	2 Q9UBM2	Q9UBM2 homo sapien
31	21	23.9	11	2 Q7M372	Q7M372 bos taurus

Q7zda8 human immun
Q6jvp5 elaphandra
Q6jvp7 dimerostemm
Q6jvq1 blainvillea
Q6jvq2 baltimora r
Q6jvq4 angelphytum
Q6jvp9 dimerostemm
Q08936 nicotiana t
Q7m279 oryza sativ
Q6lcw3 mus musculu
O07478 streptococc
Q6ua69 carassius c
Q6uvk2 malus domes
Q7rh60 plasmodium

ALIGNMENTS

RESULT 1

Q9SOV1 PRELIMINARY; PRT; 15 AA.
AC Q9SOV1;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE Dinitrogenase beta subunit (Fragment).
GN Name=anfK;
OS nitrogen fixing bacterium ANFK33.
OC Bacteria.
OX NCBI_TaxID=96027;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20011232; PubMed=10543806;
RA Noda S., Okuma M., Ueami R., Horikoshi K., Kudo T.;
RT "Culture-independent characterization of gene responsible for nitrogen fixation in the symbiotic microbial community in the gut of the termite Neotermes koshunensis";
RL Appl. Environ. Microbiol. 65:4935-4942(1999).
DR EMBL; AB027751; BAA86283.1; -.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1719 MW; 4D64BBE1338D9A9A CRC64;

Query Match 31.8%; Score 28; DB 2; Length 15;
Best Local Similarity 57.1%; Pred. No. 1.6e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 CNIKVXD 9
| : : |
DB 3 CELKXND 9

RESULT 2

Q48686 PRELIMINARY; PRT; 9 AA.
AC Q48686;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Streptococcus cremoris promoter 23 DNA. (Fragment).
OS Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1359;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88105390; PubMed=2447829;
RA van der Vossen J.M., van der Lelie D., Venema G.;
RT "Isolation and characterization of Streptococcus cremoris Wg2-specific promoters";
RL Appl. Environ. Microbiol. 53:2452-2457(1987).
DR EMBL; M24763; AAA74720.1; -.
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1080 MW; 5AF3A44AA4469443 CRC64;

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Query Match      29.5%; Score 26; DB 2; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.6e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 7 VKDVNDN 13
Db :||:|
1 MKNMNDN 7

RESULT 3
Q9ICES PRELIMINARY; PRT; 12 AA.
AC Q9ICES;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Envelope glycoprotein.
GN Name=env;
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Choroid plexus;
RA Gartner S., Liu Y., Tang X.P., McArthur J.C., Scott J.;
RT "Analysis of human immunodeficiency virus type 1 gp160 sequences from
RT a patient with HIV dementia: evidence for monocyte trafficking into
RT brain.";
RL J. Neurovirol. 0:0-0(2000).
DR EMBL; AF217155; AAF75497.1; -
DR EMBL; AF217153; AAF75495.1; -
DR EMBL; AF217154; AAF75496.1; -
DR GO; GO:0019031; C:viral envelope; IEA.
KW Envelope protein.
SQ SEQUENCE 12 AA; 1636 MW; 78D6A2917A24005B CRC64;

Query Match      28.4%; Score 25; DB 2; Length 12;
Best Local Similarity 30.0%; Pred. No. 3.9e+03;
Matches 3; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 5 IKVKVDNDF 14
Db :||:|
1 MRVKEIRKNY 10

RESULT 4
Q7S362 PRELIMINARY; PRT; 15 AA.
AC Q7S362;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Predicted protein.
GN Name=NCU08588.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kamysyssel M., Mauceli E., Bielke C., Rudd S., Frishman D.,
RA Kryzstofova S., Raasmussen C., Metznerberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmari S.A.,
RA DeSouza C.C., Glaes L., Orbach M.J., Berglund J., Voelker R.,

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RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nuebaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DDJB whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABX01000413; EAA29870.1; -
SQ SEQUENCE 15 AA; 1753 MW; 44BAA4C25D52DA9A CRC64;

Query Match      28.4%; Score 25; DB 2; Length 15;
Best Local Similarity 57.1%; Pred. No. 4.8e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 VKDVNDN 13
Db :||:|
7 IKDINLN 13

RESULT 5
PLP_BRANA STANDARD; PRT; 8 AA.
AC P81707;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Plastidial lipid-associated protein (Fragment).
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosida II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. Topaz; TISSUE=Tapetum;
RX MEDLINE=99349136; PubMed=10420651;
RA Hernandez-Pinzon I., Ross J.H.E., Barnes K.A., Damant A.P.,
RA Murphy D.J.;
RT "Composition and role of tapetal lipid bodies in the biogenesis of the
RT pollen coat of Brassica napus.";
RL Planta 208:588-598(1999).
CC -!- FUNCTION: May play a structural role in the elaioplast, a tapetum-
CC specific plastidial lipid organelle.
CC -!- TISSUE SPECIFICITY: Tapetum of anthers.
KW Direct protein sequencing.
FT NON_TER
SQ SEQUENCE 8 AA; 989 MW; 9D7B1AA452CAA042 CRC64;

Query Match      27.3%; Score 24; DB 1; Length 8;
Best Local Similarity 62.5%; Pred. No. 1.6e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 VKDVNDNF 14
Db :||:|
1 VIDVNDWE 8

RESULT 6
CS15_BACSU STANDARD; PRT; 11 AA.
ID CS15_BACSU
AC P81095;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cold shock protein CS15 (11 kDa cold shock protein) (Fragment).
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE.
RC STRAIN=168 / JH642;
RA Graumann P.L., Schmid R., Marahiel M.A.;

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RL Submitted (OCT-1997) to Swiss-Prot.
RN CHARACTERIZATION.
RP STRAIN=168 / JH642;
RX MEDLINE=96345629; PubMed=8755892;
RA Graumann P., Schroeder K., Schmid R., Marahiel M.A.;
RT "Cold shock stress-induced proteins in Bacillus subtilis.";
RL J. Bacteriol. 178:4611-4619(1996).
CC -|- SUBCELLULAR LOCATION: Cytoplasmic.
CC -|- INDUCTION: In response to low temperature.
CC -|- CAUTION: Could not be found in the genome of B. subtilis 168.
KW Direct protein sequencing.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1360 MW; 15F6ECEEE6322C330 CRC64;

Query Match 27.3%; Score 24; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NIKVK 8
Db 3 NIKVK 7

RESULT 7
Q9KHJ4 PRELIMINARY; PRT; 13 AA.
AC Q9KHJ4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Proteolysis tag (Fragment).
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
OC Caulobacteraceae; Caulobacter.
OX NCBI_TaxID=155892;
RN [1]
SQ SEQUENCE FROM N.A.
RX MEDLINE=20345063; PubMed=10884408; DOI=10.1073/pnas.97.14.7778;
RA Keiler K.C., Shapiro L., Williams K.P.;
RT "tmRNAs that encode proteolysis-inducing tags are found in all known
bacterial genomes: A two-piece tmRNA functions in Caulobacter.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:7778-7783(2000).
DR EMBL; AF255738; AAF87998.1; -.
FT NON_TER 1
SQ SEQUENCE 13 AA; 1368 MW; CE5F60C57FCE1B1D CRC64;

Query Match 27.3%; Score 24; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 NDNF 14
Db 2 NDNF 5

RESULT 8
Q661E1 PRELIMINARY; PRT; 14 AA.
AC Q661E1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Hypothetical protein.
GN ORFNames=BG0491;
OS Borrelia garinii PBI.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=290434;
RN [1]
SQ SEQUENCE FROM N.A.
RX STRAIN=PBI;
RA Gloeckner G., Lehmann R., Romualdi A., Pradella S.,
Schulte-Spechtel U., Wilske B., Suenkel J., Platzer M.;

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RT "Comparative analysis of the Borrelia garinii genome.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CP000013; AAU07330.1; -.
KW Hypothetical protein.
SQ SEQUENCE 14 AA; 1712 MW; DD3944F0FB199202 CRC64;

Query Match 27.3%; Score 24; DB 2; Length 14;
Best Local Similarity 57.1%; Pred. No. 6.5e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 KDWDNF 14
Db 5 KDVEDKY 11

RESULT 9
VSP3 AGKHP STANDARD; PRT; 15 AA.
AC P80899;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ancrod (EC 3.4.21.74) (Venombin A) (Protein C activator) (ACC-C) (Fragment).
OS Agkistrodon halys pallas (Chinese water moccasin) (Gloydius halys pallas).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Gloydius.
OX NCBI_TaxID=8714;
RN [1]
SQ SEQUENCE, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RP TISSUE=Venom;
RC Hong S.;
RL Submitted (FEB-1997) to Swiss-Prot.
CC -|- FUNCTION: Thrombin-like snake venom serine protease. Activates
protein C (by similarity).
CC -|- CATALYTIC ACTIVITY: Selective cleavage of Arg-|-Xaa bond in
fibrinogen, to form fibrin, and release fibrinopeptide A. The
specificity of further degradation of fibrinogen varies with
species origin of the enzyme.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -|- SIMILARITY: Belongs to the peptidase S1 family. Snake venom
subfamily.
DR InterPro; IPR001254; Peptidase S1.
DR PROSITE; PS00240; TRYPSIN_DOM; PARTIAL.
DR PROSITE; PS00134; TRYPSIN_HIS; PARTIAL.
DR PROSITE; PS00135; TRYPSIN_SER; PARTIAL.
KW Direct protein sequencing; Glycoprotein; Hydrolase; Serine protease.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1642 MW; 03BFE10227CD8CDA CRC64;

Query Match 27.3%; Score 24; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.9e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ECNI 5
Db 6 ECNI 9

RESULT 10
Q9PRW2 PRELIMINARY; PRT; 15 AA.
AC Q9PRW2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Alpha-FIBRINOGENASE isoform A3 (Fragment).
OS Crotalus atrox (Western diamondback rattlesnake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

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OC Viperidae; Crotalinae; Crotalus.
OX NCBI_TaxID=8730;
RN [1]_SEQUENCE.
RP MEDLINE=94296418; PubMed=8024586;
RX Hung C.C., Chiou S.H.;
RA "Isolation of multiple isoforms of alpha-fibrinogenase from the
RT Western diamondback rattlesnake, Crotalus atrox: N-terminal sequence
RT homology with anurod, an antithrombotic agent from Malayan viper.";
RL Biochem. Biophys. Res. Commun. 201:1414-1423(1994).
SQ SEQUENCE 15 AA; 1656 MW; 03EFE10227D52FDA CRC64;

Query Match 27.3%; Score 24; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.9e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ECNI 5
Db [1]
6 ECNI 9

RESULT 11
Q9PRW3 PRELIMINARY; PRT; 15 AA.
ID Q9PRW3;
AC Q9PRW3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Alpha-FIBRINOGENASE isoform A2 (fragment).
OS Crotalus atrox (Western diamondback rattlesnake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Crotalus.
OX NCBI_TaxID=8730;
RN [1]
RP MEDLINE=94296418; PubMed=8024586;
RX Hung C.C., Chiou S.H.;
RA "Isolation of multiple isoforms of alpha-fibrinogenase from the
RT Western diamondback rattlesnake, Crotalus atrox: N-terminal sequence
RT homology with anurod, an antithrombotic agent from Malayan viper.";
RL Biochem. Biophys. Res. Commun. 201:1414-1423(1994).
DR PIR; PC2215.
SQ SEQUENCE 15 AA; 1640 MW; 03EFE10227CA12DA CRC64;

Query Match 27.3%; Score 24; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.9e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ECNI 5
Db [1]
6 ECNI 9

RESULT 12
Q7X9S0 PRELIMINARY; PRT; 14 AA.
ID Q7X9S0;
AC Q7X9S0;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mallothionein-like protein (Fragment).
OS Malus domestica (apple) (Malus sylvestris).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Rosales; Rosaceae; Maloideae; Malus.
OX NCBI_TaxID=3750;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fruit pulp;
RA Pathak N., Asif M., Solomos T.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY277667; AAP34401.1; -.

GO; GO:0046872; F:metal ion binding; IEA.
DR InterPro: IPR000347; Metallthion_15p.
DR Pfam: PF01439; Metallthio_2; 1.
DR ProDom: PD001611; Metallthion_15p; 1.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1503 MW; 85ED164D6BB3E9A1 CRC64;

Query Match 26.1%; Score 23; DB 2; Length 14;
Best Local Similarity 75.0%; Pred. No. 9.3e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CECN 4
Db [1]
6 CTCN 9

RESULT 13
Q7R923 PRELIMINARY; PRT; 15 AA.
ID Q7R923;
AC Q7R923;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=PY07046;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17XNL;
RX PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Perteza M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feldlyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabi A., Cummings L.M.,
RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii.";
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABL01002504; EAA19396.1; -.
KW Hypothetical protein.
SQ SEQUENCE 15 AA; 1791 MW; 4A5B699572F38B6A CRC64;

Query Match 26.1%; Score 23; DB 2; Length 15;
Best Local Similarity 45.5%; Pred. No. 1e+04;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 3 CNIKVKVDNDN 13
Db [1]
2 CAHRVIKYNDN 12

RESULT 14
Q9TRP2 PRELIMINARY; PRT; 15 AA.
ID Q9TRP2;
AC Q9TRP2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE LOW MR zona pellucida binding protein (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;

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RN [1]
RP SEQUENCE.
RX MEDLINE=92378826; PubMed=1510840;
RA Parry R.V., Barker P.J., Jones R.;
RT "Characterization of low Mr zona pellucida binding proteins from boar
RL spermatozoa and seminal plasma.";
RL Mol. Reprod. Dev. 33:108-115(1992).
DR HSSP; P35496; ISPP.
SQ SEQUENCE 15 AA; 1643 MW; 7FB277857862B4BE CRC64;

Query Match 26.1%; Score 23; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 1e+04;
Matches 4; Conservative 1; Mismatches 0; Indels 3; Gaps 0;

QY 2 ECNIKVKD 9
Db ||:||
8 ECGRVIKD 15

RESULT 15
Q9QV01
ID Q9QV01 PRELIMINARY; PRT; 15 AA.
AC Q9QV01;
DT 01-MAY-2000 (TRENBLREL. 13, Created)
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
DT 01-MAY-2000 (TRENBLREL. 13, Last annotation update)
DE 16 kDa alpha-lactalbumin homolog (Fragment).
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE.
RX MEDLINE=95365417; PubMed=7638241;
RA Goto Y., Nagasawa H., Sasaki T., Enami J., Iguchi T.;
RT "Biochemical changes during growth and regression of pregnancy-
RT dependent mammary tumors of GR/A mice.";
RL Proc. Soc. Exp. Biol. Med. 209:343-353(1995).
SQ SEQUENCE 15 AA; 1686 MW; D6AF74D707F8A46 CRC64;

Query Match 26.1%; Score 23; DB 2; Length 15;
Best Local Similarity 30.0%; Pred. No. 1e+04;
Matches 3; Conservative 4; Mismatches 3; Indels 3; Gaps 0;

QY 1 CECNIKVKDV 10
Db |::||:
6 CKVSHAIKDI 15
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Search completed: February 22, 2005, 09:37:53
Job time : 54.6667 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 22, 2005, 08:52:23 ; Search time 65.6667 Seconds
(without alignments)
88.346 Million cell updates/sec

Title: US-08-991-628-5

Perfect score: 88

Sequence: 1 CECNIKVDVNDNFP 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 632537

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	88	100.0	15	2 AAW04845	Aaw04845 Self epit
2	45	51.1	15	6 ABR31812	Abr31812 Human can
3	45	51.1	15	6 ABR32072	Abr32072 Human can
4	45	51.1	15	6 ABR31894	Abr31894 Human can
5	45	51.1	15	6 ABR32303	Abr32303 Human can
6	45	51.1	15	6 ABR32121	Abr32121 Human can
7	45	51.1	15	6 ABR32187	Abr32187 Human can
8	44	50.0	11	2 AAW13139	Aaw13139 Human cad
9	40	45.5	15	6 ABR32064	Abr32064 Human can
10	40	45.5	15	6 ABR32177	Abr32177 Human can
11	40	45.5	15	6 ABR32247	Abr32247 Human can
12	40	45.5	15	6 ABR31714	Abr31714 Human can
13	40	45.5	15	6 ABR32176	Abr32176 Human can
14	40	45.5	15	6 ABR32292	Abr32292 Human can
15	40	45.5	15	6 ABR32186	Abr32186 Human can
16	40	45.5	15	6 ABR32178	Abr32178 Human can
17	39	44.3	10	5 AAE24278	Aae24278 Murine E-
18	38	43.2	15	6 ABR32086	Abr32086 Human can
19	38	43.2	15	6 ABR32002	Abr32002 Human can
20	38	43.2	15	6 ABR32267	Abr32267 Human can
21	38	43.2	15	6 ABR31695	Abr31695 Human can
22	38	43.2	15	6 ABR32207	Abr32207 Human can
23	38	43.2	15	6 ABR32001	Abr32001 Human can
24	37	42.0	10	6 ABR06197	Abr06197 Human can
25	36	40.9	9	6 ABR06723	Abr06723 Human can

26	36	40.9	9	6 ABR07362	Abr07362 Human can
27	36	40.9	15	4 AAG98748	Aag98748 Human cel
28	36	40.9	15	6 ABR32153	Abr32153 Human can
29	36	40.9	15	6 ABR31871	Abr31871 Human can
30	36	40.9	15	6 ABR31932	Abr31932 Human can
31	36	40.9	15	6 ABR31736	Abr31736 Human can
32	36	40.9	15	6 ABR31966	Abr31966 Human can
33	36	40.9	15	6 ABR31709	Abr31709 Human can
34	36	40.9	15	6 ABR32272	Abr32272 Human can
35	36	40.9	15	6 ABR31916	Abr31916 Human can
36	36	40.9	15	6 ABR31831	Abr31831 Human can
37	34	38.6	9	6 ABR07139	Abr07139 Human can
38	34	38.6	10	6 ABR06819	Abr06819 Human can
39	34	38.6	10	6 ABR06251	Abr06251 Human can
40	34	38.6	10	6 ABR06435	Abr06435 Human can
41	34	38.6	15	6 ABR32206	Abr32206 Human can
42	34	38.6	15	6 ABR31669	Abr31669 Human can
43	34	38.6	15	6 ABR31723	Abr31723 Human can
44	34	38.6	15	6 ABR31976	Abr31976 Human can
45	34	38.6	15	6 ABR32208	Abr32208 Human can

ALIGNMENTS

RESULT 1

AAW04845

ID AAW04845 standard; peptide; 15 AA.

XX

AC AAW04845;

XX

DT 18-FEB-1997 (first entry)

XX

DE Self epitope of desmoglein 3, implicated in autoimmune disease.

XX

KW Tolerisation; self-epitope; antigen; autoimmune disease; autoantigen;

KW HLA; human leukocyte antigen; T-cell; thymocyte; pemphigus vulgaris;

KW desmoglein; multiple sclerosis; herpes simplex virus; adenovirus;

KW phosphomannomutase; human papillomavirus; Epstein-Barr virus;

KW DNA polymerase; influenza; haemagglutinin; reovirus; sigma protein.

XX

OS Homo sapiens.

XX

PN WO9627387-A1.

XX

PD 12-SEP-1996.

XX

PF 07-MAR-1996; 96WO-US003182.

XX

PR 07-MAR-1995; 95US-00400796.

XX

PA (HARD) HARVARD COLLEGE.

XX

PI Strominger JL, Wucherpfennig KW;

XX

DR WPI; 1996-425218/42.

XX

PT Pemphigus vulgaris auto-antigens and multiple sclerosis non-self antigens

PT - useful in disease treatment, and method for identification of other

PT self and non-self antigens implicated in auto-immune disease.

XX

PS Claim 1; Page 40; 58pp; English.

XX

CC Pharmaceutical preparations for tolerisation to antigens comprise either

CC an isolated human non-collagen or non-mysin basic protein (MBP)

CC polypeptide which is capable of tolerising an individual to an

CC autoantigen; or an isolated human pathogen polypeptide capable of

CC tolerising an individual to that polypeptide. In both cases, the

CC polypeptide (whether self or non-self) includes an amino acid sequence

CC corresponding to a sequence motif for a MHC class II protein, such as HLA

CC -DR, which is associated with a human autoimmune disease and which binds

CC to the polypeptide to activate autoreactive T-cells in individuals with

CC the autoimmune disease. This peptide is derived from the human desmoglein

CC 3 protein (amino acids 251-265) and is implicated as a self epitope in
CC pemphigus vulgaris. Peptides derived from the human desmoglein protein
CC are described in AA04841-47
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 88; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CECNIKVDVNDNPP 15
 |||||
DB 1 CECNIKVDVNDNPP 15

RESULT 2
ABR31812
ID ABR31812 standard; peptide; 15 AA.
XX
AC ABR31812;
XX
XX 19-MAY-2003 (first entry)
DT
DE Human cancer-related protein 109P1D4 HLA peptide #1584.
XX
XX Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX
XX Homo sapiens.
OS
XX WO200283921-A2.
PN
XX 24-OCT-2002.
PD
XX
PF 10-APR-2002; 2002WO-US011654.
XX
XX 10-APR-2001; 2001US-0282739P.
PR
XX 10-APR-2001; 2001US-0283112P.
PR
XX 25-APR-2001; 2001US-0286630P.
XX
XX (AGEN-) AGENSYS INC.
PA
XX
XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
PI
XX WPI; 2003-075555/07.
DR
XX
PT New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.
XX
PS Claim 13; Page 499; 1021pp; English.
XX

CC The present invention relates to novel human cancer-related genes and
CC proteins (AB278120-AB278168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention
XX
SQ Sequence 15 AA;

Query Match 51.1%; Score 45; DB 6; Length 15;
Best Local Similarity 81.8%; Pred. No. 2;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;


```

XX DT 19-MAY-2003 (first entry)
XX DE Human cancer-related protein 109P1D4 HLA peptide #1666.
XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;
XX KW human leukocyte antigen.
XX OS Homo sapiens.
XX PN WO200283921-A2.
XX PD 24-OCT-2002.
XX PF 10-APR-2002; 2002WO-US011654.
XX PR 10-APR-2001; 2001US-0282739P.
XX PR 10-APR-2001; 2001US-0283112P.
XX PR 25-APR-2001; 2001US-0286630P.
XX (AGEN-) AGENSYS INC.
XX PA Jakobovits A, Challita-Bid PM, Faris M, Ge W, Hubert RS;
XX PI Morrison K, Morrison RK, Raitano AB;
XX PI WPI; 2003-075555/07.
XX DR New composition comprising a substance that modulates the structure of
XX PT proteins and polynucleotides, useful for therapeutic, prognostic and
XX PT diagnostic reagents for eliciting cellular or humoral immune response in
XX PT cancer patients.
XX PS Claim 13; Page 501; 1021pp; English.
XX CC The present invention relates to novel human cancer-related genes and
XX CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
XX CC proteins are useful for eliciting a humoral or cellular immune response.
XX CC The genes are useful as probes and primers for the amplification and/or
XX CC detection of genes, mRNAs or their fragments, as reagents for the
XX CC diagnosis and/or prognosis of cancer, as coding sequences capable of
XX CC directing the expression of the protein, as tools for modulating or
XX CC inhibiting the expression of genes and/or translation of transcripts, and
XX CC as therapeutic agents. The proteins and peptides are useful as
XX CC therapeutic, prognostic and diagnostic reagents for cancer. The present
XX CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX CC from the invention
XX SQ Sequence 15 AA;
XX Query Match 51.1%; Score 45; DB 6; Length 15;
XX Best Local Similarity 81.8%; Pred. No. 2;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 5 IKVKDNDNFP 15
DB ||||| |||||
3 IKVKDENDNAP 13
RESULT 5
ABR32303
ID ABR32303 standard; peptide; 15 AA.
XX AC ABR32303;
XX DT 19-MAY-2003 (first entry)
XX DE Human cancer-related protein 109P1D4 HLA peptide #2075.
XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;
XX KW human leukocyte antigen.
XX OS Homo sapiens.
XX PN WO200283921-A2.
XX PD 24-OCT-2002.
XX PF 10-APR-2002; 2002WO-US011654.
XX PR 10-APR-2001; 2001US-0282739P.
XX PR 10-APR-2001; 2001US-0283112P.
XX PR 25-APR-2001; 2001US-0286630P.
XX (AGEN-) AGENSYS INC.
XX PA Jakobovits A, Challita-Bid PM, Faris M, Ge W, Hubert RS;
XX PI Morrison K, Morrison RK, Raitano AB;
XX PI WPI; 2003-075555/07.
XX DR New composition comprising a substance that modulates the structure of
XX PT proteins and polynucleotides, useful for therapeutic, prognostic and
XX PT diagnostic reagents for eliciting cellular or humoral immune response in
XX PT cancer patients.
XX PS Claim 13; Page 501; 1021pp; English.
XX CC The present invention relates to novel human cancer-related genes and
XX CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
XX CC proteins are useful for eliciting a humoral or cellular immune response.
XX CC The genes are useful as probes and primers for the amplification and/or
XX CC detection of genes, mRNAs or their fragments, as reagents for the
XX CC diagnosis and/or prognosis of cancer, as coding sequences capable of
XX CC directing the expression of the protein, as tools for modulating or
XX CC inhibiting the expression of genes and/or translation of transcripts, and
XX CC as therapeutic agents. The proteins and peptides are useful as
XX CC therapeutic, prognostic and diagnostic reagents for cancer. The present
XX CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX CC from the invention
XX SQ Sequence 15 AA;
XX Query Match 51.1%; Score 45; DB 6; Length 15;
XX Best Local Similarity 81.8%; Pred. No. 2;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 5 IKVKDNDNFP 15
DB ||||| |||||
3 IKVKDENDNAP 13
RESULT 6
ABR32121
ID ABR32121 standard; peptide; 15 AA.
XX AC ABR32121;
XX DT 19-MAY-2003 (first entry)
XX DE Human cancer-related protein 109P1D4 HLA peptide #1893.
XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;
XX KW human leukocyte antigen.
XX OS Homo sapiens.
XX PN WO200283921-A2.
XX PD 24-OCT-2002.
XX PF 10-APR-2002; 2002WO-US011654.
XX PR 10-APR-2001; 2001US-0282739P.
XX PR 10-APR-2001; 2001US-0283112P.
XX PR 25-APR-2001; 2001US-0286630P.
XX (AGEN-) AGENSYS INC.
XX PA Jakobovits A, Challita-Bid PM, Faris M, Ge W, Hubert RS;
XX PI Morrison K, Morrison RK, Raitano AB;
XX PI WPI; 2003-075555/07.
XX DR New composition comprising a substance that modulates the structure of
XX PT proteins and polynucleotides, useful for therapeutic, prognostic and
XX PT diagnostic reagents for eliciting cellular or humoral immune response in
XX PT cancer patients.
XX PS Claim 13; Page 508; 1021pp; English.
XX CC The present invention relates to novel human cancer-related genes and
XX CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
XX CC proteins are useful for eliciting a humoral or cellular immune response.
XX CC The genes are useful as probes and primers for the amplification and/or
XX CC detection of genes, mRNAs or their fragments, as reagents for the
XX CC diagnosis and/or prognosis of cancer, as coding sequences capable of
XX CC directing the expression of the protein, as tools for modulating or
XX CC inhibiting the expression of genes and/or translation of transcripts, and
XX CC as therapeutic agents. The proteins and peptides are useful as
XX CC therapeutic, prognostic and diagnostic reagents for cancer. The present
XX CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX CC from the invention
XX SQ Sequence 15 AA;
XX Query Match 51.1%; Score 45; DB 6; Length 15;
XX Best Local Similarity 81.8%; Pred. No. 2;
XX Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 5 IKVKDNDNFP 15
DB ||||| |||||
5 IKVKDENDNAP 15

```

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PA (AGEN-) AGENSYS INC.
XX
PI Jakobovits A, Challita-Bid PM, Paris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
DR WPI; 2003-075555/07.
XX
PT New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.
XX
PS Claim 13; Page 505; 1021pp; English.
XX
CC The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention
XX
SQ Sequence 15 AA;
Query Match 51.1%; Score 45; DB 6; Length 15;
Best Local Similarity 81.8%; Pred. NO. 2;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 IKVKDNDNFP 15
Db ||||| ||| |
2 IKVKDENDNAP 12

RESULT 8
AAW13139
ID AAW13139 standard; protein; 11 AA.
XX
AC AAW13139;
XX
DT 25-MAR-2003 (revised)
DT 14-MAY-1997 (first entry)
XX
DE Human cadherin-5 antigenic epitope (residues 242-252).
XX
KW Ca2+ dependent; cell adhesion protein; cadherin; human; antibody;
KW purification; determination; epitope; tissue expression;
KW binding antagonist; calcium ion; antigen.
XX
OS Homo sapiens.
XX
PN US5597725-A.
XX
PD 28-JAN-1997.
XX
PF 26-JAN-1994; 94US-00188228.
XX
PR 17-APR-1992; 92US-00872643.
PR 19-APR-1993; 93US-00049460.
XX
PA (DOHE-) DOHENY EYE INST.
XX
PI Suzuki S;
XX
DR WPI; 1997-108328/10.
XX
PT Antibodies to cadherin proteins - useful as cadherin antagonists, etc.
XX
PS Claim 5; Col 112; 59pp; English.
XX
CC The present sequence is an antigenic epitope from human cadherin-5, which
CC is a Ca2+ dependent cell adhesion protein. Antibodies or fragments that
CC specifically bind the epitope can be used to purify the cadherin,
CC determine its tissue expression and antagonise its ligand/antiligand
CC binding activities. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 11 AA;
Query Match 50.0%; Score 44; DB 2; Length 11;

```

```
Best Local Similarity 54.5%; Pred. No. 2.1;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 5 IKVKDVNDNFP 15
Db 1 VTLDQINDNFP 11

RESULT 9
ABR32064
ID ABR32064 standard; peptide; 15 AA.
XX
AC ABR32064;
XX
XX 19-MAY-2003 (first entry)
DE
DE Human cancer-related protein 109P1D4 HLA peptide #1836.
XX
XX Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX
XX Homo sapiens.
XX
XX WO200283921-A2.
XX
XX 24-OCT-2002.
XX
XX 10-APR-2002; 2002WO-US011654.
XX
XX 10-APR-2001; 2001US-0282739P.
PR 10-APR-2001; 2001US-0283112P.
PR 25-APR-2001; 2001US-0286630P.
XX
XX (AGEN-) AGENSYS INC.
XX
XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
XX WPI; 2003-075555/07.
XX
XX New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.
XX
XX Claim 13; Page 504; 1021pp; English.
XX
XX The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention
XX
XX Sequence 15 AA;
QY Query Match 45.5%; Score 40; DB 6; Length 15;
Best Local Similarity 63.6%; Pred. No. 13;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 5 IKVKDVNDNFP 15
Db 3 VNVTDVNDNVP 13

RESULT 10
ABR32177
ID ABR32177 standard; peptide; 15 AA.
XX
AC ABR32177;
XX
XX 19-MAY-2003 (first entry)
DE
DE Human cancer-related protein 109P1D4 HLA peptide #1949.
XX
XX Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX
XX Homo sapiens.
XX
XX WO200283921-A2.
XX
XX 24-OCT-2002.
XX
XX 10-APR-2002; 2002WO-US011654.
XX
XX 10-APR-2001; 2001US-0282739P.
PR 10-APR-2001; 2001US-0283112P.
PR 25-APR-2001; 2001US-0286630P.
XX
XX (AGEN-) AGENSYS INC.
XX
XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
XX WPI; 2003-075555/07.
XX
XX New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.
XX
XX Claim 13; Page 506; 1021pp; English.
XX
XX The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention
XX
XX Sequence 15 AA;
QY Query Match 45.5%; Score 40; DB 6; Length 15;
Best Local Similarity 63.6%; Pred. No. 13;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 5 IKVKDVNDNFP 15
Db 4 VNVTDVNDNVP 14

RESULT 11
ABR32247
ID ABR32247 standard; peptide; 15 AA.
XX
AC ABR32247;
XX
XX 19-MAY-2003 (first entry)
DE
DE Human cancer-related protein 109P1D4 HLA peptide #2019.
XX
XX Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
```


PT New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.
XX
XX Claim 13; Page 506; 1021pp; English.
XX
XX The present invention relates to novel human cancer-related genes and
XX proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
XX proteins are useful for eliciting a humoral or cellular immune response.
XX The genes are useful as probes and primers for the amplification and/or
XX detection of genes, mRNAs or their fragments, as reagents for the
XX diagnosis and/or prognosis of cancer, as coding sequences capable of
XX directing the expression of the protein, as tools for modulating or
XX inhibiting the expression of genes and/or translation of transcripts, and
XX as therapeutic agents. The proteins and peptides are useful as
XX therapeutic, prognostic and diagnostic reagents for cancer. The present
XX sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX from the invention
XX
XX SQ Sequence 15 AA;

Query Match 45.5%; Score 40; DB 6; Length 15;
Best Local Similarity 63.6%; Pred. No. 13;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 IKVKDNDNPP 15
: | | | | |
Db 5 VNVTDVNDNVP 15

RESULT 14
ABR32292
ID ABR32292 standard; peptide; 15 AA.
XX
XX ABR32292;
XX
XX 19-MAY-2003 (first entry)
XX
XX Human cancer-related protein 109P1D4 HLA peptide #2064.
XX
XX Human; cytostatic; vaccine; cancer; immune response; HLA;
XX human leukocyte antigen.
XX
XX Homo sapiens.
XX
XX WO200283921-A2.
XX
XX 24-OCT-2002.
XX
XX 10-APR-2001; 2001US-0282739P.
XX
XX 10-APR-2001; 2001US-0283112P.
XX
XX 25-APR-2001; 2001US-0286630P.
XX
XX (AGEN-) AGENSYS INC.
XX
XX Jakobovits A, Challita-Bid PM, Faris M, Ge W, Hubert RS;
XX Morrison K, Morrison RK, Raitano AB;
XX
XX WPI; 2003-075555/07.
XX
XX New composition comprising a substance that modulates the structure of
XX proteins and polynucleotides, useful for therapeutic, prognostic and
XX diagnostic reagents for eliciting cellular or humoral immune response in
XX cancer patients.
XX
XX Claim 13; Page 508; 1021pp; English.
XX
XX The present invention relates to novel human cancer-related genes and
XX proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
XX proteins are useful for eliciting a humoral or cellular immune response.

CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention
XX
XX SQ Sequence 15 AA;

Query Match 45.5%; Score 40; DB 6; Length 15;
Best Local Similarity 88.9%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 IKVKDNDN 13
: | | | | |
Db 6 IKVKDNDN 14

RESULT 15
ABR32186
ID ABR32186 standard; peptide; 15 AA.
XX
XX ABR32186;
XX
XX 19-MAY-2003 (first entry)
XX
XX Human cancer-related protein 109P1D4 HLA peptide #1958.
XX
XX Human; cytostatic; vaccine; cancer; immune response; HLA;
XX human leukocyte antigen.
XX
XX Homo sapiens.
XX
XX WO200283921-A2.
XX
XX 24-OCT-2002.
XX
XX 10-APR-2002; 2002WO-US011654.
XX
XX 10-APR-2001; 2001US-0282739P.
XX
XX 10-APR-2001; 2001US-0283112P.
XX
XX 25-APR-2001; 2001US-0286630P.
XX
XX (AGEN-) AGENSYS INC.
XX
XX Jakobovits A, Challita-Bid PM, Faris M, Ge W, Hubert RS;
XX Morrison K, Morrison RK, Raitano AB;
XX
XX WPI; 2003-075555/07.
XX
XX New composition comprising a substance that modulates the structure of
XX proteins and polynucleotides, useful for therapeutic, prognostic and
XX diagnostic reagents for eliciting cellular or humoral immune response in
XX cancer patients.
XX
XX Claim 13; Page 506; 1021pp; English.
XX
XX The present invention relates to novel human cancer-related genes and
XX proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
XX proteins are useful for eliciting a humoral or cellular immune response.
XX The genes are useful as probes and primers for the amplification and/or
XX detection of genes, mRNAs or their fragments, as reagents for the
XX diagnosis and/or prognosis of cancer, as coding sequences capable of
XX directing the expression of the protein, as tools for modulating or
XX inhibiting the expression of genes and/or translation of transcripts, and
XX as therapeutic agents. The proteins and peptides are useful as
XX therapeutic, prognostic and diagnostic reagents for cancer. The present
XX sequence is a human leukocyte antigen (HLA) peptide, used in an example
XX from the invention
XX

SQ Sequence 15 AA;

Query Match 45.5%; Score 40; DB 6; Length 15;
Best Local Similarity 88.9%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 IKVKDVNDN 13
| | | | |
Db 7 IKVKDENDN 15

Search completed: February 22, 2005, 09:24:37
Job time : 66.6667 secs

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OM protein - protein search, using sw model

Run on: February 22, 2005, 09:08:09 ; Search time 11.1333 Seconds
(without alignments)
129.633 Million cell updates/sec

Title: US-08-991-628-6
Perfect score: 82
Sequence: 1 SARTLNRYTGPYP 15
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 2523

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	32.9	9	2 S70332	endosperm protein,
2	24	29.3	15	2 A56970	GLYMA1 - soybean (
3	23	28.0	15	2 S08209	hypothetical prote
4	22	26.8	12	2 A28856	fructose-bisphosph
5	22	26.8	12	2 PH1459	T-cell receptor be
6	22	26.8	15	2 S36893	ribosomal protein
7	22	26.8	15	2 A28497	neurotensin-relate
8	21	25.6	8	2 D47393	neuropeptide calla
9	21	25.6	13	2 PH1593	Ig H chain V-D-J r
10	21	25.6	15	2 D28587	T-cell receptor be
11	21	25.6	15	2 P28587	T-cell receptor be
12	21	25.6	15	2 I53284	T-cell receptor be
13	21	25.6	15	4 I38335	hypothetical TEL/M
14	20.5	25.0	12	2 PH1462	T-cell receptor be
15	20.5	25.0	13	2 PH0799	T-cell receptor al
16	20	24.4	10	2 PH0927	T-cell receptor be
17	20	24.4	11	2 PH1375	T antigen variant
18	20	24.4	12	2 S26546	T-cell receptor be
19	20	24.4	12	2 S23168	Z protein - guinea
20	20	24.4	12	2 PH1461	T-cell receptor be
21	20	24.4	13	2 A32734	enkephalin precurs
22	20	24.4	13	2 S23372	T-cell receptor al
23	20	24.4	13	2 PH1585	Ig H chain V-D-J r
24	20	24.4	13	2 PH0783	T-cell receptor al
25	20	24.4	14	2 PH1305	Ig heavy chain DJ
26	20	24.4	15	2 PH0004	chlorophyll a/b-bi
27	20	24.4	15	2 PH1318	Ig heavy chain DJ
28	20	24.4	15	2 B45115	peptidylprolyl iso
29	19	23.2	8	2 E47393	neuropeptide calla

30 19 23.2 9 2 S39766 cardioactive pepti
31 19 23.2 9 2 S39767 cardioactive pepti
32 19 23.2 9 2 A26363 cardioactive pepti
33 19 23.2 9 2 S27233 cardioactive pepti
34 19 23.2 10 2 C61440 polygalacturonase
35 19 23.2 10 2 S07202 phyllomedulin - tw
36 19 23.2 12 2 S17869 glutathione transf
37 19 23.2 12 2 S49547 hypothetical prote
38 19 23.2 13 2 S47377 T-cell antigen rec
39 19 23.2 13 2 S10562 zona pellucida-bin
40 19 23.2 13 2 JQ2309 hypothetical 1.6K
41 19 23.2 13 2 JQ2319 hypothetical 1.6K
42 19 23.2 14 2 B28018 very late antigen-
43 19 23.2 15 2 C48401 ribosomal protein
44 18 22.0 8 2 PT0030 inulinase [EC 3.2.
45 18 22.0 9 2 A61357 phyllocaerulein -

ALIGNMENTS

RESULT 1
S70332
endosperm protein, 10K - rye (fragment)
C;Species: Secale cereale (rye)
C;Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 17-Apr-1998
C;Accession: S70332
R;Rocher, A.; Calero, M.; Soriano, F.; Mendez, E.
Biochim. Biophys. Acta 1295, 13-22, 1996
A;Title: Identification of major rye secalins as coeliac immunoreactive proteins.
A;Reference number: S70327; MUID:96283789; PMID:8679669
A;Accession: S70332
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <ROC>
Query Match 32.9%; Score 27; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 TGPYTF 15
DB 1 TGPYEF 6

RESULT 2
A56970
GLYMA1 - soybean (fragment)
C;Species: Glycine max (soybean)
C;Date: 02-Sep-1995 #sequence_revision 08-Sep-1995 #text_change 09-Jul-2004
C;Accession: A56970
R;Codina, M.R.
submitted to the Protein Sequence Database, September 1995
A;Reference number: A56970
A;Accession: A56970
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-15 <COD>
A;Cross-references: UNIPROT:Q7M285
Query Match 29.3%; Score 24; DB 2; Length 15;
Best Local Similarity 44.4%; Pred. No. 6.3e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 LNNRYTGPY 13
DB 6 LADTYRGPF 14

RESULT 3
S08209
hypothetical protein 2 - garden pea
N;Alternate names: phytochrome

C:Species: Pisum sativum (garden pea)
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Sep-1997
C:Accession: S08209

R:Sato, N.
Plant Mol. Biol. 11, 697-710, 1988
A:Title: Nucleotide sequence and expression of the phytochrome gene in Pisum sativum: di
A:Reference number: S08856
A:Accession: S08209
A:Molecule type: DNA
A:Residues: 1-15 <SNT>
A:Cross-references: EMBL:X14077; NID:g20836; PID:g20838
C:Genes: phy

Query Match 28.0%; Score 23; DB 2; Length 15;
Best Local Similarity 57.1%; Pred. No. 9.5e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 NRYTPY 13
| | | |
| | | |
Db 8 NGYFNPY 14

RESULT 4
A28856
fructose-bisphosphate aldolase (EC 4.1.2.13) B, hepatic - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 31-Oct-1997
C:Accession: A28856
R:Hannappel, E.; MacGregor, J.S.; Davoust, S.; Horecker, B.L.
Arch. Biochem. Biophys. 214, 293-298, 1982
A:Title: Limited proteolysis of liver and muscle aldolases: effects of subtilisin, cathe
A:Reference number: A28856; MUID:82205113; PMID:7044315
A:Accession: A28856
A:Molecule type: protein
A:Residues: 1-12 <HAN>
A:Superfamily: fructose-bisphosphate aldolase
C:Keywords: aldehyde-lyase; carbon-carbon lyase; gluconeogenesis; glycolysis; liver; per

Query Match 26.8%; Score 22; DB 2; Length 12;
Best Local Similarity 42.9%; Pred. No. 1.1e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 9 YTGPTTF 15
: | | | |
: | | | |
Db 6 FTASYTY 12

RESULT 5
PH1459
T-cell receptor beta chain (clone A3/IIC7) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 15-Mar-2004
C:Accession: PH1459; PH1460
R:Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; Ko
J. Exp. Med. 177, 811-820, 1993
A:Title: T cell receptor selection by and recognition of two class I major histocompatib
A:Reference number: PH1430; MUID:93171821; PMID:8436911
A:Accession: PH1459
A:Molecule type: mRNA
A:Residues: 1-12 <CAL>
A:Experimental source: cytolytic T-lymphocyte clone A3/IIC7
A:Accession: PH1460
A:Molecule type: mRNA
A:Residues: 1-12 <CA2>
A:Experimental source: cytolytic T-lymphocyte clone 332/2A
C:Keywords: receptor; T-cell

Query Match 26.8%; Score 22; DB 2; Length 12;
Best Local Similarity 57.1%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 YTGPTTF 15

Db 5 YGSDYTF 11
| | | |

RESULT 6
S36893
ribosomal protein - Mycobacterium bovis (fragment)
C:Species: Mycobacterium bovis
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S36893
R:Ohara, N.; Kimura, M.; Higashi, Y.; Yamada, T.
FEBS Lett. 331, 9-14, 1993
A:Title: Isolation and amino acid sequence of the 30S ribosomal protein S19 from Mycobact
A:Reference number: S36887; MUID:94009653; PMID:8405418
A:Accession: S36893
A>Status: Preliminary
A:Molecule type: protein
A:Residues: 1-15 <OHA>
A:Cross-references: UNIPROT:Q9R541

Query Match 26.8%; Score 22; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 YTGPTY 14
| | | |
| | | |
Db 3 YEGPKT 8

RESULT 7
A28497
neurotensin-related protein - turkey (fragment)
C:Species: Meleagris gallopavo (common turkey)
C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C:Accession: A28497
R:Carraway, R.E.; Cochran, D.E.; Ruane, S.E.
J. Biol. Chem. 262, 15886-15889, 1987
A:Title: Isolation, structures, and biologic activity of neurotensin-related peptides ge
A:Reference number: A28497; MUID:88058942; PMID:2445741
A:Accession: A28497
A:Molecule type: protein
A:Residues: 1-15 <CAR>
A:Cross-references: UNIPROT:Q7LZA3
C:Keywords: neuropeptide

Query Match 26.8%; Score 22; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 RYTGYPY 13
| | | |
| | | |
Db 8 RTRGYPY 13

RESULT 8
D47393
neuropeptide callatostatin 4 - bluebottle fly (Calliphora vomitoria)
C:Species: Calliphora vomitoria
C>Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: D47393
R:Duve, H.; Johnsen, A.H.; Scott, A.G.; Yu, C.G.; Yagi, K.J.; Tobe, S.S.; Thorpe, A.
Proc. Natl. Acad. Sci. U.S.A. 90, 2456-2460, 1993
A:Title: Callatostatin: neuropeptides from the blowfly Calliphora vomitoria with sequen
A:Reference number: A47393; MUID:93211980; PMID:8460157
A:Accession: D47393
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <DUV>
A:Cross-references: UNIPROT:P41840
A:Experimental source: thoracic ganglia
A>Note: sequence extracted from NCBI backbone (NCBIP:128479)

Query Match 25.6%; Score 21; DB 2; Length 8;

Best Local Similarity 75.0%; Score 21; DB 2; Length 15;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 PYTF 15
||:|
Db 3 PYSF 6

RESULT 9
PH1593
IG H chain V-D-J region (wild-type clone 144) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: PH1593
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
A;Reference number: PH1580; MUID:93301609; PMID:8315387
A;Accession: PH1593
A;Molecule type: DNA
A;Residues: 1-13 <LEV>
A;Experimental source: bone marrow pre-B lymphocyte
C;Keywords: immunoglobulin

Query Match 25.6%; Score 21; DB 2; Length 13;
Best Local Similarity 41.7%; Pred. No. 1.8e+03;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2 ARTLNRYTGPY 13
||:|
Db 2 ARPLRHYAMDY 13

RESULT 10
D28587
T-cell receptor beta-2 chain J-B2.5 segment - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 05-Nov-1999
C;Accession: D28587
R;Toyonaga, B.; Yoshikai, Y.; Vadasz, V.; Chin, B.; Mak, T.W.
Proc. Natl. Acad. Sci. U.S.A. 82, 8624-8628, 1985
A;Title: Organization and sequences of the diversity, joining, and constant region genes
A;Reference number: A94081; MUID:86094276; PMID:3866244
A;Accession: D28587
A;Molecule type: DNA
A;Residues: 1-15 <TOY>
A;Cross-references: GB:M14159; NID:g338852; PIDN:AAA60679.1; PID:g553690
C;Keywords: T-cell receptor

Query Match 25.6%; Score 21; DB 2; Length 15;
Best Local Similarity 57.1%; Pred. No. 2.1e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 RYTGPTY 14
:|:|
Db 4 QYFGPGT 10

RESULT 11
F28587
T-cell receptor beta-2 chain J-B2.7 segment - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 05-Nov-1999
C;Accession: F28587
R;Toyonaga, B.; Yoshikai, Y.; Vadasz, V.; Chin, B.; Mak, T.W.
Proc. Natl. Acad. Sci. U.S.A. 82, 8624-8628, 1985
A;Title: Organization and sequences of the diversity, joining, and constant region genes
A;Reference number: A94081; MUID:86094276; PMID:3866244
A;Accession: F28587
A;Molecule type: DNA
A;Residues: 1-15 <TOY>
A;Cross-references: GB:M14159; NID:g338852; PIDN:AAA60681.1; PID:g553692
C;Keywords: T-cell receptor

Query Match 25.6%; Score 21; DB 2; Length 15;
Best Local Similarity 57.1%; Pred. No. 2.1e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 RYTGPTY 14
:|:|
Db 4 QYFGPGT 10

RESULT 12
I53284
T-cell receptor beta 2 chain J region, Jbeta2.7 - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C;Accession: I53284
R;Harindranath, N.; Alexander, C.B.; Mage, R.G.
Mol. Immunol. 28, 881-888, 1991
A;Title: Evolutionarily conserved organization and sequences of germ-line diversity and J
A;Reference number: A53284; MUID:91342695; PMID:1678859
A;Accession: I53284
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-15 <HAR>
A;Cross-references: GB:S60737; NID:g233916; PIDN:AAB19525.1; PID:g233925
A;Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBIP:60747)
C;Keywords: T-cell receptor

Query Match 25.6%; Score 21; DB 2; Length 15;
Best Local Similarity 57.1%; Pred. No. 2.1e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 RYTGPTY 14
:|:|
Db 4 QYFGPGT 10

RESULT 13
I38335
hypothetical TEL/MNI mutant fusion protein type II - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 20-Apr-2000
C;Accession: I38335
R;Builjs, A.; Sherr, S.; van Baal, S.; van Bezouw, S.; van der Plas, D.; Van Kessel, A.G.;
Oncogene 10, 1511-1519, 1995
A;Title: Translocation (12;22) (p13;q11) in myeloproliferative disorders results in fusion
A;Reference number: I38031; MUID:95249265; PMID:7731705
A;Accession: I38335
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-15 <BUI>
A;Cross-references: EMBL:X85024; NID:g971471; PIDN:CAA59397.1; PID:g971472
A;Comment: This sequence is the chimeric product of a translocation mutation.
C;Genetics:
A;Gene: ETV6/MNI; TEL/MNI
A;Map position: 22q11/12p13
C;Keywords: fusion protein

Query Match 25.6%; Score 21; DB 4; Length 15;
Best Local Similarity 42.9%; Pred. No. 2.1e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 8 RYTGPTY 14
||:|
Db 1 RYRSPHS 7

RESULT 14
PH1462
T-cell receptor beta chain (clone A24/PEF1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 15-Mar-2004
C;Accession: PH1462

R;Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; Kd
J. Exp. Med. 177, 811-820, 1993
A:Title: T cell receptor selection by and recognition of two class I major histocompatib
A:Reference number: PH1430; MUID:93171821; PMID:8436911
A:Accession: PH1462

A:Molecule type: mRNA
A:Residues: 1-12 <CAS>
A:Experimental source: cytolytic T-lymphocyte
C:Keywords: receptor; T-cell

Query Match 25.0%; Score 20.5; DB 2; Length 12;
Best Local Similarity 83.3%; Pred. No. 2e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 11 GP-YTF 15
Db 6 GPDYTF 11

RESULT 15

PH0799
T-cell receptor alpha chain (H1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PH0799
R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A:Title: T cell receptor genes in a series of class I major histocompatibility complex-r
allelic exclusion and antigen-specific repertoire.
A:Reference number: PH0746; MUID:92078846; PMID:1836010
A:Accession: PH0799
A:Molecule type: mRNA
A:Residues: 1-13 <CAS>
A:Cross-references: EMBL:X60905
A:Experimental source: T lymphocyte
C:Keywords: T-cell receptor

Query Match 25.0%; Score 20.5; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 2.2e+03;
Matches 7; Conservative 0; Mismatches 4; Indels 3; Gaps 1;

QY 2 ARTLNRRYTGPTYTF 15
Db 2 ARGTN---TGKLTTF 12

Search completed: February 22, 2005, 09:46:26
Job time : 12.1333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 22, 2005, 08:53:13 ; Search time 52.6 Seconds
(without alignments)
146.030 Million cell updates/sec

Title: US-08-991-628-6

Perfect score: 82

Sequence: 1 SARTLNRYTGPYTF 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 6622

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Uniprot_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	27	32.9	8	1	ALL5_CARMA	P81818 carcinus ma
2	26	31.7	8	1	ALL8_CARMA	P81811 carcinus ma
3	26	31.7	8	1	ALL9_CARMA	P81812 carcinus ma
4	26	31.7	12	2	Q41856	Q41856 zea mays (m
5	25	30.5	10	2	Q6EX62	Q6EX62 hyptis suav
6	25	30.5	13	2	P90442	P90442 spodoptera
7	25	30.5	15	2	Q9QV00	Q9QV00 rattus sp.
8	24	29.3	8	1	ALL6_CARMA	P81819 carcinus ma
9	24	29.3	15	2	Q9UR63	Q9UR63 emericeella
10	24	29.3	15	2	Q7M285	Q7M285 glycine max
11	23.5	28.7	15	2	P97249	P97249 nitrosospir
12	23	28.0	9	1	ALL1_CARMA	P81814 carcinus ma
13	23	28.0	15	2	Q9R4M8	Q9R4M8 bacillus fi
14	23	28.0	15	2	Q924T1	Q924T1 rattus norv
15	22	26.8	10	1	CA12_LITCI	P62540 litoria cit
16	22	26.8	10	1	CA12_LITSP	P62541 litoria spl
17	22	26.8	14	2	Q9MR76	Q9MR76 hordeum mur
18	22	26.8	15	2	Q9R341	Q9R341 mycobacteri
19	22	26.8	15	2	Q7LZA3	Q7LZA3 meleagris g
20	21	25.6	8	1	ALL3_CYPDO	P82154 cydia pomon
21	21	25.6	8	1	ALL4_CALVO	P41840 calliphora
22	21	25.6	8	1	ALL4_CYPDO	P82155 cydia pomon
23	21	25.6	9	1	FLA2_TREHY	P80159 treponema h
24	21	25.6	10	2	Q6A3T8	Q6A3T8 arhanglopt
25	21	25.6	10	2	Q71V02	Q71V02 pseudomonas
26	21	25.6	13	1	MP1_MICOC	P81532 micoplitis
27	21	25.6	15	2	Q95751	Q95751 brachylophu
28	21	25.6	15	2	Q9R564	Q9R564 escherichia
29	20	24.4	7	1	ALL3_CARMA	P81806 carcinus ma
30	20	24.4	7	1	ALL4_CARMA	P81807 carcinus ma
31	20	24.4	7	1	ALL5_CARMA	P81808 carcinus ma

32	20	24.4	7	1	MNPI_LEPDE	P42984 leptinotars
33	20	24.4	8	1	ALL7_CARMA	P81820 carcinus ma
34	20	24.4	8	1	ALL7_CARMA	P81809 carcinus ma
35	20	24.4	9	1	ALL10_CARMA	P81813 carcinus ma
36	20	24.4	11	1	TKC2_CALVO	P41518 calliphora
37	20	24.4	12	2	Q7RW16	Q7RW16 neurospora
38	20	24.4	13	2	Q7M226	Q7M226 ovis aries
39	20	24.4	13	2	Q6BCX4	Q6BCX4 oncorhynch
40	20	24.4	14	2	Q8MH00	Q8MH00 homo sapien
41	20	24.4	14	2	Q8MH01	Q8MH01 homo sapien
42	20	24.4	14	2	Q8MH02	Q8MH02 homo sapien
43	20	24.4	14	2	Q8MH03	Q8MH03 homo sapien
44	20	24.4	14	2	Q8MH04	Q8MH04 homo sapien
45	20	24.4	14	2	Q8MH05	Q8MH05 homo sapien

ALIGNMENTS

RESULT 1
AL15_CARMA
ID AL15_CARMA STANDARD; PRT; 8 AA.
AC P81818;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Carcinustatin 15.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Brachyura; Portunioidea; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P., Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997)
CC -|- FUNCTION: May act as a neurotransmitter or neuromodulator.
CC -|- SIMILARITY: Belongs to the allatostatin family.
KW Amidation; Direct protein sequencing; Multigene family; Neuropeptide.
FT MOD RES 8 Leucine amide.
SQ SEQUENCE 8 AA; 811 MW; 922879D5AB47687D CRC64;

Query Match 32.9%; Score 27; DB 1; Length 8;
Best Local Similarity 80.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 GPVTF 15
Db |||:|
2 GPYSF 6

RESULT 2
ALL8_CARMA
ID ALL8_CARMA STANDARD; PRT; 8 AA.
AC P81811;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Carcinustatin 8.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Brachyura; Portunioidea; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;

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RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734 (1997).
CC -!- FUNCTION: May act as a neurotransmitter or neuromodulator.
CC -!- SIMILARITY: Belongs to the allatostatin family.
KW Amidation; Direct protein sequencing; Multigene family; Neuropeptide.
FT MOD_RES 8 Leucine amide.
SQ SEQUENCE 8 AA; 795 MW; 922879DCB47687D CRC64;

Query Match 31.7%; Score 26; DB 1; Length 8;
Best Local Similarity 80.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GPYTF 15
DB 2 GPYAF 6

RESULT 3
ALL9_CARMA STANDARD; PRT; 8 AA.
ID ALL9_CARMA
AC P81812;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Carcinustatin 9.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubranchyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6739;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734 (1997).
CC -!- FUNCTION: May act as a neurotransmitter or neuromodulator.
CC -!- SIMILARITY: Belongs to the allatostatin family.
KW Amidation; Direct protein sequencing; Multigene family; Neuropeptide.
FT MOD_RES 8 Leucine amide.
SQ SEQUENCE 8 AA; 781 MW; 7C2879DCB476878 CRC64;

Query Match 31.7%; Score 26; DB 1; Length 8;
Best Local Similarity 80.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GPYTF 15
DB 2 GPYAF 6

RESULT 4
Q41856 PRELIMINARY; PRT; 12 AA.
ID Q41856;
AC Q41856;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
DE Sucrose synthetase gene mutant (Sh-5586 allele) containing transposon
DE Tz86, 5' end of Tz86. (fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE=85153004; PubMed=6099243;
RA Dellaporta S.L., Chomet P.S., Mottinger J.P., Wood J.A., Yu S.M.,
RA Hicks J.B.;
RT "Endogenous transposable elements associated with virus infection in
RT maize.";
RL Cold Spring Harb. Symp. Quant. Biol. 49:321-328 (1984).
DR EMBL; M10174; AAA33516.1; -.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1239 MW; 925ECBFEB0A5B861 CRC64;

Query Match 31.7%; Score 26; DB 2; Length 12;
Best Local Similarity 62.5%; Pred. No. 9.9e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 NRYTGPYT 14
DB 2 SRYTGSST 9

RESULT 5
Q6EX62 PRELIMINARY; PRT; 10 AA.
ID Q6EX62
AC Q6EX62;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Ribosomal protein (Fragment).
GN Name=rp816;
OS Hyptis suaveolens.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Hyptis.
OX NCBI_TaxID=204129;
RN [1]
RP SEQUENCE FROM N.A.
RA Paton A., Springate D.A., Sudde S., Otieno D., Grayer R., Willis F.,
RA Powell M.P., Savolainen V.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ505341; CAD45464.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
KW Chloroplast; Ribosomal protein.
FT NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 1087 MW; 3783107729D1BB47 CRC64;

Query Match 30.5%; Score 25; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 PYTF 15
DB 3 PYTF 6

RESULT 6
P90442 PRELIMINARY; PRT; 13 AA.
ID P90442
AC P90442;
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Polyhedrin (Fragment).
OS Spodoptera littoralis nuclear polyhedrosis virus (SlNPV).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=10456;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97300849; PubMed=9155869;
RA Faktor O., Toister-Achituv M., Nachum O.;
RT "Enhancer element, repetitive sequences and gene organization in an 8-

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RT kbp region containing the polyhedrin gene of the Spodoptera littoralis
 RT nucleopolyhedrovirus.";
 RL Arch. Virol. 142:1-15(1997).
 DR EMBL: X99711; CAA68046.1; -;
 DR GO: GO:0005198; F: structural molecule activity; IEA.
 DR InterPro: IPR001746; Polyhedrin.
 DR Pfam: PF00738; Polyhedrin; 1.
 FT NON_TER 1
 SQ SEQUENCE 13 AA; 1383 MW; 2B0CD62832655737 CRC64;
 Query Match 30.5%; Score 25; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.6e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 YTGP 12
 Db 8 YTGP 11
 RESULT 7
 Q9QV00 PRELIMINARY; PRT; 15 AA.
 ID Q9QV00
 AC Q9QV00
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE Eosinophil cationic protein (Fragment).
 OS Rattus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10118;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95375557; PubMed=7647580;
 RA Watanabe M., Nittoh T., Suzuki T., Kitoh A., Mue S., Ohuchi K.;
 RT "Isolation and partial characterization of eosinophil granule proteins
 in rats--eosinophil cationic protein and major basic protein.";
 RL Int. Arch. Allergy Immunol. 108:11-18(1995).
 SQ SEQUENCE 15 AA; 1785 MW; 2AF6D99C12EBD794 CRC64;
 Query Match 30.5%; Score 25; DB 2; Length 15;
 Best Local Similarity 80.0%; Pred. No. 1.9e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 7 NRYTG 11
 Db 4 NRYTG 8
 RESULT 8
 AL16_CARMA STANDARD; PRT; 8 AA.
 ID AL16_CARMA
 AC P818T9;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Carcinus matting 16.
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Plecocyemata; Brachyura;
 OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 RT allatostatin superfamily in the shore crab Carcinus maenas.";
 RL Eur. J. Biochem. 250:727-734(1997).
 CC -!- FUNCTION: May act as a neurotransmitter or neuromodulator.
 CC -!- SIMILARITY: Belongs to the allatostatin family.

KW Amidation; Direct protein sequencing; Multigene family; Neuropeptide.
 FT MOD_RES 8
 SQ SEQUENCE 8 AA; 813 MW; 7C286B45AB476878 CRC64;
 Query Match 29.3%; Score 24; DB 1; Length 8;
 Best Local Similarity 60.0%; Pred. No. 1.6e+06;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 11 GPYTF 15
 Db 2 GPYSY 6
 RESULT 9
 Q9UR63 PRELIMINARY; PRT; 15 AA.
 ID Q9UR63
 AC Q9UR63
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Beta-D-FRUCTOFURANOSIDE FRUCTOHYDROLASE 60 kDa high molecular weight
 DE isoform (EC 3.2.1.26) (Fragment).
 OS Emericella nidulans (Aspergillus nidulans).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; Emericella.
 OX NCBI_TaxID=162425;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=96409246; PubMed=8814228; DOI=10.1016/0167-4838(96)00073-8;
 RA Chen J.S., Saxton J., Hemming F.W., Peberdy J.F.;
 RT "Purification and partial characterization of the high and low
 RT molecular weight form (S- and F-form) of invertase secreted by
 RT Aspergillus nidulans.";
 RL Biochim. Biophys. Acta 1296:207-218(1996).
 DR GO: GO:0004564; F:beta-fructofuranosidase activity; IEA.
 SQ SEQUENCE 15 AA; 1588 MW; 2C992B42211366BB CRC64;
 Query Match 29.3%; Score 24; DB 2; Length 15;
 Best Local Similarity 80.0%; Pred. No. 2.9e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 9 YTGYP 13
 Db 11 YTEPY 15
 RESULT 10
 Q7M285 PRELIMINARY; PRT; 15 AA.
 ID Q7M285
 AC Q7M285;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE GLYMA1 (Fragment).
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 OX NCBI_TaxID=3847;
 RN [1]
 RP SEQUENCE.
 RA Codina M.R.;
 RL Submitted (SEP-1995) to the PIR data bank.
 DR PIR; A56970; A56970.
 FT NON_TER 1
 FT NON_TER 15
 SQ SEQUENCE 15 AA; 1795 MW; 9F02F7DE3A760BD7 CRC64;
 Query Match 29.3%; Score 24; DB 2; Length 15;
 Best Local Similarity 44.4%; Pred. No. 2.9e+03;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 5 LNNRYTGPY 13

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Db          6 LADTYRGPF 14
| : | | |
RESULT 11
P97249
ID P97249 PRELIMINARY; PRT; 15 AA.
AC P97249;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Ammonia monooxygenase subunit Amoc3 (Ammonia monooxygenase subunit
DE Amoc2) (Fragment).
GN Name=amoc3; Synonyms=amoc2;
OS Nitrosospira multiformis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
OC Nitrosomonadaceae; Nitrosospira.
OX NCBI_TaxID=1231;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 25196;
RX MEDLINE=21665709; PubMed=11807563;
RA Norton J.M., Alzerreca J.J., Suwa Y., Klotz M.G.;
RT "Diversity of ammonia monooxygenase operon in autotrophic ammonia-
RT oxidizing bacteria.";
RL Arch. Microbiol. 177:139-149(2002).
DR EMBL; U99833; AAB48532.1; -.
DR EMBL; U15733; AAB48013.1; -.
DR GO; GO:0004497; F:monooxygenase activity; IEA.
KW Monooxygenase.
FT NON_TER 1
SQ SEQUENCE 15 AA; 1790 MW; 030B79929D28A467 CRC64;

Query Match 28.7%; Score 23.5; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 3.6e+03;
Matches 6; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 5 LNNRYTGPY 13
| | | | |
Db 4 LNNRIV-PY 11

RESULT 12
AL11 CARMA
ID AL11 CARMA STANDARD; PRT; 9 AA.
AC P81814;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Carcinustatin 11.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunioidea; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -!- FUNCTION: May act as a neurotransmitter or neuromodulator.
CC -!- SIMILARITY: Belongs to the allatostatin family.
KW Amidation; Direct protein sequencing; Multigene family; Neuropeptide.
FT MOD_RES 9
FT MOD_RES 9 Leucine amide.
SQ SEQUENCE 9 AA; 927 MW; 832D79CDBC46D861 CRC64;

Query Match 28.0%; Score 23; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 10 TGPYTF 15
| | | | |
Db 2 TQYAP 7

RESULT 13
Q9R4M8
ID Q9R4M8 PRELIMINARY; PRT; 15 AA.
AC Q9R4M8;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE Catalase isozyme I (Fragment).
OS Bacillus firmus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1399;
RN [1]
RP SEQUENCE.
RX MEDLINE=95267795; PubMed=7748885; DOI=10.1016/0005-2728(95)00016-C;
RA Hicks D.B.;
RT "Purification of three catalase isozymes from facultatively
RT alkaliphilic Bacillus firmus OF4.";
RL Biochim. Biophys. Acta 1229:347-355(1995).
SQ SEQUENCE 15 AA; 1677 MW; 12E47DC8F66876ED CRC64;

Query Match 28.0%; Score 23; DB 2; Length 15;
Best Local Similarity 46.2%; Pred. No. 4.4e+03;
Matches 6; Conservative 1; Mismatches 4; Indels 2; Gaps 1;

QY 4 TLNRYTGT--PYT 14
| | | | |
Db 3 TQNNENAGKXKPT 15

RESULT 14
Q924T1
ID Q924T1 PRELIMINARY; PRT; 15 AA.
AC Q924T1;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE DNase I (Fragment).
GN Name=DNASE1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21226133; PubMed=11327695; DOI=10.1006/bbrc.2001.4770;
RA Yasuda T., Takeshita H., Ueki M., Iida R., Nakajima T., Mori S.,
RA Mogi K., Kaneko Y., Kishi K.;
RT "Tissue-specific in vivo inhibition of DNase I gene expression by
RT somatostatin.";
RL Biochem. Biophys. Res. Commun. 283:287-291(2001).
DR EMBL; AB057442; BAB62091.1; -.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1743 MW; 35D288B8AED1DE561 CRC64;

Query Match 28.0%; Score 23; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 RYTG 11
| | | | |
Db 2 RYTG 5

RESULT 15
CA12_LITCI
ID CA12_LITCI STANDARD; PRT; 10 AA.
AC P62540; P82086;

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DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
-DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Caerulein 1.2/1.2Y4.
OS Litoria citropa (Australian blue mountains tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=94770;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RX MEDLINE=20057701; PubMed=10589099;
RA Wabnitz P.A., Bowie J.H., Tyler M.J.;
RT "Caerulein-like peptides from the skin glands of the Australian blue
mountains tree frog Litoria citropa. Part 1. Sequence determination
using electrospray mass spectrometry.";
RL Rapid Commun. Mass Spectrom. 13:2498-2502(1999).
CC -1- FUNCTION: Hypotensive neuropeptide (Probable).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin dorsal glands.
CC -1- PTM: Isoform 1.2Y4 differs from isoform 1.2 in not being sulfated.
CC -1- MASS SPECTROMETRY: MW=1366; METHOD=Electrospray; RANGE=1-10
(Isoform caerulein 1.2); NOTE=Ref.1.
CC -1- MASS SPECTROMETRY: MW=1286; METHOD=Electrospray; RANGE=1-10
(Isoform caerulein 1.2Y4); NOTE=Ref.1.
CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; FALSE NEG.
KW Amidation; Amphibian defense peptide; Direct protein sequencing;
KW Hypotensive agent; Pyrrolidone carboxylic acid; Sulfation.
FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
FT MOD_RES 4 4 Sulfotyrosine (in form caerulein 1.2).
FT MOD_RES 10 10 Phenylalanine amide.
SQ SEQUENCE 10 AA; 1306 MW; 99DBFCD37861BB5A CRC64;

Query Match 26.8%; Score 22; DB 1; Length 10;
Best Local Similarity 57.1%; Pred. No. 4.2e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 YTGPTTF 15
||| : |
Db 4 YTGWDFD 10

Search completed: February 22, 2005, 09:37:54
Job time : 53.6667 secs

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OM protein - protein search, using sw model

Run on: February 22, 2005, 08:52:23 ; Search time 65.6667 Seconds
(without alignments)
88.346 Million cell updates/sec

Title: US-08-991-628-6

Perfect score: 82

Sequence: 1 SARTLNRRVTPYTF 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 632537

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	82	100.0	15	2	AAW04846 Self epit
2	36	43.9	10	3	AAE77563 GPCR-B4 p
3	34	41.5	13	5	AAE20719 Human Mls
4	34	41.5	13	5	AAE21020 Human Icr
5	31	37.8	12	2	AAW23267 Tumour ne
6	31	37.8	12	2	AAW23269 Tumour ne
7	31	37.8	13	2	AAW23268 Tumour ne
8	31	37.8	13	8	ADP44318 Chaperone
9	31	37.8	14	6	ABR55893 CDR3-junc
10	31	37.8	15	6	ABR33651 Human can
11	31	37.8	15	6	ABR33761 Human can
12	31	37.8	15	6	ABR33743 Human can
13	30	36.6	12	2	AAW16032 Peptide c
14	30	36.6	12	2	AAW68670 Peptide b
15	30	36.6	12	2	AAW58149 IL-1RI b
16	30	36.6	12	2	AAW09793 Interleuk
17	30	36.6	12	3	ABR17593 IL-1 anta
18	30	36.6	12	5	ABR72489 Interleuk
19	30	36.6	12	7	ADJ72682 Interleuk
20	30	36.6	12	8	ADJ52317 CH1 delet
21	30	36.6	12	8	ADJ51280 CH1 delet
22	30	36.6	13	7	ADM75241 Potential
23	29	35.4	10	2	AAW67679 Go-alpha
24	29	35.4	10	3	AAW79428 Tie2 rece
25	29	35.4	10	7	ADM08993 Canine im

26	29	35.4	10	7	ADM08999 Canine im
27	29	35.4	12	3	AAV56630 Virus-lik
28	29	35.4	12	3	AAV56273 Human cat
29	29	35.4	13	3	AAV39640 Anti-IL12
30	29	35.4	14	7	ADC83481 Asparagin
31	29	35.4	14	7	ADC83531 Asparagin
32	29	35.4	14	7	ADC83579 Asparagin
33	28	34.1	9	6	ABO10713 Murine J4
34	28	34.1	9	6	ABR44657 Murine J4
35	28	34.1	9	8	ADQ90785 Mouse com
36	28	34.1	10	4	AAU25785 Breast ca
37	28	34.1	11	8	ADR25847 Anti-alpha
38	28	34.1	14	2	AAW60752 Lolium pe
39	28	34.1	14	7	ADC83623 Asparagin
40	28	34.1	14	8	ADH89412 Human tra
41	27	32.9	6	2	AAW25089 bGRF prod
42	27	32.9	8	2	AAW25090 bGRF prod
43	27	32.9	9	2	AAW27420 CDR3 from
44	27	32.9	9	4	AAW63652 Complemen
45	27	32.9	9	6	ABJ38610 Hepatitis

ALIGNMENTS

RESULT 1
AAW04846
ID AAW04846 standard; peptide; 15 AA.
XX
AC AAW04846;

DT 18-FEB-1997 (first entry)

DE Self epitope of desmoglein 3, implicated in autoimmune disease.

XX Tolerisation; self-epitope; antigen; autoimmune disease; autoantigen;
KW HLA; human leukocyte antigen; T-cell; thymocyte; pemphigus vulgaris;
KW desmoglein; multiple sclerosis; herpes simplex virus; adenovirus;
KW phosphonannomutase; human papillomavirus; Epstein-Barr virus;
KW DNA polymerase; influenza; haemagglutinin; reovirus; sigma protein.

XX Homo sapiens.

XX WO9627387-A1.

XX 12-SEP-1996.

XX 07-MAR-1996; 96WO-US003182.

XX 07-MAR-1995; 95US-00400796.

(HARD) HARVARD COLLEGE.

PI Strominger JL, Wucherpfennig KW;

XX WPI; 1996-425218/42.

XX Pemphigus vulgaris auto-antigens and multiple sclerosis non-self antigens
PT - useful in disease treatment, and method for identification of other
PT self and non-self antigens implicated in autoimmune disease.

XX Claim 1; Page 41; 58pp; English.

CC Pharmaceutical preparations for tolerisation to antigens comprise either
CC an isolated human non-collagen or non-mysin basic protein (MBP)
CC polypeptide which is capable of tolerising an individual to an
CC autoantigen; or an isolated human pathogen polypeptide capable of
CC tolerising an individual to that polypeptide. In both cases, the
CC polypeptide (whether self or non-self) includes an amino acid sequence
CC corresponding to a sequence motif for a MHC class II protein, such as HLA
CC -DR, which is associated with a human autoimmune disease and which binds
CC to the polypeptide to activate autoreactive T-cells in individuals with
CC the autoimmune disease. This peptide is derived from the human desmoglein

CC 3 protein (amino acids 512-526) and is implicated as a self epitope in
 CC pemphigus vulgaris. Peptides derived from the human desmoglein protein
 CC are described in AA04841-47
 XX
 SQ Sequence 15 AA;

Query Match 100.0%; Score 82; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.7e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SARTLNRYTGPYTF 15
 |||||
 DB 1 SARTLNRYTGPYTF 15
 |||||

RESULT 2

AAAY77563
 ID AAY77563 standard; peptide; 10 AA.

AC AAY77563;
 DT 08-MAY-2000 (first entry)
 XX
 DE GPCR-B4 peptide fragment.
 XX
 KW Sensory transduction G-protein coupled receptor; GPCR; GPCR-B4; rat;
 KW taste transduction pathway; taste receptor; foliate; fungiform; food;
 KW circumvallate; taste signaling; pharmaceutical.

OS Rattus sp.
 OS Mus sp.

PN WO200006593-A1.

PD 10-FEB-2000.

PF 27-JUL-1999; 99WO-US017104.

PR 28-JUL-1998; 98US-0095464P.

PR 17-DEC-1998; 98US-0112747P.

PA (REGC) UNIV CALIFORNIA.

PI Zuker CS, Adler JE, Lindemeier J;

DR WPI; 2000-195257/17.

PT New isolated sensory transduction G-protein coupled receptor, useful for
 PT developing products for use in studying and modulating the taste
 PT transduction pathway and for generating taste topographic maps.

PS Claim 7; Page 58; 76pp; English.

XX The invention provides nucleic acids encoding rat, mouse and human
 CC sensory transduction G-protein coupled receptor (GPCR) polypeptides. The
 CC GPCR polypeptides are components of the taste transduction pathway. The
 CC nucleic acids can be used to identify taste cells and as tools for the
 CC generation of taste topographic maps that elucidate the relationship
 CC between the taste cells of the tongue and taste sensory neurons leading
 CC to taste centers in the brain. GPCR-B4 is useful as a nucleic acid probe
 CC for identifying subpopulations of taste receptor cells such as foliate,
 CC fungiform, and circumvallate taste receptor cells. The polypeptides can
 CC be used for identifying compounds that modulate sensory signaling in
 CC sensory cells. Such modulators of taste transduction are useful for
 CC pharmacological and genetic modulation of taste signaling pathways. These
 CC modulatory compounds can then be used in the food and pharmaceutical
 CC industries to customize taste. The present sequence represents a GPCR-B4
 CC peptide fragment

XX Sequence 10 AA;

Query Match 43.9%; Score 36; DB 3; Length 10;
 Best Local Similarity 75.0%; Pred. No. 17;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 8 RYTGPTVF 15
 |||||
 DB 3 RYHGPTVF 10
 |||||

RESULT 3

AAE20719
 ID AAE20719 standard; peptide; 13 AA.

XX AAE20719;

DT 01-JUL-2002 (first entry)

DE Human Mlsn1 intra-cellular loop 2 peptide #1.

XX Human; Mlsn1 protein; calcium channel; immune system; macrophage; T-cell;
 KW monocyte; B-cell; mast cell; lcrac; immuno degenerative disorder; COPD;
 KW biomarker; autoimmune disease; inflammatory disease; organ rejection;
 KW arthritis; antisense gene therapy; intra-cellular loop 2.

XX Homo sapiens.

PN EP1184457-A1.

PD 06-MAR-2002.

PF 03-SEP-2001; 2001EP-00402283.

PR 05-SEP-2000; 2000EP-00402436.

PA (WARN) WARNER LAMBERT CO.

PI Schindler V, Bloes C, Fink M, Allen J, Grentzmann G;

DR WPI; 2002-271038/32.

DR N-PSDB; AAD33208.

PT Novel Mlsn1 polypeptide and nucleic acid encoding the polypeptide, useful
 PT for screening Mlsn1 modulators and for diagnosing disorders associated
 PT with aberrant lcrac function in immune cells.

PS Claim 16; Page 37; 63pp; English.

XX The patent discloses novel human Mlsn1 polypeptides and polynucleotides
 CC encoding them. The invention also relates to the characterisation of
 CC capacitative calcium channel homologue for the activation of immune
 CC system. Mlsn1 gene products contain a novel calcium pore sequence which
 CC is a part of the capacitative calcium channel in immune cells such as
 CC macrophages, monocytes, T-cells, B-cells and mast cells. Mlsn1 sequences
 CC are useful for screening Mlsn1 modulators and for diagnosing disorders
 CC associated with aberrant lcrac function in immune cells. They are useful
 CC for screening ligand substances or molecules that are able to modulate
 CC the biological activity of Mlsn1. The compound identified as modulator is
 CC the biological activity of Mlsn1. The compound identified as modulator is
 CC that bind and/or modulate the biological activity of Mlsn1. Sequences of
 CC the invention are useful for treating immuno degenerative disorders. They
 CC are also useful for developing biomarkers for immune system activation or
 CC autoimmune or inflammatory diseases (e.g., arthritis, organ rejection,
 CC COPD), as modulators of immune system activation and as therapeutic
 CC targets. Mlsn1 sequences are also used for antisense gene therapy. The
 CC present sequence is human mlsn1 intra-cellular loop 2 peptide

XX Sequence 13 AA;

Query Match 41.5%; Score 34; DB 5; Length 13;
 Best Local Similarity 71.4%; Pred. No. 53;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 NRYTGPY 13

DB 1 NKYLGPY 7

RESULT 4
AAE21020
ID AAE21020 standard; peptide; 13 AA.
XX
AC AAE21020;
XX
DT 01-JUL-2002 (first entry)
XX
DE Human Icrac-Mlsn1 protein fragment #6.
XX
KW Human; Icrac-Mlsn1; major capacitative calcium channel; ligand screening;
KW macrophage maturation; detection.
XX
OS Homo sapiens.
XX
PN EP1186661-A1.
XX
PD 13-MAR-2002.
XX
PF 05-SEP-2000; 2000EP-00402436.
XX
PR 05-SEP-2000; 2000EP-00402436.
XX
PA (WARN) WARNER LAMBERT CO.
XX
PI Allen J, Grentzmann G, Fink M, Schindler V, Bloss C;
XX
DR WPI; 2002-282883/33.
DR N-PSDB; AAD33455.
XX
XX Polypeptide regions of major capacitative calcium channel and
PT polynucleotide regions useful for screening modulators of channel
PT activity for regulating activity of antigen presenting cell especially of
PT macrophages.
XX
PS Claim 16; Page 36; 62pp; English.
XX
XX The invention relates to a purified or isolated N-terminal polypeptide
CC region, C-terminal polypeptide region, extracellular and intracellular
CC loop regions, of human Icrac-Mlsn1 (major capacitative calcium channel).
CC Icrac-Mlsn1 DNA and protein are useful for screening ligand substances or
CC molecules that are able to bind to a Icrac-Mlsn1 and modulates the
CC activity of antigen presenting cells especially macrophages maturation.
CC Icrac-Mlsn1 is also useful for screening ligand substances or molecules
CC that are able to modulate the biological activity of Icrac-Mlsn1, where a
CC change in calcium flux or activation potential within the exposed
CC recombinant cell is measured, and where the recombinant cell expresses a
CC reporter molecule under the control of Icrac-Mlsn1 DNA, where a
CC competitor Mlsn1 binding ligand, is selected from the class of pyrazol
CC compounds is added and the binding of the competitor in the presence
CC and/or absence of a test compound is determined. Icrac-Mlsn1 useful for
CC detecting Icrac-Mlsn1 DNA in a blood sample. The present sequence is
CC human Icrac-Mlsn1 protein intracellular loop 2
XX
SQ Sequence 13 AA;
Query Match 41.5%; Score 34; DB 5; Length 13;
Best Local Similarity 71.4%; Pred. No. 53;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 7 NRYTGPY 13
|:|:|:|
DB 1 NKYLGPY 7
RESULT 5
AAW23267
ID AAW23267 standard; peptide; 12 AA.
XX
AC AAW23267;
XX

DT 03-NOV-1997 (first entry)
XX
DE Tumour necrosis factor alpha inhibiting peptide.
XX
KW Tumour necrosis factor; alpha; TNF-alpha; inhibition; treatment;
KW mediation; disorder; septic shock; bacterium; virus; fungus; infection;
KW autoimmune; disease; alcohol induced hepatitis; sarcoiditis; Crohn's;
KW disseminated intravascular coagulation; graft versus host; Rawasaki's;
KW tumour; bacteria.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "acetylated"
FT Modified-site 12 /note= "amidated"
FT
XX US5641751-A.
PN XX
PD 24-JUN-1997.
XX
PF 01-MAY-1995; 95US-00432694.
XX
PR 01-MAY-1995; 95US-00432694.
XX
PA (CENZ) CENTOCOR INC.
XX
PI Heavner GA;
XX
DR WPI; 1997-340972/31.
XX
XX Peptide inhibiting tumour necrosis factor alpha - useful for treating
PT septic shock, infections, autoimmune diseases, etc.
XX
XX Example 2; Col 23-24; 15pp; English.
XX
CC The present peptide is a tumour necrosis factor alpha (TNF-alpha)
CC inhibitor, which can be used to treat TNF-alpha mediated disorders, e.g.
CC septic shock, bacterial, viral and fungal infections, autoimmune
CC diseases, alcohol induced hepatitis, sarcoiditis, Crohn's disease,
CC disseminated intravascular coagulation, graft versus host disease,
CC Rawasaki's disease and TNF-alpha secreting tumours. The peptide is
CC preferably given as a daily dose of 1-1000, preferably 1-10 mg/kg, and
CC has an IC50 of 155 microm against binding of TNF-alpha to a p55TNFr-IgG
CC construct
XX
SQ Sequence 12 AA;
Query Match 37.8%; Score 31; DB 2; Length 12;
Best Local Similarity 71.4%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 5 LNNRYTG 11
|:|:|:|
DB 6 VSNRYTG 12
RESULT 6
AAW23269
ID AAW23269 standard; peptide; 12 AA.
XX
AC AAW23269;
XX
DT 03-NOV-1997 (first entry)
XX
DE Tumour necrosis factor alpha inhibiting peptide.
XX
KW Tumour necrosis factor; alpha; TNF-alpha; inhibition; treatment;
KW mediation; disorder; septic shock; bacterium; virus; fungus; infection;
KW autoimmune; disease; alcohol induced hepatitis; sarcoiditis; Crohn's;
KW disseminated intravascular coagulation; graft versus host; Rawasaki's;
KW tumour; bacteria.

OS Synthetic.
 XX US5641751-A.
 PN 24-JUN-1997.
 PD 01-MAY-1995; 95US-00432694.
 PF 01-MAY-1995; 95US-00432694.
 XX 01-MAY-1995; 95US-00432694.
 XX (CENZ) CENTOCOR INC.
 PA Heavner GA;
 XX WPI; 1997-340972/31.
 DR Peptide inhibiting tumour necrosis factor alpha - useful for treating
 PT septic shock, infections, autoimmune diseases, etc.
 XX Disclosure; Col 23-24; 15pp; English.
 XX The present peptide is a tumour necrosis factor alpha (TNF-alpha)
 CC inhibitor, which can be used to treat TNF-alpha mediated disorders, e.g.
 CC septic shock, bacterial, viral and fungal infections, autoimmune
 CC diseases, alcohol induced hepatitis, sarcoiditis, Crohn's disease,
 CC disseminated intravascular coagulation, graft versus host disease,
 CC Kawasaki's disease and TNF-alpha secreting tumours. The peptide is
 CC preferably given as a daily dose of 1-1000, preferably 1-10 mg/kg
 XX SQ Sequence 12 AA;
 Query Match 37.8%; Score 31; DB 2; Length 12;
 Best Local Similarity 71.4%; Pred. No. 1.7e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 5 LNNRYTG 11
 Db ::|||
 6 VSNRYTG 12
 RESULT 7
 AAW23268
 ID AAW23268 standard; peptide; 13 AA.
 AC AAW23268;
 XX 03-NOV-1997 (first entry)
 DT Tumour necrosis factor alpha inhibiting peptide.
 DE
 XX Tumour necrosis factor; alpha; TNF-alpha; inhibition; treatment;
 KW mediation; disorder; septic shock; bacterium; virus; fungus; infection;
 KW autoimmune; disease; alcohol induced hepatitis; sarcoiditis; Crohn's;
 KW disseminated intravascular coagulation; graft versus host; Kawasaki's;
 KW tumour; bacteria.
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 XX Modified-site 1
 FT /note= "acetylated"
 FT Modified-site 13
 FT /note= "amidated"
 XX US5641751-A.
 PN 24-JUN-1997.
 XX 01-MAY-1995; 95US-00432694.
 XX 01-MAY-1995; 95US-00432694.
 PR

PA (CENZ) CENTOCOR INC.
 XX Heavner GA;
 XX WPI; 1997-340972/31.
 DR Peptide inhibiting tumour necrosis factor alpha - useful for treating
 PT septic shock, infections, autoimmune diseases, etc.
 XX Example 2; Col 23-24; 15pp; English.
 XX The present peptide is a tumour necrosis factor alpha (TNF-alpha)
 CC inhibitor, which can be used to treat TNF-alpha mediated disorders, e.g.
 CC septic shock, bacterial, viral and fungal infections, autoimmune
 CC diseases, alcohol induced hepatitis, sarcoiditis, Crohn's disease,
 CC disseminated intravascular coagulation, graft versus host disease,
 CC Kawasaki's disease and TNF-alpha secreting tumours. The peptide is
 CC preferably given as a daily dose of 1-1000, preferably 1-10 mg/kg, and
 CC has an IC50 of 307 microM against binding of TNF-alpha to a p55TNFr-IgG
 CC construct
 XX Sequence 13 AA;
 SQ Query Match 37.8%; Score 31; DB 2; Length 13;
 Best Local Similarity 71.4%; Pred. No. 1.8e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 5 LNNRYTG 11
 Db ::|||
 6 VSNRYTG 12
 RESULT 8
 ADP44318
 ID ADP44318 standard; peptide; 13 AA.
 XX ADP44318;
 AC 26-AUG-2004 (first entry)
 DT Chapterone-related peptide #5.
 XX Chapterone peptide; transmissible spongiform encephalopathy;
 KW Creutzfeld-Jakob disease; scrapie; bovine spongiform encephalopathy.
 XX Synthetic.
 OS JP2004155688-A.
 PN 03-JUN-2004.
 XX 05-NOV-2002; 2002JP-00321436.
 PF 30-APR-2002; 2002JP-00128976.
 PR 10-JUL-2002; 2002JP-00200884.
 PR 13-SEP-2002; 2002JP-00268260.
 XX (BIOF-) BIO FRONTIER KENKYUSHO KK.
 PA WPI; 2004-424357/40.
 XX New synthetic peptide having chaperone activity, useful for treating
 PT transmissible spongiform encephalopathies such as Creutzfeld-Jakob
 PT disease and scrapie.
 XX Example; SEQ ID NO 7; 22pp; Japanese.
 XX The invention comprises synthetic peptides that have chaperone activity.
 CC The peptides of the invention are useful in the treatment of
 CC transmissible spongiform encephalopathies, Creutzfeld-Jakob disease,
 CC scrapie and bovine spongiform encephalopathy. The present amino acid
 CC sequence represents a peptide that was used in the exemplification of the
 CC invention.

```
XX SQ Sequence 13 AA;
Query Match 37.8%; Score 31; DB 8; Length 13;
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SARTLNRY 9
   |||:|
Db 5 SGRTWSNRY 13

RESULT 9
ABR55893
ID ABR55893 standard; protein; 14 AA.
XX AC ABR55893;
XX DT 02-SEP-2003 (first entry)
XX DE CDR3-junction sequence of kappa light chain of mAb 2C8.
XX KW Mitochondrial antigen; autoantibody; biliary cirrhosis; transgenic;
XX KW monoclonal antibody; mAb.
XX OS Homo sapiens.
XX PN WO200276406-A2.
XX PD 03-OCT-2002.
XX PF 27-MAR-2002; 2002WO-US009694.
XX PR 27-MAR-2001; 2001US-0279052P.
XX PR 21-SEP-2001; 2001US-0323920P.
XX PA (GERS/) GERSHWIN M E.
XX PI Gershwin ME;
XX PI WPI; 2003-018851/01.
XX DR
XX CC New anti-mitochondrial antigen specific human monoclonal antibodies from
PT patients with primary biliary cirrhosis (PBC), useful as a diagnostic
PT reagent, or as a reagent for screening antagonists for treating patients
PT with PBC.
XX PS Claim 34; Page 101; 150pp; English.
XX CC The invention relates to an isolated human antibody or its antigen-
CC binding portions, which binds a mitochondrial antigen bound by a human
CC autoantibody found in patients with primary biliary cirrhosis. The
CC antibody is useful as a diagnostic reagent, e.g. for monitoring whether a
CC transplanted liver in a patient with primary biliary cirrhosis, is
CC expressing a mitochondrial antigen bound by an autoantibody. The antibody
CC is also useful for purifying an antigen to which it binds, for producing
CC an anti-idiotype antibody to it, or as a reagent to screen for
CC antagonists to it, either in vivo or in vitro. The antagonist is useful
CC for treating a patient with primary biliary cirrhosis, or for
CC prophylactically treating a patient about to have primary biliary
CC cirrhosis. Sequences ABR55890-98 represent CDR3- junction sequences of
CC the kappa light chains of the anti-mitochondrial antigen human monoclonal
CC antibodies (mAbs) 2E6, 4D11, 1C7, 2C8, 3B4, 4G6, 4C2, 2E11 and 3B10
XX SQ Sequence 14 AA;
Query Match 37.8%; Score 31; DB 6; Length 14;
Best Local Similarity 62.5%; Pred. No. 2e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 RYTGPTTF 15
   |||:|
Db 4 RYNTPTTF 11

RESULT 10
ABR33651
ID ABR33651 standard; peptide; 15 AA.
XX AC ABR33651;
XX DT 19-MAY-2003 (first entry)
XX DE Human cancer-related protein 159P2B5 HLA peptide #41.
XX KW Human; cytostatic; vaccine; cancer; immune response; HLA;
XX KW human leukocyte antigen.
XX OS Homo sapiens.
XX PN WO200283921-A2.
XX PD 24-OCT-2002.
XX PF 10-APR-2002; 2002WO-US011654.
XX PR 10-APR-2001; 2001US-0282739P.
XX PR 10-APR-2001; 2001US-0283112P.
XX PR 25-APR-2001; 2001US-0286630P.
XX PA (AGEN-) AGENSYS INC.
XX PI Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX WPI; 2003-075555/07.
XX DR
XX CC New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.
XX PS Claim 13; Page 533; 1021pp; English.
XX CC The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention
XX SQ Sequence 15 AA;
Query Match 37.8%; Score 31; DB 6; Length 15;
Best Local Similarity 60.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 RTLNRYTGP 12
   |||:|
Db 1 RTQARRHTGP 10

RESULT 11
ABR33761
ID ABR33761 standard; peptide; 15 AA.
XX AC ABR33761;
XX DT 19-MAY-2003 (first entry)
XX DR
```

DE Human cancer-related protein 159P2B5 HLA peptide #151.
 XX Human; cytostatic; vaccine; cancer; immune response; HLA;
 KW human leukocyte antigen.
 XX
 OS Homo sapiens.
 XX
 PN WO200283921-A2.
 XX
 PD 24-OCT-2002.
 XX
 PF 10-APR-2002; 2002WO-US011654.
 XX
 PR 10-APR-2001; 2001US-0282739P.
 PR 10-APR-2001; 2001US-0283112P.
 PR 25-APR-2001; 2001US-0286630P.
 XX
 PA (AGEN-) AGENSYS INC.
 XX
 PI Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;
 XX
 DR WPI; 2003-075555/07.
 XX
 PT New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response in
 PT cancer patients.
 XX
 PS Claim 13; Page 535; 1021pp; English.
 XX
 CC The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention
 XX
 SQ Sequence 15 AA;
 Query Match 37.8%; Score 31; DB 6; Length 15;
 Best Local Similarity 60.0%; Pred. No. 2.1e+02;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 3 RTLNRYTGP 12
 DB ||| :|||
 3 RTQARRHTGP 12
 RESULT 12
 ABR33743
 ID ABR33743 standard; peptide; 15 AA.
 XX
 AC ABR33743;
 XX
 DT 19-MAY-2003 (first entry)
 XX
 DE Human cancer-related protein 159P2B5 HLA peptide #133.
 XX
 KW Human; cytostatic; vaccine; cancer; immune response; HLA;
 KW human leukocyte antigen.
 XX
 OS Homo sapiens.
 XX
 PN WO200283921-A2.
 XX
 PD 24-OCT-2002.

XX 10-APR-2002; 2002WO-US011654.
 PF
 XX 10-APR-2001; 2001US-0282739P.
 PR
 PR 10-APR-2001; 2001US-0283112P.
 PR 25-APR-2001; 2001US-0286630P.
 XX
 PA (AGEN-) AGENSYS INC.
 XX
 PI Jakobovits A, Challita-Eid PM, Paris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;
 XX
 DR WPI; 2003-075555/07.
 XX
 PT New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response in
 PT cancer patients.
 XX
 PS Claim 13; Page 535; 1021pp; English.
 XX
 CC The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer. The present
 CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
 CC from the invention
 XX
 SQ Sequence 15 AA;
 Query Match 37.8%; Score 31; DB 6; Length 15;
 Best Local Similarity 60.0%; Pred. No. 2.1e+02;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 3 RTLNRYTGP 12
 DB ||| :|||
 4 RTQARRHTGP 13
 RESULT 13
 AAW16032
 ID AAW16032 standard; peptide; 12 AA.
 XX
 AC AAW16032;
 XX
 DT 19-AUG-1997 (first entry)
 XX
 DE Peptide containing QPY or QPY-like motif.
 XX
 KW interleukin-1; type I receptor; IL-1r1; agonist; antagonist.
 XX
 OS Synthetic.
 XX
 PN WO9639165-A1.
 XX
 PD 12-DEC-1996.
 XX
 PF 05-JUN-1996; 96WO-US009835.
 XX
 PR 05-JUN-1995; 95US-00464538.
 XX
 PA (AFFV-) AFFYMAX TECHNOLOGIES NV.
 XX
 PI Barrett RW, Yanofsky SD, Baldwin D, Jacobs JW, Bovy PR, Leahy EM;
 PI Pottorf RS, Dharanipragada R, Tomlinson RC;
 XX
 DR WPI; 1997-042846/04.

XX Interleukin-1 type I receptor inhibitor peptide(s) and compounds - used
PT to antagonise the activity of IL-1, for treatment of e.g. AIDS,
PT rheumatoid arthritis, chronic hepatitis B, etc.
XX
XX Disclosure; Page 22; 74pp; English.
XX
XX The invention relates to peptides which bind to the IL-1 type I receptor
CC and which comprise the motif WXXG-Z1-W or the motif XXQ-Z5-Y-Z6-XX, in
CC which X can be any one of the 20 genetically coded L-amino acids or the
CC stereoisomeric D-amino acids or unnatural amino acids; Z1 is L, I, A or Q
CC; Z5 is P or azetidine (presumably intended to be azetidine carboxylic
CC acid); and Z6 is S, A, V or L. The present sequence is that of a random
CC peptide from a library of peptides containing the "XXQ-Z5-Y-Z6-XX" motif,
CC the library being constructed to screen the peptides for activity. IL-1
CC type I receptor-binding peptides may be useful in the treatment of a
CC variety of IL-1 related disorders including atherosclerosis, rheumatoid
CC arthritis, osteoporosis, HIV infection and AIDS, bacterial infection,
CC respiratory distress syndrome, acute myelogenous leukaemia, graft versus
CC host disease, coal miner pneumoconiosis, alcoholic cirrhosis, cuprophane
CC haemodialysis, cardiopulmonary bypass, chronic hepatitis B, tuberculosis,
CC obstructive jaundice, Paget's disease and osteomalacia, IDDM, Kawasaki's
CC disease, inflammatory bowel disease, sepsis, toxic shock and luteal phase
XX
SQ Sequence 12 AA;

Query Match 36.6%; Score 30; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 6 NNRYTGPYTF 15
| | | | |
Db 1 NGNYWQPYSF 10

RESULT 14

AAW68670
ID AAW68670 standard; peptide; 12 AA.

XX
XX AAW68670;

XX
XX 01-OCT-1998 (first entry)

XX Peptide binding interleukin-1 type I receptor.

XX Antagonist; interleukin-1; IL-1; IL-1 type I receptor; IL-1rTi;
KW treatment; IL-1 disorder.

XX Synthetic.

XX US5786331-A.

XX 28-JUL-1998.

XX 05-JUN-1995; 95US-00465391.

XX 02-FEB-1994; 94US-00190788.

XX 01-FEB-1995; 95US-00383474.

XX (HMRI) HOECHST MARION ROUSSEL INC.

PA (AFFY-) AFFYMAX TECHNOLOGIES NV.

XX Yanofsky SD, Jacobs JW, Bovy PR, Leahy EM, Barrett RW;

PI Pottorf RS, Baldwin D;

XX WPI; 1998-436582/37.

XX Antagonisation of action of interleukin-1 on type I receptor - by

PT contacting receptor with selected peptides.

XX Disclosure; Col 13; 118pp; English.

XX AAW68666-75 represent random peptide sequences, identified from a peptide

CC library based on the peptide AAW68899. The peptides antagonise the action
CC of interleukin-1 (IL-1) by binding to an IL-1 type I receptor (IL-1rTi).
CC The peptides are used in the treatment of disorders mediated by IL-1,
CC e.g. atherosclerosis, arthritis, osteoporosis, AIDS, bacterial
CC infections, respiratory distress syndrome, acute myelogenous leukaemia,
CC graft-versus-host disease, pneumoconiosis, cirrhosis, cuprophane
CC haemodialysis, cardiopulmonary bypass, hepatitis B, thermal injury,
CC reticulohistiocytosis, sarcoidosis, tuberculosis, obstructive jaundice,
CC Paget's disease, osteomalacia, diabetes, Kawasaki's disease, inflammatory
CC bowel disease, sepsis, toxic shock and luteal phase
XX
SQ Sequence 12 AA;

Query Match 36.6%; Score 30; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 6 NNRYTGPYTF 15
| | | | |
Db 1 NGNYWQPYSF 10

RESULT 15

AAW58149
ID AAW58149 standard; peptide; 12 AA.

XX
XX AAW58149;

XX 14-AUG-1998 (first entry)

XX IL-1rTi binding peptide SEQ ID NO:75 based in SEQ ID NO:45.

XX Interleukin-1 type I receptor; binding peptide; IL-1R; IL-1rTi;
KW competitive inhibition; cytokine; blocker; IL-1 related disorder;
KW diagnosis; atherosclerosis; rheumatoid arthritis; osteoporosis.

XX Synthetic.

XX Homo sapiens.

XX US5767234-A.

XX 16-JUN-1998.

XX 01-FEB-1995; 95US-00383474.

XX 02-FEB-1994; 94US-00190788.

XX (AFFY-) AFFYMAX TECHNOLOGIES NV.

XX Baldwin D, Jacobs JW, Yanofsky SD, Barrett RW;

PI WPI; 1998-361782/31.

XX Peptide(s) that bind to interleukin-1 type I receptor - useful in
PT screening assays for interleukin receptors blockers, diagnosis and
PT therapy.

XX Disclosure; Col 11; 89pp; English.

XX A compound has been developed that binds to an interleukin-1 (IL-1) type
CC I receptor with an IC50 of 2.5 mM or less and has a molecular weight of
CC <3 kD, where the binding of the compound to the receptor is competitively
CC inhibited by a peptide of 8-25 amino acids comprising the core sequence:
CC 27-Z8-Q-Z5-Y-Z6-Z9-Z10, where Z5 = Pro or azetidine; Z6 = Ser, Ala, Val
CC or Leu; Z7 = Tyr, Trp or Phe; Z8 = Glu, Phe, Val, Trp or Tyr; Z9 = Met,
CC Phe, Val, Arg, Gln, Lys, Thr, Ser, Asp, Leu, Ile or Glu; and Z10 = Glu,
CC Leu, Trp, Val, His, Ile, Gly, Ala, Asp, Tyr, Asn, Gln or Pro. Peptides of
CC the invention are used in screening assays for IL-1 receptor blockers.
CC They are also used as probes for detecting IL-1 type I receptor
CC expression on the surface of cells. The peptides are useful in treating
CC IL-1-related disorders, e.g. atherosclerosis, rheumatoid arthritis,
CC osteoporosis, HIV infection, AIDS, bacterial infection, respiratory
CC distress syndrome, acute myelogenous leukaemia (AML), graft versus host

CC disease, coal miner pneumoconiosis, alcoholic cirrhosis, cuprophane
CC haemodialysis, cardiopulmonary bypass, chronic hepatitis B, thermal
CC injury, reticulohistiocytosis, sarcoidosis, tuberculosis, obstructive
CC jaundice, Paget's disease and osteomalacia, Kawasaki's disease,
CC inflammatory bowel disease, sepsis, toxic shock, and luteal phase. The
CC present sequence represents a peptide from the present invention

Query Match 36.6%; Score 30; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 6 NNRYTGPYTF 15
Db 1 NGNIWQPYSF 10

Search completed: February 22, 2005, 09:24:40
Job time : 68.6667 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 22, 2005, 09:08:09 ; Search time 11.1333 Seconds
(without alignments)
129.633 Million cell updates/sec

Title: US-08-991-628-7

Perfect score: 80

Sequence: 1 QSGTMRHSTGQTN 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 2523

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	35.0	11	2 A61512	variant surface gl
2	23	28.7	14	2 PH0776	T-cell receptor al
3	22	27.5	9	1 YFRG	thymic factor - pi
4	22	27.5	9	2 A60557	thymocyte growth p
5	22	27.5	15	2 PH0751	T-cell receptor be
6	21	26.2	8	2 PT0639	T-cell receptor be
7	21	26.2	11	2 PH0919	T-cell receptor be
8	21	26.2	11	2 S05002	corazonin - Americ
9	21	26.2	15	2 S57577	T cell receptor V-
10	20	25.0	8	2 A54823	olfactory receptor
11	20	25.0	12	2 D20907	Ig kappa-1 chain J
12	20	25.0	12	2 PH1464	T-cell receptor be
13	20	25.0	14	2 I51432	histone H4-1 precu
14	20	25.0	15	2 C43334	orf3 3' to aadr -
15	20	25.0	15	2 A28497	neurotensin-relate
16	19	23.8	6	2 PT0512	T-cell receptor be
17	19	23.8	9	2 PT0231	Ig heavy chain CDR
18	19	23.8	9	2 D44787	callicliffamide 13
19	19	23.8	10	2 S19296	16K protein - poul
20	19	23.8	10	2 E61512	variant surface gl
21	19	23.8	11	2 PT0287	Ig heavy chain CRD
22	19	23.8	12	2 A49033	T-cell receptor de
23	19	23.8	12	2 PH0931	T-cell receptor be
24	19	23.8	14	2 S58426	spermadesin AWN h
25	19	23.8	15	2 A38304	heterogeneous ribo
26	19	23.8	15	2 PA0099	phenotypic variati
27	18	22.5	8	2 PT0588	T-cell receptor be
28	18	22.5	9	2 D28854	fibrinopeptide B -
29	18	22.5	10	2 B38887	T-cell receptor ga

30 18 22.5 11 2 PN0167 ribosomal protein
31 18 22.5 11 2 PT0302 Ig heavy chain CRD
32 18 22.5 11 2 B41946 T-cell receptor ga
33 18 22.5 11 2 C49037 TcR gamma V-J regi
34 18 22.5 12 2 C49033 T-cell receptor de
35 18 22.5 12 2 PT0216 T-cell receptor be
36 18 22.5 13 2 A23695 myosin heavy chain
37 18 22.5 13 2 S74130 NADH oxidase - Gia
38 18 22.5 14 2 A42473 ermK leader peptid
39 18 22.5 14 2 A32654 fibrinopeptide A -
40 18 22.5 15 2 S42741 ubiquinol-cytochro
41 18 22.5 15 2 S26791 Ig heavy chain V r
42 18 22.5 15 2 S10388 Ig heavy chain J r
43 18 22.5 15 2 S10386 Ig heavy chain J r
44 18 22.5 15 2 PH0780 T-cell receptor al
45 18 22.5 15 2 PC4213 bphB protein - Com

ALIGNMENTS

RESULT 1

A61512

variant surface glycoprotein MITat 1.7 - Trypanosoma brucei (fragment)

C;Species: Trypanosoma brucei

C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004

C;Accession: A61512

R;Holder, A.A.; Cross, G.A.M.

Mol. Biochem. Parasitol. 2, 135-150, 1981

A;Title: Glycopeptides from variant surface glycoproteins of Trypanosoma brucei. C-termin

A;Reference number: A61512; MUID:81172836; PMID:6163983

A;Accession: A61512

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-11 <HOL>

A;Cross-references: UNIPROT:Q7M3S1

C;Keywords: glycoprotein

Query Match 35.0%; Score 28; DB 2; Length 11;

Best Local Similarity 50.0%; Pred. No. 77;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 GTWTRHSTG 12

Db 1 GTAETQBTG 10

RESULT 2

PH0776

T-cell receptor alpha chain (M1 V-alpha-8.F3.3) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C;Accession: PH0776

R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.

J. Exp. Med. 174, 1371-1383, 1991

A;Title: T cell receptor genes in a series of class I major histocompatibility complex-r

allelic exclusion and antigen-specific repertoire.

A;Reference number: PH0746; MUID:92078846; PMID:1836010

A;Accession: PH0776

A;Molecule type: mRNA

A;Residues: 1-14 <CAS>

A;Cross-references: EMBL:X60873

A;Experimental source: T lymphocyte

C;Keywords: T-cell receptor

Query Match 28.7%; Score 23; DB 2; Length 14;

Best Local Similarity 80.0%; Pred. No. 7.6e+02;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 TGGTN 15

Db 5 TGGNN 9

RESULT 3

YPPG
thymic factor - pig
N;Alternate names: FTS (facteur thymique serique)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 09-Jul-2004
C;Accession: A01523; A60983
R;Pleau, J.M.; Dardenne, M.; Blouquit, Y.; Bach, J.F.
J. Biol. Chem. 252, 8045-8047, 1977
A;Title: Structural study of circulating thymic factor: a peptide isolated from pig serum
A;Reference number: A01523; MUID:78026571; PMID:914862
A;Accession: A01523
A;Molecule type: protein
A;Residues: 1-9 <PLE>
A;Cross-references: UNIPROT:P01255
R;Bach, J.F.; Dardenne, M.; Pleau, J.M.; Rosa, J.
Nature 266, 55-57, 1977
A;Title: Biochemical characterisation of a serum thymic factor.
A;Reference number: A60983; MUID:77123829; PMID:300146
A;Accession: A60983
A;Molecule type: protein
A;Residues: 'Z', 2-4, 'Z', 6-9 <BAC>
C;Comment: This peptide induces DNA synthesis in immature thymocytes, but not peripheral in a variety of immunoassays.
C;Comment: See PIR:A60957 (sheep) for discussion of another possible N-terminal modification
C;Superfamily: thymic factor
C;Keywords: pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 27.5%; Score 22; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 STGGTN 15

Db 4 SQGGSN 9

RESULT 4

A60957
thymocyte growth peptide - sheep
N;Contains: FTS (facteur thymique serique)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: A60957
R;Ernstroem, U.; Gafvelin, G.; Rudja, J.M.
Biosci. Rep. 10, 403-412, 1990
A;Title: Purification of thymocyte growth peptide (TGP) from sheep thymus. Relationship
A;Reference number: A60957; MUID:91064427; PMID:2249004
A;Accession: A60957
A;Molecule type: protein
A;Residues: 1-9 <ERN>
A;Cross-references: UNIPROT:Q7M3C5
C;Comment: This peptide induces DNA synthesis in immature thymocytes, but not peripheral in a variety of immunoassays.
C;Comment: This peptide was isolated in two forms. One form contained the pyrrolidone carboxylic acid (Gln) in thymocyte growth peptide (TGP) from sheep thymus. Relationship
F;1/Modified site: blocked amino end (Glx) (in thymocyte growth peptide) #status experimental

Query Match 27.5%; Score 22; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 STGGTN 15

Db 4 SQGGSN 9

RESULT 5

PH0751

T-cell receptor beta chain (F12) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
C;Accession: PH0751
R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A;Title: T cell receptor genes in a series of class I major histocompatibility complex-related alleles exclusion and antigen-specific repertoire.
A;Reference number: PH0746; MUID:92078846; PMID:1836010
A;Accession: PH0751
A;Molecule type: mRNA
A;Residues: 1-15 <CAS>
A;Cross-references: EMBL:X60843; NID:g50931; PIDN:CAA43235.1; PID:g50932
A;Experimental source: T lymphocyte
C;Keywords: T-cell receptor

Query Match 27.5%; Score 22; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 TGGT 14

Db 6 TGGT 9

RESULT 6

PH0639
T-cell receptor beta chain V-D-J region (111-1AA) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0639
R;Peeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0639
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-8 <FEE>
A;Experimental source: newborn thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 26.2%; Score 21; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 STGG 13

Db 3 STGG 6

RESULT 7

PH0919
T-cell receptor beta chain V-D-J region (isolate 5) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0919
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic encephalomyelitis
A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0919
A;Molecule type: mRNA
A;Residues: 1-11 <GOL>
A;Experimental source: concanavalin A-activated lymphoblast
A;Note: the authors translated the codon CAG for residue 11 as Glu
C;Keywords: T-cell receptor

Query Match 26.2%; Score 21; DB 2; Length 11;
Best Local Similarity 57.1%; Pred. No. 1.3e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 RTRHSTG 12
| | : | |
Db 4 RDRRTNG 10

RESULT 8
S05002
corazonin - American cockroach
C:Species: Periplaneta americana (American cockroach)
C>Date: 07-Sep-1990 #sequence_revision 09-Apr-1998 #text_change 09-Jul-2004
C:Accession: S05002
R:Veenstra, J.A.
FEBS Lett. 250, 231-234, 1989
A:Title: Isolation and structure of corazonin, a cardioactive peptide from the american
A:Reference number: S05002; MUID:89325572; PMID:2753132
A:Accession: S05002
A:Molecule type: protein
A:Residues: 1-11 <VEE>
A:Cross-references: UNIPROT:P11496
C:Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:11/Modified site: amidated carboxyl end (Asn) #status experimental

Query Match 26.2%; Score 21; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 1.3e+03; Mismatches 2; Indels 0; Gaps 0;
Matches 4; Conservative 2;

QY 8 RHSTGNTN 15
: | | | |
Db 4 QYSGWTN 11

RESULT 9
S57577
T cell receptor V-J junctional alpha chain region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 19-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 05-Nov-1999
R:Burrows, S.R.; Silins, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Argat, V.P.
submitted to the EMBL Data Library, June 1995
A:Description: T cell receptor repertoire for a viral epitope in humans is diversified
A:Reference number: S57494
A:Accession: S57577
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-15 <BUR>
A:Cross-references: EMBL:Z49945; NID:g887492; PIDN:CAA90216.1; PID:g887493
C:Keywords: T-cell receptor

Query Match 26.2%; Score 21; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.8e+03; Mismatches 4; Indels 0; Gaps 0;
Matches 4; Conservative 0;

QY 8 RHSTGNTN 15
| | | | |
Db 4 RDQTGANN 11

RESULT 10
A54823
olfactory receptor I7 - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 09-Jul-2004
C:Accession: A54823
R:Chese, A.; Simon, I.; Cedar, H.; Axel, R.
Cell 78, 823-834, 1994
A:Title: Allelic inactivation regulates olfactory receptor gene expression.
A:Reference number: A54823; MUID:94373818; PMID:8087849
A:Accession: A54823
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-8 <CHE>
A:Cross-references: UNIPROT:Q9QWU6

Query Match 25.0%; Score 20; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.8e+05; Mismatches 3; Indels 0; Gaps 0;
Matches 4; Conservative 1;

QY 5 MTRHSTG 12
| | : | |
Db 1 MERRNHTG 8

RESULT 11
D20907
Ig kappa-1 chain J4 segment (b95 allotype) - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 10-Aug-1990 #sequence_revision 10-Aug-1990 #text_change 05-Nov-1999
C:Accession: D20907; D53275
R:Emorine, L.; Max, E.E.
Nucleic Acids Res. 11, 8877-8890, 1983
A:Title: Structural analysis of a rabbit immunoglobulin kappa2 J-C locus reveals multiple
A:Reference number: A20907; MUID:84169523; PMID:6324107
A:Accession: D20907
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-12 <EMO>
A:Cross-references: GB:X00231; NID:g1577; PIDN:CAA25049.1; PID:e8275; PID:g1364234
R:Ayadi, H.; Marche, P.N.; Cazenave, P.A.
Immunogenetics 34, 201-207, 1991
A:Title: Evolution of the rabbit immunoglobulin kappa chain genes.
A:Reference number: A53275; MUID:91372868; PMID:1909995
A:Accession: D53275
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-12 <AYA>
A>Note: sequence extracted from NCBI backbone (NCBIN:56069, NCBIP:56166)
C:Comment: This J4 segment may not be functional because of a short space between the 7 n
C:Keywords: heterotetramer; immunoglobulin

Query Match 25.0%; Score 20; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.2e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0;

QY 2 SGTGM 5
| | | | |
Db 5 SGTGM 8

RESULT 12
PHI464
T-cell receptor beta chain (clone A3/63) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 15-Mar-2004
C:Accession: PHI464
R:Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; Koi
J. Exp. Med. 177, 811-820, 1993
A:Title: T cell receptor selection by and recognition of two class I major histocompatibili
A:Reference number: PHI430; MUID:93171821; PMID:8436911
A:Accession: PHI464
A:Molecule type: mRNA
A:Residues: 1-12 <CAS>
A:Experimental source: cytolytic T-lymphocyte
C:Keywords: receptor; T-cell

Query Match 25.0%; Score 20; DB 2; Length 12;
Best Local Similarity 80.0%; Pred. No. 2.2e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0;

QY 10 STGCT 14
| | | | |
Db 4 STGNT 8

RESULT 13
IS1432

Search completed: February 22, 2005, 09:46:26
Job time : 11.1333 secs

histone H4-1 precursor - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: I51432
R:Gargiulo, G.; Razvi, F.; Ruberti, I.; Mohr, I.; Worcel, A.
J. Mol. Biol. 181, 333-349, 1985
A:Title: Chromatin-specific hypersensitive sites are assembled on a Xenopus histone gene
A:Reference number: I51431, MUID:85160855; PMID:4039007
A:Accession: I51432
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-14 <GAR>
A:Cross-references: UNIPROT:P70007; GB:M23777; NID:G214219; PIDN:AAA49737.1; PID:G214222
C:Superfamily: histone H4

Query Match 25.0%; Score 20; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 2.6e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 RTRHSTGG 13
||| . ||
Db 7 RTLYGFGG 14

RESULT 14
C43334
orf3 3' to aadR - Rhodopseudomonas palustris (fragment)
C:Species: Rhodopseudomonas palustris
C>Date: 10-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: C43334
R:Dispensa, M.; Thomas, C.T.; Kim, M.K.; Perrotta, J.A.; Gibson, J.; Harwood, C.S.
J. Bacteriol. 174, 5803-5813, 1992
A:Title: Anaerobic growth of Rhodopseudomonas palustris on 4-hydroxybenzoate is dependent
A:Reference number: A43334; MUID:92394882; PMID:1522059
A:Accession: C43334
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-15 <DIS>
A:Cross-references: UNIPROT:Q02006; GB:M92426; NID:G151870; PIDN:AAA26091.1; PID:G551951
A>Note: sequence extracted from NCBI backbone (NCBIN:112964, NCBIF:112967)

Query Match 25.0%; Score 20; DB 2; Length 15;
Best Local Similarity 60.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 MTRH 9
: || ||
Db 9 LRARH 13

RESULT 15
A28497
neurotensin-related protein - turkey (fragment)
C:Species: Meleagris gallopavo (common turkey)
C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C:Accession: A28497
R:Carraway, R.E.; Cochran, D.E.; Ruane, S.E.
J. Biol. Chem. 262, 15886-15889, 1987
A:Title: Isolation, structures, and biologic activity of neurotensin-related peptides ge
A:Reference number: A28497; MUID:88058942; PMID:2445741
A:Accession: A28497
A:Molecule type: protein
A:Residues: 1-15 <CAR>
A:Cross-references: UNIPROT:Q7LZA3
C:Keywords: neuropeptide

Query Match 25.0%; Score 20; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 MTRH 8
||| |
Db 7 MTRH 10

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 22, 2005, 08:53:13 ; Search time 52.6 Seconds
(without alignments)
146.030 Million cell updates/sec

Title: US-08-991-628-7
Perfect score: 80
Sequence: 1 QSGTMRHSTGCTN 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 6622

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	35.0	11	2 Q7M3S1	Q7M3S1 trypanosoma
2	26	32.5	13	2 Q9REI2	Q9REI2 acidiphilium
3	23	28.7	8	2 Q15894	Q15894 homo sapien
4	23	28.7	13	2 Q8I8F3	Q8I8F3 drosophila
5	23	28.7	13	2 P97944	P97944 mus musculus
6	23	28.7	13	2 Q65331	Q65331 autographa
7	23	28.7	15	2 Q95770	Q95770 cyclura ric
8	22	27.5	9	1 THYF_PIG	P01255 sus scrofa
9	22	27.5	9	2 Q7M3C5	Q7M3C5 ovis aries
10	22	27.5	12	2 Q6LQD6	Q6LQD6 mus musculus
11	22	27.5	13	2 Q6PJ24	Q6PJ24 homo sapien
12	22	27.5	14	2 Q642Z4	Q642Z4 brachytherci
13	22	27.5	14	2 Q642Z5	Q642Z5 brachytherci
14	22	27.5	14	2 Q642Z8	Q642Z8 brachytherci
15	22	27.5	14	2 Q643A0	Q643A0 brachytherci
16	22	27.5	14	2 P83424	P83424 morus nigra
17	22	27.5	15	2 Q95762	Q95762 ctenosaura
18	22	27.5	15	2 Q6XEW6	Q6XEW6 platyomell
19	22	27.5	15	2 Q422Z3	Q422Z3 arabisidopsis
20	21	26.2	8	2 Q6J0R5	Q6J0R5 paracentrot
21	21	26.2	8	2 O19956	O19956 gossypium a
22	21	26.2	8	2 O19958	O19958 gossypium b
23	21	26.2	8	2 O19959	O19959 gossypium c
24	21	26.2	8	2 O19960	O19960 gossypium m
25	21	26.2	8	2 O19961	O19961 gossypium d
26	21	26.2	10	2 Q8SAC2	Q8SAC2 amblystegiu
27	21	26.2	11	1 CORZ_PERAM	P11496 periplaneta
28	21	26.2	14	2 Q79AV9	Q79AV9 klebsiella
29	20	25.0	8	2 Q80WD6	Q80WD6 mus musculus
30	20	25.0	12	2 Q841R5	Q841R5 agrobacteri
31	20	25.0	13	2 Q7RDM8	Q7RDM8 plasmodium

32	20	25.0	13	2 P97140	P97140 borrelia bu
33	20	25.0	13	2 Q53693	Q53693 streptomyce
34	20	25.0	14	2 P70007	P70007 xenopus lae
35	20	25.0	15	2 Q7TRP3	Q7TRP3 sus scrofa
36	20	25.0	15	2 Q7LZA3	Q7LZA3 meleagris g
37	19	23.8	8	2 Q841S6	Q841S6 orf virus
38	19	23.8	8	2 Q84271	Q84271 human papil
39	19	23.8	9	1 FARD_CALVO	F41868 calliphora
40	19	23.8	9	2 Q6LEH2	Q6LEH2 homo sapien
41	19	23.8	10	2 Q7M3S4	Q7M3S4 trypanosoma
42	19	23.8	10	2 Q7M278	Q7M278 triticum tu
43	19	23.8	11	2 Q9BJ61	Q9BJ61 dictyosteli
44	19	23.8	12	2 Q6DUJ5	Q6DUJ5 rattus norv
45	19	23.8	15	2 Q9UWG1	Q9UWG1 pyrococcus

ALIGNMENTS

RESULT 1
Q7M3S1 PRELIMINARY; PRT; 11 AA.
AC Q7M3S1;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE Variant surface glycoprotein Mitat 1.7 (Fragment).
OS Trypanosoma brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5691;
RN [1]
RP SEQUENCE.
RX MEDLINE=81172836; PubMed=6163983; DOI=10.1016/0166-6851(81)90095-5;
RA Holder A.A., Cross G.A.M.;
RT "Glycopeptides from variant surface glycoproteins of Trypanosoma
brucei. C-terminal location of antigenically cross-reacting
RT carbohydrate moieties.";
RL Mol. Biochem. Parasitol. 2:135-150 (1981).
DR PIR; A61512; A61512.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1067 MW; 64FD322AAF16C1AB CRC64;

Query Match 35.0%; Score 28; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 3.1e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GTMTRHSTG 12
||| : : ||
Db 1 GTAETOBTTG 10

RESULT 2
Q9REI2 PRELIMINARY; PRT; 13 AA.
AC Q9REI2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Acidiphilium symbioticum.
OG Plasmid pAS3.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
OC Acetobacteraceae; Acidiphilium.
OX NCBI_TaxID=94005;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KM2;
RX MEDLINE=22165970; PubMed=12177739;
RA Mahapatra N.R., Ghosh S., Deb C., Banerjee P.C.;
RT "Resistance to cadmium and zinc in Acidiphilium symbioticum KM2 is
plasmid mediated.";
RL Curr. Microbiol. 45:180-186(2002).

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DR EMBL; AJ239066; CAB65725.1; -.
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 13 AA; 1361 MW; 6811778519FD11B4 CRC64;

Query Match 32.5%; Score 26; DB 2; Length 13;
Best Local Similarity 55.6%; Pred. No. 8.5e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 MRTRHSTGG 13
Db 5 IRTAARGG 13

RESULT 3
Q15894 PRELIMINARY; PRT; 8 AA.
AC Q15894;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Homo sapiens (clone XP587B) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindate E.A., Zhao Z.-Y.,
RA Caskey C.T.H.;
RT "Isolation of chromosome-specific genes by reciprocal probing of
RT arrayed cDNAs and cosmid libraries.";
RL Hum. Mol. Genet. 0:0-0(1995).
DR EMBL; L32074; AAA73884.1; -.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 952 MW; EBC735B1E1F1B6D6 CRC64;

Query Match 28.7%; Score 23; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.6e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 MRTRHS 10
Db 1 MQTHS 6

RESULT 4
Q818F3 PRELIMINARY; PRT; 13 AA.
AC Q818F3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Acetylcholinesterase (Fragment).
GN Name-Ace; Synonyms=ache;
OS Drosophila parisiensis.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila; mayaguana subcluster.
OX NCBI_TaxID=214822;
RN [1]
RP SEQUENCE FROM N.A.
RA O'Grady P.M. II, Durando C.M., Heed W.B., Wasserman M., Etges W.,
RA DeSalle R.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AV154986; AAO13634.1; -.
DR FlyBase; FBgn0064412; Dpaf\Ace.
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1451 MW; 67DAF26C3079B774 CRC64;

Query Match 28.7%; Score 23; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 2.9e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 SGTMRHST 11
Db 3 SGTFRATPTT 12

RESULT 5
P97944 PRELIMINARY; PRT; 13 AA.
AC P97944;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Calcium channel beta subunit (Fragment).
GN Name=Cacnb4; Synonyms=Cchb4;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=lethargic, and BALB/c;
RX MEDLINE=97191307; PubMed=9039265; DOI=10.1016/S0092-8674(00)81877-2;
RA Burgess D.L., Jones J.M., Meisler M.H., Noebels J.L.;
RT "Mutation of the Ca2+ channel beta subunit gene Cchb4 is associated
RT with ataxia and seizures in the lethargic (lh) mouse.";
RL Cell 88:385-392(1997).
DR EMBL; U80986; AAC53037.1; -.
DR MGD; MGI:103301; Cacnb4.
DR GO; GO:0005891; C:voltage-gated calcium channel complex; TAS.
DR GO; GO:0008331; C:high voltage-gated calcium channel activity; TAS.
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1370 MW; DFE26C2AA094C409 CRC64;

Query Match 28.7%; Score 23; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 2.9e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 SGTMRHST 11
Db 3 SGTFRATPTT 12

RESULT 6
Q65331 PRELIMINARY; PRT; 13 AA.
AC Q65331;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Basic protein (Fragment).
OS Autographa californica nuclear polyhedrosis virus (AcMNPV).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=46015;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C6;
RX MEDLINE=90218045; PubMed=2109042;
RA Hill-Perkins M.S., Possee R.D.;
RT "A baculovirus expression vector derived from the basic protein
RT promoter of Autographa californica nuclear polyhedrosis virus.";
RL J. Gen. Virol. 71:971-976(1990).
DR EMBL; D00864; BAA00738.1; -.
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1626 MW; 6C75B58A749D1414 CRC64;

Query Match 28.7%; Score 23; DB 2; Length 13;

```

Best Local Similarity 71.4%; Pred. No. 2.9e+03; Mismatches 2; Indels 0; Gaps 0;

QY 6 RTRHSTG 12
| | | | |

Db 6 RRSSTG 12

RESULT 7

Q95770 ID Q95770 PRELIMINARY; PRT; 15 AA.

AC Q95770; DT 01-FEB-1997 (TrEMBLrel. 02, Created)

DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE NADH dehydrogenase subunit 4 (Fragment).

GN Names=ND4;

OS Cyclura ricordi (Ricord's rock iguana).

OG Mitochondrion.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Iguania; Iguanidae; Cyclura.

OC NCBI_TaxID=51215;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=97019047; PubMed=8865663;

RA Sites J.W. Jr., Davis S.K., Guerra T., Iverson J.B., Snell H.L.;

RT "Character congruence and phylogenetic signal in molecular and

RT morphological data sets: a case study in the living Iguanas (Squamata,

RT Iguanidae).";

RL Mol. Biol. Evol. 13:1087-1105(1996).

RN [2]

RP SEQUENCE FROM N.A.

RA Sites J.W., Davis S.K., Guerra T., Iverson J.B., Snell H.L.;

RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL; U66237; AAB07473.1; -;

DR GO; GO:0005739; C-mitochondrion; IEA.

KW Mitochondrion.

FT NON TER 1 1

SQ SEQUENCE 15 AA; 1715 MW; 8327178E7927A57E CRC64;

Query Match 28.7%; Score 23; DB 2; Length 15;

Best Local Similarity 80.0%; Pred. No. 3.4e+03;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 TRHST 11
| | | | |

Db 9 SRHST 13

RESULT 8

THYF PIG

ID THYF PIG STANDARD; PRT; 9 AA.

AC P01255;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Thymic factor.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Cetartiodactyla; Suina; Suidae; Sus.

OC NCBI_TaxID=9823;

RN [1]

RP SEQUENCE.

RX MEDLINE=78026571; PubMed=914862;

RA Pleau J.-M., Dardenne M., Blouquit Y., Bach J.-F.;

RT "Structural study of circulating thymic factor: a peptide isolated

RT from pig serum. II. Amino acid sequence.;"

RL J. Biol. Chem. 252:8045-8047(1977).

CC -I- MISCELLANEOUS: The biological source(s) and physiological

CC activities of this peptide have not been determined.

DR PIR; A01523; YFPG.

KW Direct protein sequencing; Pyrrolidone carboxylic acid.

FT MOD_RES 1 1

SQ SEQUENCE 15 AA; 1715 MW; 8327178E7927A57E CRC64;

SQ SEQUENCE 9 AA; 876 MW; D500B87866C5B33D CRC64;

Query Match 27.5%; Score 22; DB 1; Length 9;

Best Local Similarity 66.7%; Pred. No. 1.6e+06;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 STGGTN 15
| | | | |

Db 4 SQGGSN 9

RESULT 9

Q7M3C5 ID Q7M3C5 PRELIMINARY; PRT; 9 AA.

AC Q7M3C5; DT 01-MAR-2004 (TrEMBLrel. 26, Created)

DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Thymocyte growth peptide.

OS Ovis aries (Sheep).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Caprinae; Ovis.

OC NCBI_TaxID=9940;

RN [1]

RP SEQUENCE.

RA Ernstrom U., Gafvelin G., Rudja J.M.;

RT "Purification of thymocyte growth peptide (TGP) from sheep thymus.

RT Relationship to FTS/thymulin.;"

RL Biosci. Rep. 10:403-412(1990).

DR PIR; A60957; A60957.

SQ SEQUENCE 9 AA; 876 MW; DCE7B87866C5B33D CRC64;

Query Match 27.5%; Score 22; DB 2; Length 9;

Best Local Similarity 66.7%; Pred. No. 1.6e+06;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 STGGTN 15
| | | | |

Db 4 SQGGSN 9

RESULT 10

Q6LDQ6

ID Q6LDQ6 PRELIMINARY; PRT; 12 AA.

AC Q6LDQ6;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE C-myb oncogene, exon 1 and exon 2. (Fragment).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OC NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=90017472; PubMed=2678098;

RA Reddy C.D., Reddy P.E.;

RT "Differential binding of nuclear factors to intron-1 containing the

RT transcriptional pause site correlates with c-myb expression.;"

RL Proc. Natl. Acad. Sci. U.S.A. 86:7326-7330(1989).

DR EMBL; M26185; AAA37505.1; -;

FT NON TER 12 12

SQ SEQUENCE 12 AA; 1461 MW; 32769A1F9CB1F417 CRC64;

Query Match 27.5%; Score 22; DB 2; Length 12;

Best Local Similarity 66.7%; Pred. No. 4e+03;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 RTRHST 11
| | | | |

Db 4 RPRHSS 9

```

RESULT 11
Q6PJ24
ID Q6PJ24 PRELIMINARY; PRT; 13 AA.
AC Q6PJ24;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE POLRMT protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Capletton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC024170; AHA24170.1;
SQ SEQUENCE 13 AA; 1266 MW; 7D6737769FD0734 CRC64;

Query Match 27.5%; Score 22; DB 2; Length 13;
Best Local Similarity 36.4%; Pred. No. 4.4e+03;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 SGTMRTRHSTG 12
Db 2 AGACRLRSASG 12

RESULT 12
Q642Z4
ID Q642Z4 PRELIMINARY; PRT; 14 AA.
AC Q642Z4;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE AtPB (Fragment).
GN Name=atpB;
OS Brachytheciastrum venustum.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Bryidae; Hypnales; Brachytheciaceae; Brachytheciastrum.
OX NCBI_TaxID=292614;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=venustum1704, and Venustum1705;
RA Vanderpoorten A.;
RT "A molecular and morphological recircumscription of Brachytheciastrum

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RT (Brachytheciaceae, Bryopsida).";
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY736270; AAU25912.1;
DR EMBL; AY736271; AAU25913.1;
KW Chloroplast.
FT NON_TER 14
SQ SEQUENCE 14 AA; 1544 MW; 811BBAA1FD5040D1 CRC64;

Query Match 27.5%; Score 22; DB 2; Length 14;
Best Local Similarity 45.5%; Pred. No. 4.8e+03;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 5 MTRHSTGTGTN 15
Db 1 MKTDSRTFGTS 11

RESULT 13
Q642Z5
ID Q642Z5 PRELIMINARY; PRT; 14 AA.
AC Q642Z5;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE AtPB (Fragment).
GN Name=atpB;
OS Brachytheciastrum velutinum.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Bryidae; Hypnales; Brachytheciaceae; Brachytheciastrum.
OX NCBI_TaxID=113273;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Velut1771;
RA Vanderpoorten A.;
RT "A molecular and morphological recircumscription of Brachytheciastrum
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY736269; AAU25911.1;
KW Chloroplast.
FT NON_TER 14
SQ SEQUENCE 14 AA; 1544 MW; 811BBAA1FD5040D1 CRC64;

Query Match 27.5%; Score 22; DB 2; Length 14;
Best Local Similarity 45.5%; Pred. No. 4.8e+03;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 5 MTRHSTGTGTN 15
Db 1 MKTDSRTFGTS 11

RESULT 14
Q642Z8
ID Q642Z8 PRELIMINARY; PRT; 14 AA.
AC Q642Z8;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE AtPB (Fragment).
GN Name=atpB;
OS Brachytheciastrum trachypodium.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Bryidae; Hypnales; Brachytheciaceae; Brachytheciastrum.
OX NCBI_TaxID=292612;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Trachypol1762, Trachypol1766, and Trachypol1770;
RA Vanderpoorten A.;
RT "A molecular and morphological recircumscription of Brachytheciastrum
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.

```



```
DR EMBL; AY736266; AAU25908.1; -.
DR EMBL; AY736267; AAU25909.1; -.
DR EMBL; AY736268; AAU25910.1; -.
KW Chloroplast.
FT NON TER      14      14
SQ SEQUENCE     14 AA; 1544 MW; 811BBAA1FD5040D1 CRC64;

Query Match
Best Local Similarity  27.5%; Score 22; DB 2; Length 14;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 5 MRTRHSTGGTN 15
Db 1 MKTDSRTFGTS 11

RESULT 15
Q643A0
ID Q643A0 PRELIMINARY; PRT; 14 AA.
AC Q643A0;
DT 25-OCT-2004 (T-EMBLrel. 28, Created)
DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
DE AtpB (Fragment).
GN Name-atpB;
OS Brachytheciastrum collinum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Bryidae; Hypnales; Brachytheciaceae; Brachytheciastrum.
OX NCBI_TaxID=219719;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Collinum1767, Collinum1769, and Collinum1765;
RA Vanderpoorten A.;
RT "A molecular and morphological recircumscription of Brachytheciastrum
RL (Brachytheciaceae, Bryopsida).";
DR EMBL; AY736264; AAU25906.1; -.
DR EMBL; AY736265; AAU25907.1; -.
DR EMBL; AY736263; AAU25905.1; -.
KW Chloroplast.
FT NON TER      14      14
SQ SEQUENCE     14 AA; 1544 MW; 811BBAA1FD5040D1 CRC64;

Query Match
Best Local Similarity  27.5%; Score 22; DB 2; Length 14;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 5 MRTRHSTGGTN 15
Db 1 MKTDSRTFGTS 11
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Search completed: February 22, 2005, 09:37:56
Job time : 54.6667 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 22, 2005, 08:52:23 ; Search time 65.6667 Seconds
(without alignments)
88.346 Million cell updates/sec

Title: US-08-991-628-7

Perfect score: 80

Sequence: 1 QSGWTRHSTGCTN 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 632537

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	80	100.0	15	2	AAW04847 Self epit
2	41	51.2	14	4	ABBS56600 Human SNP
3	34	42.5	10	4	AAG86787 Saccharom
4	31	38.8	12	2	AAR13070 SIV500 fu
5	30	37.5	15	7	ADM37098 Mutated I
6	30	37.5	15	7	ADM53386 Mutant NF
7	30	37.5	15	7	ADM53392 Mutant NF
8	30	37.5	15	7	ADM53392 Converted
9	30	37.5	15	8	ADR31520 IkappaB-a
10	30	37.5	15	8	ADR31534 IkappaB-a
11	29	36.2	7	2	AAW59304 Non-polio
12	29	36.2	7	2	AAW50064 Coxsackie
13	29	36.2	11	3	AAB26509 Human Ige
14	29	36.2	11	4	AAB16840 Peptide P
15	29	36.2	11	5	ABJ00284 Human Ige
16	29	36.2	14	3	AAB26512 Human Ige
17	29	36.2	14	4	AAU16843 Human pro
18	29	36.2	14	4	AAU16843 Peptide P
19	29	36.2	14	5	ABJ00287 Human Ige
20	28	35.0	7	5	ABP49196 Zinc fing
21	28	35.0	7	7	ADM63567 Zinc fing
22	28	35.0	7	7	ADM22065 Synthetic
23	28	35.0	8	7	ADF66168 Mouse ubi
24	28	35.0	10	4	AAG63152 Peptide d
25	28	35.0	10	4	AAG97581 Human com

26	28	35.0	10	4	AAG97582 Human com
27	28	35.0	13	3	AAY66866 T cell an
28	28	35.0	13	5	ADG67012 Ricin tox
29	28	35.0	13	5	ADG67013 Ricin tox
30	28	35.0	13	5	ADG67014 Ricin tox
31	28	35.0	13	5	ADG67015 Ricin tox
32	28	35.0	14	3	ADCL6855 Human sin
33	28	35.0	14	6	ABR75388 Biologica
34	27.5	34.4	13	2	AAR77321 Human apo
35	27	33.8	7	3	AAB02885 Nucleotid
36	27	33.8	7	5	ABP49458 Zinc fing
37	27	33.8	7	5	ABP49464 Zinc fing
38	27	33.8	7	5	ABP50954 Zinc fing
39	27	33.8	7	5	ABP48644 Zinc fing
40	27	33.8	7	5	ABP49467 Zinc fing
41	27	33.8	7	5	ABP48647 Zinc fing
42	27	33.8	7	5	ABP49461 Zinc fing
43	27	33.8	7	7	ADA63126 Zinc fing
44	27	33.8	7	7	ADA63760 Zinc fing
45	27	33.8	7	7	ADA63758 Zinc fing

ALIGNMENTS

RESULT 1
AAW04847
ID AAW04847 standard; peptide; 15 AA.

XX

AC AAW04847;

XX

DT 18-FEB-1997 (first entry)

XX

DE Self epitope of desmoglein 3, implicated in autoimmune disease.

XX

XX Tolerisation; self-epitope; antigen; autoimmune disease; autoantigen;

KW HLA; human leukocyte antigen; T-cell; thymocyte; pemphigus vulgaris;

KW desmoglein; multiple sclerosis; herpes simplex virus; adenovirus;

KW phosphomannomutase; human papillomavirus; Epstein-Barr virus;

KW DNA polymerase; influenza; haemagglutinin; reovirus; sigma protein.

XX

OS Homo sapiens.

XX

PN W09627387-A1.

XX

PD 12-SEP-1996.

XX

PD 07-MAR-1996; 96WO-US003182.

XX

PR 07-MAR-1995; 95US-00400796.

XX

PA (HARD) HARVARD COLLEGE.

XX

PI Strominger JL, Wucherpfennig KW;

XX

XX WPI; 1996-425218/42.

XX

XX Pemphigus vulgaris auto-antigens and multiple sclerosis non-self antigens

PT - useful in disease treatment, and method for identification of other

PT self and non-self antigens implicated in autoimmune disease.

XX

XX Claim 1; Page 42; 58pp; English.

XX

XX Pharmaceutical preparations for tolerisation to antigens comprise either

CC an isolated human non-collagen or non-mysin basic protein (MBP),

CC polypeptide which is capable of tolerising an individual to an

CC autoantigen; or an isolated human pathogen polypeptide capable of

CC tolerising an individual to that polypeptide. In both cases, the

CC polypeptide (whether self or non-self) includes an amino acid sequence

CC corresponding to a sequence motif for a MHC class II protein, such as HLA

CC -DR, which is associated with a human autoimmune disease and which binds

CC to the polypeptide to activate autoreactive T-cells in individuals with

CC the autoimmune disease. This peptide is derived from the human desmoglein

CC 3 protein (amino acids 762-786) and is implicated as a self epitope in
CC pemphigus vulgaris. Peptides derived from the human desmoglein protein
CC are described in AA04841-47
XX
SQ Sequence 15 AA;
Query Match 100.0%; Score 80; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 6e-07; Mismatches 0; Indels 0; Gaps 0;
Matches 15; Conservative 0;
QY 1 QSGTMRTRHSTGGTN 15
DB 1 QSGTMRTRHSTGGTN 15
RESULT 2
ID ABB56600 standard; peptide; 14 AA.
AC ABB56600;
XX
DT 05-MAR-2002 (first entry)
XX
DE Human SNP related amino acid sequence SEQ ID NO:1165.
XX
KW Human; single nucleotide polymorphism; SNP; polymorphism; cytostatic;
KW immunosuppressive; antiinflammatory; neuroprotective; antimicrobial;
KW autoimmune disease; inflammation; cancer; nervous system disease;
KW infection; polymorphic protein.
XX
OS Homo sapiens.
XX
PN WO200138586-A2.
XX
PD 31-MAY-2001.
XX
PF 22-NOV-2000; 2000WO-US032311.
XX
PR 24-NOV-1999; 99US-0167383P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA, Leach M;
XX
DR WPI; 2001-355949/37.
XX
PT Isolated human nucleic acids comprising one or more single nucleotide
PT polymorphisms, useful for treating a subject suffering from a pathology,
PT e.g. autoimmune diseases, ascribed to the presence of a sequence
PT polymorphism.
XX
PS Claim 1; Page 600; 674pp; English.
XX
CC ABL00010 to ABL01104 represent human nucleic acid oligonucleotides
CC comprising one or more single nucleotide polymorphisms (SNPs). ABB56531
CC to ABB56903 represent human peptides encoded by some of the SNP
CC oligonucleotides. The sequences from the present invention can have
CC immunosuppressive, cytostatic, antiinflammatory, neuroprotective and
CC antimicrobial activities. Nucleic acids, polypeptides, oligonucleotides
CC and antibodies from the present invention can be used for treating a
CC subject suffering from, at risk for, or suspected of, suffering from a
CC pathology ascribed to the presence of a sequence polymorphism. The
CC pathology may be autoimmune diseases, inflammation, cancer, diseases of
CC the nervous system, and infection by pathogenic microorganisms. The SNPs
CC are also useful for determining which forms of a characterised
CC polymorphism are present in individuals. The antibodies may be used in
CC the detection, quantitation and/or cellular or tissue localisation of a
CC polymorphic protein (e.g., for use in measuring levels of the polymorphic
CC protein within appropriate physiological samples)
XX
SQ Sequence 14 AA;
Query Match 51.2%; Score 41; DB 4; Length 14;

Best Local Similarity 70.0%; Pred. No. 3.4;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 6 RTRHSTGGTN 15
DB 1 QARHRTGGTN 10
RESULT 3
ID AAG86787 standard; peptide; 10 AA.
XX
AC AAG86787;
XX
DT 11-SEP-2001 (first entry)
XX
DE Saccharomyces cerevisiae peptide, SEQ ID NO: 1736.
XX
KW Saccharomyces cerevisiae; complementary peptide; peptide identification;
KW drug discovery; drug design.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200142276-A1.
XX
PD 14-JUN-2001.
XX
PF 13-DEC-2000; 2000WO-GB004773.
XX
PR 13-DEC-1999; 99GB-00029471.
XX
PA (PROT-) PROTEOM LTD.
XX
PI Roberts GW, Heal JR;
XX
DR WPI; 2001-367863/38.
XX
PT Identifying complementary peptides by analysis of protein and nucleotide
PT sequence databases, useful in drug design.
XX
PS Example 3; Page 269; 489pp; English.
XX
CC The invention relates to the identification of complementary peptides by
CC analysis of protein and nucleotide sequence databases from higher
CC eukaryotic genomes, excluding human and plants. The specific
CC complementary peptides interact with their relevant target proteins
CC encoded in the eukaryote genome. The peptides may be used as reagents and
CC drugs for drug discovery and as lead ligands for drug design and
CC development. The present sequence is a complementary peptide from
CC Saccharomyces cerevisiae
XX
SQ Sequence 10 AA;
Query Match 42.5%; Score 34; DB 4; Length 10;
Best Local Similarity 70.0%; Pred. No. 38;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 6 RTRHSTGGTN 15
DB 1 RTRASRGGAN 10
RESULT 4
ID AAR13070 standard; protein; 12 AA.
XX
AC AAR13070;
XX
DT 04-OCT-1991 (first entry)
XX
DE SIV500 fusion protein.
XX
KW SIV; beta-galactosidase; vaccine; immunotoxin; antibodies.

XX OS Synthetic.
 XX PN WO9109872-A.
 XX XX
 XX PD 11-JUL-1991.
 XX PF 13-DEC-1989; 89US-00450150.
 XX PR 13-DEC-1989; 89US-00450150.
 XX PA (UNIV-) UNIVAX BIOLOGICS IN.
 XX PI Shafferman A;
 XX DR WPI; 1991-222846/30.
 XX DR N-PSDB; AAQ12645.
 XX PT New fusion proteins for diagnosis and treatment of HIV infection -
 PT comprise synthetic antigenic determinants of HIV fused to non-HIV
 PT polypeptide, preferably beta galactosidase.
 XX PS Disclosure; Fig 2B; 58pp; English.
 XX CC The sequence identified from SiVmac env is equivalent to HIV500
 CC (AAQ12641). Because of the criteria used to correlate HIV and SiV
 CC sequences, observation of the antibody response of monkeys immunised with
 CC an SiV sequence could be used to assess the antibody response of humans
 CC immunised with the corresp. HIV sequence. See also AAQ12640-47
 XX XX
 XX SQ Sequence 12 AA;
 Query Match 38.8%; Score 31; DB 2; Length 12;
 Best Local Similarity 62.5%; Pred. No. 1.6e+02;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 8 RHSTGCTN 15
 |::|||:
 Db 1 RYTTGTS 8

RESULT 5
 ADM37098
 ID ADM37098 standard; peptide; 15 AA.
 XX AC
 XX ADM37098;
 XX DT 03-JUN-2004 (first entry)
 XX DE Mutated IkappaB-alpha 26-40.
 XX KW IkappaB-alpha; AKT kinase; beta-TrCP; kinase; phosphorylation substrate;
 KW kinase recognition domain; E3 binding region; mutant; mutein.
 XX OS Synthetic.
 OS Unidentified.
 XX Key Location/Qualifiers
 FH Misc-difference 2 /note= "Wild-type Asp substituted by Arg"
 FT Misc-difference 7 /note= "Wild-type Ser substituted by Thr"
 FT US2003170611-A1.
 XX PN 11-SEP-2003.
 XX PD
 XX PF 09-MAR-2002; 2002US-00093840.
 XX PR 09-MAR-2002; 2002US-00093840.
 XX PA (CARD/) CARDONE M H.
 PA (YAFFE/) YAFFE M.

XX PI Cardone MH, Yaffe M;
 XX DR WPI; 2003-863752/80.
 XX PT Identifying a molecule capable of modulating a kinase activity in situ
 PT using a substrate with an altered kinase recognition domain and an
 PT associated label is useful in drug discovery.
 XX PS Disclosure; Fig 3a; 25pp; English.
 XX CC The invention relates to identifying a molecule capable of modulating a
 CC kinase activity in situ, comprising exposing a candidate molecule to a
 CC cell comprising a phosphorylation substrate associated with a detectable
 CC label and having a kinase recognition domain altered to be recognised by
 CC a kinase that does not recognise the substrate in its unaltered state,
 CC and determining whether the candidate molecule causes a change in an
 CC expression of the label. Also included are a molecule capable of
 CC modulating activity of at least one kinase in situ identified by the
 CC claimed method, a fusion protein (comprising an E3 binding region, a
 CC kinase recognition domain and a green fluorescent protein, where the
 CC kinase recognition domain is the domain of beta-catenin, HIV protein VP1,
 CC p27, Bcl-2 or c-Jun), a fusion protein (comprising an E3 binding region,
 CC a kinase recognition domain and an enzyme capable of producing a
 CC detectable enzymatic product, where the kinase recognition domain is the
 CC domain of beta-catenin, HIV protein VP1, p27, Bcl-2 or c-Jun), an
 CC isolated genetic molecule encoding one of the above fusion proteins, a
 CC vector capable of expressing the above genetic molecule and a cell
 CC transfected with the above vector. Expression of the label requires
 CC phosphorylation of the phosphorylation substrate by the kinase. The
 CC kinase recognition domain is altered to include a consensus recognition
 CC motif for the kinase (e.g. AKT kinase). The invention is useful to study
 CC kinase activity in situ and to screen for molecules that modulate kinase
 CC activities in situ, for example in drug discovery. The invention allows
 CC for information on multiple kinases to be provided simultaneously, which
 CC prior art does not provide. The present sequence is a mutated Beta-TrCP
 CC binding region of IkappaB-alpha, which is mutated to an AKT or IKK (both
 CC not defined) phosphorylation site.
 XX XX
 XX SQ Sequence 15 AA;
 Query Match 37.5%; Score 30; DB 7; Length 15;
 Best Local Similarity 62.5%; Pred. No. 3e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 5 MTRHSTG 12
 :|||:
 Db 1 LRDRHDTG 8

RESULT 6
 ADM53386
 ID ADM53386 standard; peptide; 15 AA.
 XX AC ADM53386;
 XX DT 03-JUN-2004 (first entry)
 XX DE Mutant NFkB-regulating protein Ikb-alpha IKK recognition #1.
 XX KW kinase activity modulator; signaling enzyme; drug design; anti-tumour;
 KW anti-inflammation; anti-ischaemia;
 KW necrosis factor kappa B regulating protein; NFkB-regulating protein;
 KW I kappa B-alpha; cytokine inducible IkappaB kinase recognition site;
 KW IKK recognition site; phosphorylation; serine/threonine kinase; AKT;
 KW mutant; mutein.
 XX OS Unidentified.
 OS Synthetic.
 XX PN US2003170737-A1.
 XX PD 11-SEP-2003.

```

XX PF 09-MAR-2002; 2002US-00093945..
XX XX
XX PD 09-MAR-2002; 2002US-00093945..
XX XX
XX PF (CARD/) CARDONE M H.
XX PA (YAFFE/) YAFFE M.
XX XX
XX PI Cardone MH, Yaffe M;
XX XX
XX DR WPI; 2003-787546/74.
XX XX
XX PT A method for identifying a molecule capable of modulating a kinase
XX PT activity in situ and is useful in drug design to screen for molecules
XX PT that are candidates for anti-tumor, anti-inflammation, and anti-ischemia
XX PT therapy.
XX XX
XX PS Disclosure; Fig 3A; 25pp; English.
XX CC
XX CC The invention describes a method of identifying a molecule capable of
XX CC modulating a kinase activity in situ, comprising exposing a candidate
XX CC molecule to a cell comprising a signaling enzyme altered so as to bind a
XX CC phosphorylation substrate, where the substrate is associated with
XX CC detectable label and the binding is regulated by a kinase, and
XX CC determining whether the candidate causes a change in expression of the
XX CC label. Also described are: a molecule capable of modulating a kinase
XX CC activity in situ identified by the claimed method; a fusion protein
XX CC comprising a genetically altered signaling enzyme and a label, where the
XX CC alteration produces an adapter molecule in the signaling enzyme capable
XX CC of binding to a phosphorylation substrate that the enzyme does not bind
XX CC in its unaltered state, where the binding is regulated by a kinase; an
XX CC isolated genetic molecule encoding the above fusion protein; a vector
XX CC capable of expressing the above genetic molecule; and a cell transfected
XX CC with the above vector. The invention is useful in drug design to screen
XX CC for molecules that are candidates for anti-tumor, anti-inflammation, and
XX CC anti-ischaemia therapy. This is the amino acid sequence of a necrosis
XX CC factor kappa B (NFkB)-regulating protein I kappa B-alpha cytokine
XX CC inducible IkappaB kinase (IKK) recognition site that has been altered to
XX CC allow phosphorylation by serine/threonine kinase AKT.
XX XX
XX SQ Sequence 15 AA;
XX
XX Query Match 37.5%; Score 30; DB 7; Length 15;
XX Best Local Similarity 62.5%; Pred. No. 3e+02;
XX Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 5 MTRHSTG 12
XX Db : || || ||
XX 1 LRDRHDTG 8
XX
XX RESULT 7
XX ID ADM53392
XX XX ADM53392 standard; peptide; 15 AA.
XX AC ADM53392;
XX XX
XX XX 03-JUN-2004 (first entry)
XX DE Mutant NFkB-regulating protein Ikb-alpha IKK recognition #2.
XX DE
XX DE kinase activity modulator; signaling enzyme; drug design; anti-tumour;
XX KW anti-inflammation; anti-ischaemia;
XX KW necrosis factor kappa B regulating protein; NFkB-regulating protein;
XX KW I kappa B-alpha; cytokine inducible IkappaB kinase recognition site;
XX KW IKK recognition site; phosphorylation; serine/threonine kinase; AKT;
XX KW mutant; mutein.
XX XX
XX OS Unidentified.
XX OS Synthetic.
XX XX
XX XX Key Location/Qualifiers
XX FH Misc-difference 11
XX FT

```

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FT XX /label= Asp, Glu
XX XX
XX PN US2003170737-A1.
XX XX
XX PD 11-SEP-2003.
XX XX
XX PF 09-MAR-2002; 2002US-00093945.
XX XX
XX PR 09-MAR-2002; 2002US-00093945.
XX XX
XX PA (CARD/) CARDONE M H.
XX PA (YAFFE/) YAFFE M.
XX XX
XX PI Cardone MH, Yaffe M;
XX XX
XX DR WPI; 2003-787546/74.
XX XX
XX PT A method for identifying a molecule capable of modulating a kinase
XX PT activity in situ and is useful in drug design to screen for molecules
XX PT that are candidates for anti-tumor, anti-inflammation, and anti-ischemia
XX PT therapy.
XX XX
XX PS Disclosure; Page 7; 25pp; English.
XX CC
XX CC The invention describes a method of identifying a molecule capable of
XX CC modulating a kinase activity in situ, comprising exposing a candidate
XX CC molecule to a cell comprising a signaling enzyme altered so as to bind a
XX CC phosphorylation substrate, where the substrate is associated with
XX CC detectable label and the binding is regulated by a kinase, and
XX CC determining whether the candidate causes a change in expression of the
XX CC label. Also described are: a molecule capable of modulating a kinase
XX CC activity in situ identified by the claimed method; a fusion protein
XX CC comprising a genetically altered signaling enzyme and a label, where the
XX CC alteration produces an adapter molecule in the signaling enzyme capable
XX CC of binding to a phosphorylation substrate that the enzyme does not bind
XX CC in its unaltered state, where the binding is regulated by a kinase; an
XX CC isolated genetic molecule encoding the above fusion protein; a vector
XX CC capable of expressing the above genetic molecule; and a cell transfected
XX CC with the above vector. The invention is useful in drug design to screen
XX CC for molecules that are candidates for anti-tumour, anti-inflammation, and
XX CC anti-ischaemia therapy. This is the amino acid sequence of a necrosis
XX CC factor kappa B (NFkB)-regulating protein I kappa B-alpha cytokine
XX CC inducible IkappaB kinase (IKK) recognition site that has been altered to
XX CC stop Ikb-alpha phosphorylation.
XX XX
XX SQ Sequence 15 AA;
XX
XX Query Match 37.5%; Score 30; DB 7; Length 15;
XX Best Local Similarity 62.5%; Pred. No. 3e+02;
XX Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 5 MTRHSTG 12
XX Db : || || ||
XX 1 LRDRHDTG 8
XX
XX RESULT 8
XX ID ADM95020
XX XX ADM95020 standard; peptide; 15 AA.
XX AC ADM95020;
XX XX
XX XX 17-JUN-2004 (first entry)
XX DE Converted I kappa B (Ikb) kinase recognition domain.
XX DE
XX DE drug design; anti-inflammatory; anti-tumour; immune response;
XX KW anti-ischaemic; I kappa B kinase; Ikb kinase.
XX KW
XX OS Synthetic.
XX OS
XX XX Key Location/Qualifiers
XX FH Misc-difference 11
XX FT

```

FT XX /note= "Optionally Asp or Glu"

PN US2003170850-A1.

XX 11-SEP-2003.

XX 09-MAR-2002; 2002US-00093838.

XX 09-MAR-2002; 2002US-00093838.

XX (CARD/) CARDONE M H.

XX (YAFFE/) YAFFE M.

XX Cardone MH, Yaffe M;

XX WPI; 2003-863758/80.

XX A fusion protein comprising a pair of sequestering motifs, an enzyme-binding region and a label is useful to test and design drugs e.g. anti-inflammatory, anti-tumour, immune response regulating and anti-ischaemic drugs.

XX Disclosure; Fig 3A; 24pp; English.

XX The invention relates to a fusion protein comprising a pair of sequestering motifs, an enzyme-binding region and a label, where the sequestering motifs flank each side of the enzyme-binding region which is prevented from binding to a signalling enzyme when the motifs interact with each other and the interaction is regulated by a kinase. The sequestering motifs comprise a phosphorylation substrate for the kinase and a binding motif for the phosphorylation substrate. Interaction between the phosphorylation substrate and the binding motif requires phosphorylation of the substrate by the kinase. The binding motif comprises substantially a ligand-binding region of a 14-3-3 protein or an SH2 domain and an adapter molecule which is a PDZ, SH3, WW, PTB or FHA domain. The signalling enzyme is a ubiquitin E3 ligase and the enzyme-binding region is an E3-binding region, preferably comprising a PST element or a cyclin destruction box. Alternatively the signalling enzyme is a transporting protein. The label is fluorescent, preferably green fluorescent protein or an enzyme, preferably beta-galactosidase, a phosphatase or luciferase. The method is useful to test and design drugs with various clinical applications including anti-inflammatory candidate molecules, anti-tumour therapies, immune response regulating drugs and anti-ischaemic drugs. The present sequence represents an enzyme binding region used in the fusion protein of the invention.

XX Sequence 15 AA;

Query Match 37.5%; Score 30; DB 7; Length 15;
Best Local Similarity 62.5%; Pred. No. 3e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 MTRRHSTG 12
: |||||

Db 1 LRDRHDTG 8

RESULT 9

ADR31520

ID ADR31520 standard; peptide; 15 AA.

XX ADR31520;

XX 04-NOV-2004 (first entry)

XX IkappaB-alpha mutant substrate peptide #1.

XX Drug designing; clinical application; anti-inflammatory; anti-tumour; immune response; anti-ischaemic; artherosclerosis; therapy;

KW IkappaB-alpha; mutant; mutein.

XX Unidentified.

OS

FT Key Location/Qualifiers

FT Misc-difference 2 /note= "Wild type Asp substituted with Arg"

FT Binding-site 6..11

FT /note= "Beta-TrCP binding region 11"

FT Misc-difference 7 /note= "Wild type Ser substituted with Thr"

FT /note= "Phosphorylated"

FT Modified-site 7 /note= "Phosphorylated"

FT Modified-site 11 /note= "Phosphorylated"

XX US2004157272-A1.

XX 12-AUG-2004.

XX 03-FEB-2004; 2004US-00771035.

XX 09-MAR-2002; 2002US-00093945.

XX (MERR-) MERRIMACK PHARM INC.

XX Cardone MH, Yaffe M;

XX WPI; 2004-580267/56.

XX Identifying molecule capable of modulating kinase activity in situ, by exposing candidate molecule to cell comprising signalling enzyme altered to bind substrate having label and determining whether molecule changes expression of label.

XX Disclosure; Fig 3A; 25pp; English.

XX The invention relates to a method for identifying molecule capable of modulating kinase activity in situ. The method involves exposing candidate molecule to cell having signalling enzyme altered to bind phosphorylation substrate associated with detectable label where the binding between altered signalling enzyme and substrate is regulated by a kinase and determining if the candidate molecule cause a change in expression of label. The method is useful for testing and designing drugs with various clinical application e.g. anti-inflammatory candidate molecules. The invention is useful in the field of anti-tumour therapeutics and immune response regulating drugs. The method is also useful for developing anti-ischaemic drugs that are useful for treating artherosclerosis. The present sequence is IkappaB-alpha mutant substrate peptide. This sequence is used to illustrate the method of the invention.

XX Sequence 15 AA;

Query Match 37.5%; Score 30; DB 8; Length 15;
Best Local Similarity 62.5%; Pred. No. 3e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 MTRRHSTG 12
: |||||

Db 1 LRDRHDTG 8

RESULT 10

ADR31534

ID ADR31534 standard; peptide; 15 AA.

XX ADR31534;

XX 04-NOV-2004 (first entry)

XX IkappaB-alpha mutant substrate peptide #2.

XX Drug designing; clinical application; anti-inflammatory; anti-tumour; immune response; anti-ischaemic; artherosclerosis; therapy;

KW IkappaB-alpha; mutant; mutein.

XX

OS	Unidentified.
XX	
XX	
Key	Location/Qualifiers
FH	Key
FT	Misc-difference 11
FT	/note= "Wild type Ser substituted with Xaa"
FT	/note= "Xaa corresponds to Asp, Glu"
XX	
US	US2004157272-A1.
FN	
XX	
PD	12-AUG-2004.
XX	
XX	
Pf	03-FEB-2004; 2004US-00771035.
XX	
PR	09-MAR-2002; 2002US-00093945.
XX	
PA	(MERR-) MERRIMACK PHARM INC.
XX	
PI	Cardone MH, Yaffe M;
XX	
DR	WPI; 2004-580267/56.
XX	
PT	Identifying molecule capable of modulating kinase activity in situ, by
PT	exposing candidate molecule to cell comprising signaling enzyme altered
PT	to bind substrate having label and determining whether molecule changes
PT	expression of label.
XX	
PS	Disclosure; Page 7; 25pp; English.
XX	
CC	The invention relates to a method for identifying molecule capable of
CC	modulating kinase activity in situ. The method involves exposing
CC	candidate molecule to cell having signalling enzyme altered to bind
CC	phosphorylation substrate associated with detectable label where the
CC	binding between altered signalling enzyme and substrate is regulated by a
CC	kinase and determining if the candidate molecule cause a change in
CC	expression of label. The method is useful for testing and designing drugs
CC	with various clinical application e.g. anti-inflammatory candidate
CC	molecules. The invention is useful in the field of anti-tumour
CC	therapeutics and immune response regulating drugs. The method is also
CC	useful for developing anti-ischaemic drugs that are useful for treating
CC	atherosclerosis. The present sequence is IkappaB-alpha mutant substrate
CC	peptide. This sequence is used to illustrate the method of the invention.
XX	
SQ	Sequence 15 AA;
Query Match	37.5%; Score 30; DB 8; Length 15;
Best Local Similarity	62.5%; Pred. No. 3e+02;
Matches	5; Conservative 1; Mismatches 2; Indels 0; Gaps 0
Qy	5 MRTRHSTG 12
	:
Db	1 LRDRHDTG 8
RESULT 11	
AASW59304	
ID	AASW59304 standard; peptide; 7 AA.
XX	
AC	AASW59304;
XX	
DT	24-SEP-1998 (first entry)
XX	
DE	Non-polio enterovirus peptide fragment 11A.
XX	
KW	Non-polio enterovirus; NPEV; enteroviral disease; aseptic meningitis;
KW	vaccination.
XX	
OS	Enterovirus sp.
XX	
PN	WO9814611-A2.
XX	
PD	09-APR-1998.
XX	
PF	01-OCT-1997; 97WO-US017734.

CC epitope. The invention relates to a novel method for designing degenerate
 CC PCR primers (AAZ30975-231000, AAZ32601- AAZ32611) for amplifying target
 CC polynucleotides. This method comprises identifying uniquely conserved
 CC amino acid sequences (e.g. this epitope) in target proteins; synthesizing
 CC degenerate polynucleotides encoding the conserved sequences; and
 CC substituting the synthesized polynucleotides with up to four
 CC predetermined nucleotides (e.g., inosine) at degenerate nucleotide
 CC positions. The nucleic acids comprise no more than 7 degenerate
 CC positions, have no more than 2 adjacent predetermined nucleotides and the
 CC predetermined nucleotides are 3 bases away from the 3' end of the
 CC synthesised strand. The degenerate primers are useful for amplifying
 CC target polynucleotides by the polymerase chain reaction (PCR). The use of
 CC the method of designing degenerate primers useful for the detection of
 CC polioviruses in clinical samples is described in US85477. The degenerate
 CC primers facilitate PCR amplification of unknown polynucleotides, where
 CC the amino acid sequence encoded is known. The primers also allow for the
 CC correlation of the subsequent molecular based diagnosis with a
 CC serologically derived diagnosis

XX SQ Sequence 7 AA;

Query Match 36.2%; Score 29; DB 2; Length 7;
 Best Local Similarity 83.3%; Pred. No. 1.8e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 TMRTRH 9
 Db 1 TMRTRH 6

RESULT 13

AAZ26509
 ID AAB26509 standard; peptide; 11 AA.

XX AC AAB26509;

XX DT 11-JAN-2001 (first entry)

DE Human IgE C epsilon3 domain mimotope P1la.

XX IgE; C epsilon3; C epsilon4; histamine release inhibitor; vaccine;
 KW antibody; epitope; mimotope; human.

XX OS Homo sapiens.
 OS Synthetic.

XX FH Key Location/Qualifiers

XX FT Modified-site 1 /note= "N-terminal acetyl"

XX WO200050461-A1.

XX PD 31-AUG-2000.

XX PF 22-FEB-2000; 2000WO-EP001456.

XX PR 25-FEB-1999; 99GB-00004408.

XX PR 21-JUL-1999; 99GB-00017144.

XX PR 07-AUG-1999; 99GB-00018598.

XX PR 07-AUG-1999; 99GB-00018599.

XX PR 07-AUG-1999; 99GB-00018601.

XX PR 07-AUG-1999; 99GB-00018604.

XX PR 07-AUG-1999; 99GB-00018606.

XX PR 29-OCT-1999; 99GB-00025618.

XX PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
 PA (PEPT-) PEPTIDE THERAPEUTICS LTD.

XX PI Friede M, Mason S, Turnell WG, Van Mechelen MP;
 PI Vinals Y De BassolsC;

XX XX WPI; 2000-572074/53.

PT Peptides comprising surface exposed epitopes or mimotopes derived from C-
 PT epsilon3 or C-epsilon4 domains of IgE, useful for preventing or
 PT treating allergy.

XX PS Disclosure; Page 8; 76pp; English.

XX CC The present invention relates epitopes and mimotopes of an isolated
 CC surface exposed epitope of C epsilon3 or C epsilon4 domain of IgE. The
 CC epitopes were identified by calculating the accessible surface of each
 CC IgE residue. Mimotopes were designed to be similar to the epitopes. The
 CC epitopes are useful in preparing medicaments for treating or preventing
 CC allergies. The epitopes and mimotopes of the invention induce anti-IgE
 CC antibodies which are capable of raising non-anaphylactic antibodies and
 CC inhibiting histamine release. The present sequence is a IgE C epsilon3
 CC domain mimotope

XX SQ Sequence 11 AA;

Query Match 36.2%; Score 29; DB 3; Length 11;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 HSTGG 13
 Db 6 HSTGG 10

RESULT 14

AAU16840
 ID AAU16840 standard; peptide; 11 AA.

XX AC AAU16840;

XX DT 07-NOV-2001 (first entry)

DE Peptide P1la derived as mimotope of Cepsilon3/4 region of human IgE.

XX Human; linkage technology; conjugated compound; carrier vehicle; epitope;
 KW Cepsilon2; Cepsilon3; Cepsilon4; immunoglobulin E; IgE mediated disease;
 KW antibody response.

XX OS Homo sapiens.
 OS Synthetic.

XX WO200145745-A2.

XX PD 28-JUN-2001.

XX PF 21-DEC-2000; 2000WO-GE004935.

XX PR 21-DEC-1999; 99GB-00030233.

XX PR 22-FEB-2000; 2000GB-00004096.

XX PR 22-AUG-2000; 2000GB-00020707.

XX PR 22-AUG-2000; 2000GB-00020708.

XX PA (ACAM-) ACAMBI RES LTD.
 PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.

XX PI Flinn N, Johnson T;

XX DR WPI; 2001-521967/57.

XX PT A linkage comprising an immunogenic conjugate useful treatment of IgE
 XX mediated diseases.

XX PS Example 5; Page 25; 48pp; English.

XX CC The present invention relates to linkage methodology for use in the
 CC conjugation of compounds (e.g. peptides) to carrier vehicles (e.g.
 CC macromolecules, polymers, dendrimers, proteins) to produce biological and
 CC immunological constructs. The invention provides a method for linking an
 CC epitope (e.g. a peptide) to a carrier (e.g. a protein) for use in a
 CC pharmaceutical composition or a vaccine. The invention describes peptides

CC derived from or mimotopes of the Cepsilon2, Cepsilon3 or Cepsilon4
CC regions of human immunoglobulin E (IgE) which are used to produce
CC conjugated compounds. The compounds or compositions of the invention are
CC useful in the manufacture of a medicament for the treatment of IgE
CC mediated diseases. The invention allows for controlled conjugation of a
CC peptide epitope (antigen) to a protein so as to form an immunogenic
CC conjugate which may be able to raise a protective antibody response in an
CC animal or human patient. AAU16632-AAU16913 represent peptides derived
CC from or mimotopes of the Cepsilon2/Cepsilon3/Cepsilon4 region of human
CC IgE
XX
SQ Sequence 11 AA;

Query Match 36.2%; Score 29; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 HSTGG 13
Db |||||
6 HSTGG 10

RESULT 15
ABJ00284
ID ABJ00284 standard; peptide; 11 AA.
XX
AC ABJ00284;
XX
DT 02-SEP-2002 (first entry)
XX
DE Human IgE immunogenic peptide SEQ ID NO: 68.
XX
KW Immunogen; human; IgE; immunoglobulin E; allergy; thio-ether linkage;
KW vaccine; antiallergic.
XX
OS Homo sapiens.
XX
PN WO200216409-A2.
XX
PD 28-FEB-2002.
XX
PF 17-AUG-2001; 2001WO-BF009576.
XX
PR 22-AUG-2000; 2000GB-00020717.
XX
PA (SMIX) SMITHKLINE BEECHAM BIOLOGICALS.
PA (PEPT-) PEPTIDE THERAPEUTICS LTD.
XX
PI Friede M, Mason S, Turnell WG, Vinals Y BassolsC;
XX WPI; 2002-489648/52.
XX
DR Conjugate for use in vaccine for treatment of allergy, comprises
PT disulfide bridge cyclized peptide and immunogenic carrier.
XX
PS Claim 4; Page 10; 45pp; English.
XX
CC The present invention relates to conjugates suitable for use in vaccines,
CC where the conjugate comprises a disulphide bridge cyclised peptide and an
CC immunogenic carrier. The vaccines can be used in the treatment of
CC allergies. The present sequence is a peptide immunogen derived from human
CC immunoglobulin E (IgE) suitable to be cyclised and used in the invention
XX
SQ Sequence 11 AA;

Query Match 36.2%; Score 29; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 HSTGG 13
Db |||||
6 HSTGG 10

Search completed: February 22, 2005, 09:24:42
Job time : 67.6667 secs

Result No.	Score	Query			DB	ID	Description
		Match	Length	%			
1	21	27.6	15	2	C48401	ribosomal protein	
2	21	27.6	15	4	I52698	hypothetical protein	
3	19	25.0	12	5	S68271	major urinary protein	
4	19	25.0	14	2	C39170	acyl-[acyl]-carrier	
5	19	25.0	14	2	S29485	GTP-binding protein	
6	18	23.7	7	2	B39127	phosphotransferase	
7	18	23.7	10	2	A58365	neuropeptide FFRPa	
8	18	23.7	10	2	S23307	neurokinin A - rat	
9	18	23.7	10	2	S23186	neurokinin A - At1	
10	18	23.7	11	2	PD0441	translation elonga	
11	18	23.7	12	2	S65738	hemoglobin, extrac	
12	18	23.7	12	2	PT0228	IG heavy chain CDR	
13	18	23.7	14	2	PA0104	protein QP200070 -	
14	18	23.7	14	2	S38307	DEB-A protein - fr	
15	18	23.7	14	2	S29632	xylan 1,4-beta-xy	
16	18	23.7	14	2	A47421	leukotriene B-4 12	
17	18	23.7	15	2	PQ0193	stylar glycoprotei	
18	18	23.7	15	2	PQ0194	Sz-glycoprotein -	
19	18	23.7	15	2	PA0054	protein QP200017 -	
20	17	22.4	9	2	C36730	hutu protein - Kle	
21	17	22.4	9	2	A47487	calliFWamide 10	
22	17	22.4	10	2	PT0284	IG heavy chain CDR	
23	17	22.4	11	2	PH1600	IG H chain V-D-J r	
24	17	22.4	12	2	PH1182	T-cell receptor al	
25	17	22.4	12	2	PH1174	T-cell receptor al	
26	17	22.4	12	2	PH1181	T-cell receptor al	
27	17	22.4	12	2	A34858	proteinase E - bla	
28	17	22.4	15	2	S26525	T-cell receptor al	
29	17	22.4	15	2	S26518	T-cell receptor al	

```

Db          7 FRQVHVS 14

RESULT 3
S68271
major urinary protein VIII - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 07-May-1999
C:Accession: S68271
R:Robertson, D.H.L.; Cox, K.A.; Gaskell, S.J.; Evershed, R.P.; Beynon, R.J.
Biochem. J. 316, 265-272, 1996
A:Title: Molecular heterogeneity in the major urinary proteins of the house mouse
A:Reference number: S68271; MUID:96235201; PMID:8645216
A:Accession: S68271
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-12 <ROB>

Query Match      25.0%; Score 19; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 FAQL 14
        ||||
Db       3 FAQL 6

RESULT 4
C39170
acyl-l[acyl-carrier-protein] desaturase (EC 1.14.19.2) - avocado (fragments)
C:Species: Persea americana (avocado)
C:Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 03-Jun-2002
C:Accession: C39170
R:Shanklin, J.; Somerville, C.
Proc. Natl. Acad. Sci. U.S.A. 88, 2510-2514, 1991
A:Title: Stearoyl-acyl-carrier-protein desaturase from higher plants is structurally un
A:Reference number: A39170; MUID:91172837; PMID:2006187
A:Accession: C39170
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-14 <SHA>
C:Keywords: oxidoreductase

Query Match      25.0%; Score 19; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 3.9e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      10 DFAQL 15
        ||:|
Db       8 DVADIL 13

RESULT 5
S29485
GTP-binding protein o-xal - Pacific electric ray (fragment)
C:Species: Torpedo californica (Pacific electric ray)
C:Date: 22-Nov-1993 #sequence_revision 27-Feb-1997 #text_change 13-Mar-1997
C:Accession: S29485
R:Volkmann, W.; Pevsner, J.; Elferink, L.A.; Scheller, R.H.
FEBS Lett. 317, 53-56, 1993
A:Title: Association of three small GTP-binding proteins with cholinergic synaptic vesic
A:Reference number: S29485; MUID:93154521; PMID:8428634
A:Accession: S29485
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <VOL>

Query Match      25.0%; Score 19; DB 2; Length 15;
Best Local Similarity 60.0%; Pred. No. 4.2e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      7 FVRDF 11
        |||

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Db          5 FVEDY 9

RESULT 6
B39127
phosphotransferase system enzyme II (EC 2.7.1.69) - Escherichia coli (fragment)
C:Species: Escherichia coli
C:Date: 27-Nov-1991 #sequence_revision 27-Nov-1991 #text_change 08-Oct-1999
C:Accession: B39127
R:Hardesty, C.; Ferran, C.; DiRienzo, J.M.
J. Bacteriol. 173, 449-456, 1991
A:Title: Plasmid-mediated sucrose metabolism in Escherichia coli: characterization of sc
rin.
A:Reference number: A39127; MUID:91100329; PMID:1846143
A:Accession: B39127
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-7 <HAR>
A:Cross-references: GB:M38416; NID:g155142; PIDN:AAA98418.1; PID:g155144
C:Keywords: phosphotransferase

Query Match      23.7%; Score 18; DB 2; Length 7;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      10 DFAQL 14
        |||
Db       2 DFEQI 6

RESULT 7
A58365
neuropeptide FFRFamide - blue mussel
N:Alternate names: FMRFamide-related decapeptide; Mytilus FFRFamide
C:Species: Mytilus edulis (blue mussel)
C:Date: 20-Nov-1996 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
C:Accession: A58365
R:Fujisawa, Y.; Ikeda, T.; Nomoto, K.; Yasuda-Kamatani, Y.; Minakata, H.; Kenny, P.T.M.;
Comp. Biochem. Physiol. C 102, 91-95, 1992
A:Title: The FMRFamide-related decapeptide of Mytilus contains a D-amino acid residue.
A:Reference number: A58365; MUID:93047882; PMID:1358533
A:Accession: A58365
A:Molecule type: protein
A:Residues: 1-10 <FUJ>
A:Cross-references: UNIPROT:P42560
A:Experimental source: anterior byssus retractor muscle
C:Keywords: amidated carboxyl end; D-amino acid; neuropeptide
F;2/Modified site: D-leucine (Leu) #status experimental
F;10/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match      23.7%; Score 18; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      6 HFVR 9
        |||
Db       6 HFVR 9

RESULT 8
S23307
neurokinin A - rainbow trout
C:Species: Oncorhynchus mykiss (rainbow trout)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Aug-2004
C:Accession: S23307
R:Jensen, J.; Conlon, J.M.
Eur. J. Biochem. 206, 659-664, 1992
A:Title: Substance-P-related and neurokinin-A-related peptides from the brain of the cod
A:Reference number: S23186; MUID:92298992; PMID:1376687
A:Accession: S23307
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <JEN>

```

A;Cross-references: UNIPROT:P28500

Query Match 23.7%; Score 18; DB 2; Length 10;
Best Local Similarity 30.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 6 HFVRDFAQLL 15
| : | : | :
Db 1 HKINSFVGLM 10

RESULT 9

S23186
neurokinin A - Atlantic cod
C;Species: Gadus morhua (Atlantic cod)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Aug-2004
C;Accession: S23186
R;Jensen, J.; Conlon, J.M.
Eur. J. Biochem. 206, 659-664, 1992
A;Title: Substance-P-related and neurokinin-A-related peptides from the brain of the cod
A;Reference number: S23186; MUID:92298992; PMID:1376687
A;Accession: S23186
A;Molecule type: protein
A;Residues: 1-10 <JEN>
A;Cross-references: UNIPROT:P28500
A;Experimental source: brain
C;Function:
A;Note: neurokinin A is derived by post-translational processing of preprotachykinin A
C;Keywords: neuropeptide; amidated carboxyl end; tachykinin
F;10/Modified site: amidated carboxyl end (Met) #status predicted

Query Match 23.7%; Score 18; DB 2; Length 10;
Best Local Similarity 30.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 6 HFVRDFAQLL 15
| : | : | :
Db 1 HKINSFVGLM 10

RESULT 10

PD0441
translation elongation factor TU-like protein P43, mitochondrial - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 21-Aug-1998
C;Accession: PD0441
R;Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Morimasa, T.; Tsugita, A.
submitted to JIPID, August 1998
A;Description: Proteome analysis of mouse brain.

A;Reference number: PD0441

A;Accession: PD0441

A;Molecule type: protein

A;Residues: 1-11 <KAW>

A;Experimental source: striatum

C;Keywords: mitochondrion

Query Match 23.7%; Score 18; DB 2; Length 11;
Best Local Similarity 75.0%; Pred. No. 4.5e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 FVRD 10
| : | : | :
Db 8 YVRD 11

RESULT 11

S65730
hemoglobin, extracellular, component - earthworm (lumbricus terrestris) (fragment)
C;Species: Lumbricus terrestris (common earthworm)
C;Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C;Accession: S65730

R;Fushitani, K.; Higashiyama, K.; Asao, M.; Hosokawa, K.

Biochim. Biophys. Acta 1292, 273-280, 1996

A;Title: Characterization of the constituent polypeptides of the extracellular hemoglobin

A;Reference number: S65721; MUID:96176855; PMID:8597573

A;Accession: S65730

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-12 <FUS>

Query Match 23.7%; Score 18; DB 2; Length 12;
Best Local Similarity 40.0%; Pred. No. 5e+03;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 HFVRD 10
| : | : | :
Db 8 HLIQD 12

RESULT 12

PT0228

Ig heavy chain CDR3 region (clone 1-112) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C;Accession: PT0228

R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j

A;Reference number: PT0222; MUID:91108337; PMID:1899102

A;Accession: PT0228

A;Molecule type: DNA

A;Residues: 1-12 <YAM>

A;Experimental source: B lymphocyte

C;Keywords: heterotrimer; immunoglobulin

Query Match 23.7%; Score 18; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 5e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 FVRD 10
| : | : | :
Db 3 YVRD 6

RESULT 13

PA0104

protein QP200070 - fungus (Fusarium sporotrichioides) (fragment)

C;Species: Fusarium sporotrichioides

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001

C;Accession: PA0104

R;Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.

submitted to JIPID, October 1994

A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichi

A;Reference number: PA0051

A;Accession: PA0104

A;Molecule type: protein

A;Residues: 1-14 <CHO>

Query Match 23.7%; Score 18; DB 2; Length 14;
Best Local Similarity 60.0%; Pred. No. 5.8e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 RQLVH 6
| : | : | :
Db 10 RQIVY 14

RESULT 14

S38307

DEB-A protein - fruit fly (Drosophila melanogaster) (fragment)

C;Species: Drosophila melanogaster

C;Date: 19-May-1994 #sequence_revision 27-Feb-1997 #text_change 17-Mar-1999

C;Accession: S38307

R;Wang, G.L.; Goldstein, E.S.

Biochim. Biophys. Acta 1216, 94-104, 1993

A:Title: An AP-1 binding site in the upstream region of DEB-A is part of a developmental
A:Reference number: S38307; MUID:94032494; PMID:8218421
A:Accession: S38307
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-14 <WAN>

Query Match 23.7%; Score 18; DB 2; Length 14;
Best Local Similarity 33.3%; Pred. No. 5.8e+03;
Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 7 FVRDFA 12
::|||:
Db 6 YIRSFS 11

RESULT 15

S29632
xylan 1,4-beta-xylosidase (EC 3.2.1.37) - Thermotoga sp. (strain FJSS3-B.1) (fragment)
N:Alternate names: beta-xylosidase
C:Species: Thermotoga sp.
A:Variety: FJSS3-B.1
C:date: 19-Mar-1997 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C:Accession: S29632
R:Ruttersmith, L.D.; Daniel, R.M.
Biochim. Biophys. Acta 1156, 167-172, 1993
A:Title: Thermostable beta-glucosidase and beta-xylosidase from Thermotoga sp. strain FJ
A:Reference number: S29631; MUID:93152594; PMID:8427876
A:Accession: S29632
A:Molecule type: protein
A:Residues: 1-14 <RUT>
A:Cross-references: UNIPROT:Q7M0O6
A:Experimental source: strain FJSS3-B.1
C:Comment: Although the beta-xylosidase enzyme activity was apparently confirmed for thi
A:Description: hydrolyzes short chain oligosaccharides and xylobiose to produce D-xylose
A:Note: Plays an important role in the relief of end-product inhibition of endoxylanase
C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 23.7%; Score 18; DB 2; Length 14;
Best Local Similarity 33.3%; Pred. No. 5.8e+03;
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 ROLVHFVRD 10
::|||:
Db 2 KKYVYFFAD 10

Search completed: February 22, 2005, 09:46:27
Job time : 12.1333 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 22, 2005, 08:53:13 ; Search time 52.6 Seconds
(without alignments)
146.030 Million cell updates/sec

Title: US-08-991-628-8

Perfect score: 76

Sequence: 1 FROLVHFVRDFAQLL 15

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 6622

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	34.2	15	2 Q54325	Q54325 staphylococ
2	23	30.3	9	2 Q8GIZ6	Q8GIZ6 lactobacill
3	23	30.3	13	2 Q7XB02	Q7XB02 zea mays (m
4	23	30.3	13	2 Q6XFQ8	Q6XFQ8 bacillus cl
5	23	30.3	14	2 Q7X8P6	Q7X8P6 zea mays (m
6	23	30.3	15	2 Q7XB01	Q7XB01 zea mays (m
7	22	28.9	12	2 Q9U7R8	Q9U7R8 conus querc
8	21	27.6	10	2 Q9TS43	Q9TS43 sus scrofa
9	21	27.6	11	2 Q90735	Q90735 gallus gall
10	21	27.6	13	2 Q6LAU9	Q6LAU9 homo sapien
11	20	26.3	10	2 Q9TWU1	Q9TWU1 fusinus fer
12	20	26.3	10	2 Q6R7V4	Q6R7V4 carlia zuma
13	20	26.3	11	2 Q68LE0	Q68LE0 pyriglena l
14	20	26.3	11	2 Q68LE9	Q68LE9 myrmotherul
15	20	26.3	13	2 Q6TKD3	Q6TKD3 praecitrull
16	20	26.3	13	2 Q6TKD4	Q6TKD4 sechium edu
17	20	26.3	13	2 Q6TKD5	Q6TKD5 sicyos angu
18	20	26.3	13	2 Q6TKD6	Q6TKD6 trichosanthe
19	20	26.3	13	2 Q6TKD7	Q6TKD7 luffa grave
20	20	26.3	13	2 Q6TKD8	Q6TKD8 luffa echin
21	20	26.3	13	2 Q6TKD9	Q6TKD9 cucurbita p
22	20	26.3	13	2 Q6TKD0	Q6TKD0 benincasa h
23	20	26.3	13	2 Q6TKD1	Q6TKD1 marah orega
24	20	26.3	13	2 Q6TKD2	Q6TKD2 cycianthera
25	20	26.3	13	2 Q6TKD3	Q6TKD3 echinocyti
26	20	26.3	13	2 Q6TKD4	Q6TKD4 luffa quing
27	20	26.3	13	2 Q6TKD5	Q6TKD5 lagenaria l
28	20	26.3	13	2 Q6TKD6	Q6TKD6 citrullus l
29	20	26.3	13	2 Q6TKD7	Q6TKD7 citrullus c
30	20	26.3	13	2 Q6TKD8	Q6TKD8 acanthosicy
31	20	26.3	13	2 Q6TKD9	Q6TKD9 bryonia dio

32	20	26.3	13	2 Q6TKF0	Q6TKF0 coccinia pa
33	20	26.3	13	2 Q6TKF1	Q6TKF1 diplocyclos
34	20	26.3	13	2 Q6TKF2	Q6TKF2 ecballium e
35	20	26.3	13	2 Q9MQK3	Q9MQK3 capra ibex
36	20	26.3	14	2 Q14342	Q14342 homo sapien
37	20	26.3	14	2 Q6R7V0	Q6R7V0 carlia viva
38	20	26.3	15	2 Q6LAI1	Q6LAI1 drosophila
39	19	25.0	10	1 AKHX_LOCOMI	P81626 locusta mig
40	19	25.0	11	2 Q8MM58	Q8MM58 heliconius
41	19	25.0	11	2 Q9QVF6	Q9QVF6 mus musculu
42	19	25.0	12	2 Q8MUN4	Q8MUN4 heliconius
43	19	25.0	12	2 Q8MUN9	Q8MUN9 heliconius
44	19	25.0	12	2 Q9TJ34	Q9TJ34 bacterioph
45	19	25.0	13	1 TEML_RANTE	P57104 rana tempor

ALIGNMENTS

RESULT 1					
Q54325	Q54325	PRELIMINARY;	PRT;	15 AA.	
AC	Q54325;				
DT	01-NOV-1996	(TrEMBLrel. 01, Created)			
DT	01-NOV-1996	(TrEMBLrel. 01, Last sequence update)			
DT	01-JUN-2003	(TrEMBLrel. 24, Last annotation update)			
DE	Chloramphenicol acetyltransferase (Fragment)				
GN	Name=cat;				
OS	Staphylococcus intermedius.				
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.				
OX	NCBI_TaxID=1285;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=96379895; PubMed=8787908;				
RA	Lodder G., Schwarz S., Gregory P., Dyke K.;				
RT	tandem duplication in ermC translational attenuator of the macrolide-				
RT	lincosamide-streptogramin B resistance plasmid pSE56 from				
RT	Staphylococcus equorum."				
RL	Antimicrob. Agents Chemother. 40:215-217(1996).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RA	Schwarz S.P.;				
RL	Submitted (NOV-1994) to the EMBL/GenBank/DBDJ databases.				
DR	EMBL; X82666; CAA57981.1; -.				
DR	GO; GO:0016740; F:transferase activity; IEA.				
KW	Transferase.				
FT	NON_TER	1	1		
SQ	SEQUENCE	15 AA;	1931 MW;	173A6AA93999A8D9 CRC64;	
Query Match 34.2%; Score 26; DB 2; Length 15;					
Best Local Similarity 36.4%; Pred. No. 1.4e+03;					
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;					
QY	1 FROLVHFVRDVF 11				
	: : :				
DB	4 FQDIHVRVDDW 14				
RESULT 2					
Q8GIZ6	Q8GIZ6	PRELIMINARY;	PRT;	9 AA.	
AC	Q8GIZ6;				
DT	01-MAR-2003	(TrEMBLrel. 23, Created)			
DT	01-MAR-2003	(TrEMBLrel. 23, Last sequence update)			
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)			
DE	Glyceraldhyde 3-phosphate dehydrogenase (EC 1.2.1.12)				
DE	(Fragment)				
GN	Name=gap;				
OS	Lactobacillus delbrueckii (subsp. lactis).				
OC	Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;				
OC	Lactobacillus.				
OX	NCBI_TaxID=29397;				
RN	[1]				

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RP SEQUENCE FROM N.A.
RC STRAIN=NCC88;
RA Bourniquel A.A., Mollet B.;
RT "Purification and characterization of the 3-phosphoglycerate kinase
from the thermophile Lactobacillus delbrueckii subsp. lactis.";
RL Int. Dairy J. 12:723-728(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NCC88;
RA Bourniquel A.A.;
RT "Molecular insights into the metabolism and physiology of the lactic
acid bacterium Lactobacillus delbrueckii subsp. lactis.";
RL Thesis (2000), Department of Molecular Microbiology, Biozentrum der
Universitaet Basel, (PhD work conducted at the Nestle Research Center,
RL Lausanne), Switzerland.
DR EMBL; AJ15554; CAD56494.1; -.
DR GO; GO:0004365; F:glyceraldehyde-3-phosphate dehydrogenase (p. . .; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
KW Oxidoreductase.
FT NON_TER 1
SQ SEQUENCE 9 AA; 1071 MW; 94ABADD9C1E72731 CRC64;

Query Match 30.3%; Score 23; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.6e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ROLVHF 7
DB 1 RLLHF 6

RESULT 3
Q7XB02 PRELIMINARY; PRT; 13 AA.
AC Q7XB02;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE Phytoene synthase 2 (Fragment).
GN Name=psv2;
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B73;
RX MEDLINE=22779048; PubMed=12897253;
RA Palaisa K.A., Morgante M., Williams M., Rafalski A.;
RT "Contrasting effects of selection on sequence diversity and linkage
disequilibrium at two phytoene synthase loci.";
RL Plant Cell 15:1795-1806(2003).
DR EMBL; AY300613; AAP55352.1; -.
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1443 MW; 1D425AC312022054 CRC64;

Query Match 30.3%; Score 23; DB 2; Length 13;
Best Local Similarity 36.4%; Pred. No. 4.1e+03;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 QLVHFVRDFAQ 13
DB 3 QLTNIIRDVG 13

RESULT 4
Q6XF08 PRELIMINARY; PRT; 13 AA.
AC Q6XF08;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

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DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative leader peptide.
OS Bacillus clausii.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=79880;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM8716;
RX PubMed=14711653; DOI=10.1128/AEM.70.1.280-284.2004;
RA Bozdogan B., Galopin S., Leclercq R.;
RT "Characterization of a new erm-related macrolide resistance gene
present in probiotic strains of Bacillus clausii.";
RL Appl. Environ. Microbiol. 70:280-284(2004).
DR EMBL; AY234334; AAP74656.1; -.
SQ SEQUENCE 13 AA; 1687 MW; 48F43CB7F010D407 CRC64;

Query Match 30.3%; Score 23; DB 2; Length 13;
Best Local Similarity 60.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 VHFVR 9
DB 1 MHFIR 5

RESULT 5
Q7X8P6 PRELIMINARY; PRT; 14 AA.
AC Q7X8P6;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Phytoene synthase 2 (Fragment).
GN Name=psv2;
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PI58332; PIS95566, Ames22026, and PIS95546;
RX MEDLINE=22779048; PubMed=12897253;
RA Palaisa K.A., Morgante M., Williams M., Rafalski A.;
RT "Contrasting effects of selection on sequence diversity and linkage
disequilibrium at two phytoene synthase loci.";
RL Plant Cell 15:1795-1806(2003).
DR EMBL; AY300630; AAP55368.1; -.
DR EMBL; AY300637; AAP55375.1; -.
DR EMBL; AY300643; AAP55381.1; -.
DR EMBL; AY300662; AAP55400.1; -.
DR InterPro; IPR008949; Terpenoid_synth.
FT NON_TER 1
FT NON_TER 14
SQ SEQUENCE 14 AA; 1556 MW; 1D425AC312580D54 CRC64;

Query Match 30.3%; Score 23; DB 2; Length 14;
Best Local Similarity 36.4%; Pred. No. 4.1e+03;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 QLVHFVRDFAQ 13
DB 4 QLTNIIRDVG 14

RESULT 6
Q7XB01 PRELIMINARY; PRT; 15 AA.
AC Q7XB01;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Phytoene synthase 2 (Fragment).

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GN Name=psy2;
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=P1270297;
RX MEDLINE=22779048; PubMed=12897253;
RA Palaisa K.A., Morgante M., Williams M., Rafalski A.;
RT "Contrasting effects of selection on sequence diversity and linkage
RT disequilibrium at two phycoene synthase loci.";
RL Plant Cell 15:1795-1806 (2003).
DR EMBL; AY300625; AAP55363.1; -.
DR InterPro; IPR008949; Terpenoid_synth.
FT NON_TER 1
FT NON_TER 15
SQ SEQUENCE 15 AA; 1613 MW; 1D425AC312585ACF CRC64;

Query Match 30.3%; Score 23; DB 2; Length 15;
Best Local Similarity 36.4%; Pred. No. 4.8e+03;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 QLVHFVRDFAQ 13
DB 5 QLTNILDVGS 15

RESULT 7
Q9U7R8 PRELIMINARY; PRT; 12 AA.
ID Q9U7R8
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Calmodulin (Fragment).
OS Conus quercinus (Oak cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=101313;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=99398698; PubMed=10468598; DOI=10.1073/pnas.96.18.10272;
RA Duda T.F. Jr., Palumbi S.R.;
RT "Developmental shifts and species selection in gastropods.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:10272-10277 (1999).
DR EMBL; AF113305; AAD49168.1; -.
FT NON_TER 1
FT NON_TER 12
SQ SEQUENCE 12 AA; 1284 MW; 1CF4EE6A86D9CAA0 CRC64;

Query Match 28.9%; Score 22; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 5.7e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 DFAQLL 15
DB 6 DFAEFL 11

RESULT 8
Q9TS43 PRELIMINARY; PRT; 10 AA.
ID Q9TS43
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE OSTRADIOL-RECEPTOR-P1 peptide (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI_TaxID=9823;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=91291128; PubMed=2064608;
RA Thole H.H., Jungblut P.W., Jakob F.;
RT "The proton-driven dissociation of oestradiol-receptor dimers as a
RT preparative tool: Isolation of a 32 kDa fragment from porcine uteri
RL and assignment of C-terminal origin by partial sequencing.";
RL Biochem. J. 276:709-714 (1991).
FT NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 1240 MW; D314D274405691F2 CRC64;

Query Match 27.6%; Score 21; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 QLVHVF 8
DB 1 ELVHMI 6

RESULT 9
Q90735 PRELIMINARY; PRT; 11 AA.
ID Q90735
AC Q90735;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Gallus gallus beta-globin gene. (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=81208060; PubMed=6263308;
RA Day L.E., Hirst A.J., Lai E.C., Mace M.Jr., Woo S.L.C.;
RT "5' Domain and nucleotide sequence of an adult chicken chromosomal
RT beta-globin gene.";
RL Biochemistry 20:2091-2098 (1981).
DR EMBL; V00378; CAA23677.1; -.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1372 MW; 271C02021B1DC1B3 CRC64;

Query Match 27.6%; Score 21; DB 2; Length 11;
Best Local Similarity 36.4%; Pred. No. 7.9e+03;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 LVHFVRDFAQL 14
DB 1 MVHWTAEKQL 11

RESULT 10
Q6LAU9 PRELIMINARY; PRT; 13 AA.
ID Q6LAU9
AC Q6LAU9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE B2-bradykinin receptor gene protein (Fragment).
GN Names=B2-bradykinin receptor gene;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE=95298027; PubMed=7779089;
RA Kammerer S., Braun A., Arnold N., Roscher A.A.;
RT "The human bradykinin B2 receptor gene: full length cDNA, genomic
```

RT organization and identification of the regulatory region."
 RL Biochem. Biophys. Res. Commun. 211:226-233(1995).
 DR EMBL; X86163; CAA60107.1; -.
 DR GO; GO:0004872; F:receptor activity; IEA.
 KW Receptor.
 FT NON_TER
 SQ SEQUENCE 13 AA; 1567 MW; DDE0E98A14967AB6 CRC64;

Query Match 27.6%; Score 21; DB 2; Length 13;
 Best Local Similarity 37.5%; Pred. No. 9.3e+03;
 Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 5 VHFVRDFA 12
 Db 2 IHKLQDMA 9

RESULT 11

ID Q9TWU1 PRELIMINARY; PRT; 10 AA.
 AC Q9TWU1;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE FMRFAMIDE-related peptide.
 OS Fusinus ferrugineus (Ferruginous spindle).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
 OC Neogastropoda; Buccinoidea; Fascioliariidae; Fusinus.
 OX NCBI_TaxID=6488;
 RN [1]
 RP SEQUENCE.
 RA Kuroki Y., Kanda T., Kubota I., Ikeda T., Fujisawa Y., Minakata H.,
 RA Muneoka Y.;
 RT "FMRFamide-related peptides isolated from the prosobranch mollusc
 RT Fusinus ferrugineus."
 RL Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.
 SQ SEQUENCE 10 AA; 1233 MW; 83F80229C1EAA451 CRC64;

Query Match 26.3%; Score 20; DB 2; Length 10;
 Best Local Similarity 75.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 HFVR 9

Db 6 HFVR 9

RESULT 12

ID Q6R7V4 PRELIMINARY; PRT; 10 AA.
 AC Q6R7V4;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Glyceraldehyde-3-phosphate dehydrogenase (Fragment).
 GN Name=GAPDH;
 OS Carlia zuma.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Scincomorpha; Scincoidea;
 OC Scincidae; Carlia.
 OX NCBI_TaxID=260893;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Dolman G., Phillips B.;
 RT "Single copy nuclear DNA markers characterized for comparative
 RT phylogeography in Australian wet tropics rainforest skinks."
 RL Mol. Ecol. Notes 4:185-187(2004).
 DR EMBL; AY508912; AAS09890.1; -.
 FT NON_TER
 FT NON_TER

SQ SEQUENCE 10 AA; 1171 MW; 9D0AB2322C9C1EA CRC64;

Query Match 26.3%; Score 20; DB 2; Length 10;
 Best Local Similarity 75.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 HFVR 9

Db 4 HFVR 7

RESULT 13

ID Q68LE0 PRELIMINARY; PRT; 11 AA.
 AC Q68LE0;
 DT 25-OCT-2004 (TREMBLrel. 28, Created)
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
 DE Glyceraldehyde-3-phosphate dehydrogenase (Fragment).
 GN Name=NAPDH;
 OS Pyriglena leuconota.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Passeriformes; Formicariidae;
 OC Pyriglena.
 OX NCBI_TaxID=183187;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Irestedt M., Fjeldsa J., Nylander J.A., Ericson P.G.;
 RT "Phylogenetic relationships of typical antbirds (Thamnophilidae) and
 RT test of incongruence based on Bayes factors."
 RL BMC Evol. Biol. 4:23-23(2004).
 DR EMBL; AY677056; AAT96981.1; -.
 FT NON_TER
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 11 AA; 1242 MW; 9D0AEB2622C9C1EA CRC64;

Query Match 26.3%; Score 20; DB 2; Length 11;
 Best Local Similarity 75.0%; Pred. No. 1.2e+04;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 HFVR 9

Db 5 HFVR 8

RESULT 14

ID Q68LE9 PRELIMINARY; PRT; 11 AA.
 AC Q68LE9;
 DT 25-OCT-2004 (TREMBLrel. 28, Created)
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
 DE Glyceraldehyde-3-phosphate dehydrogenase (Fragment).
 GN Name=NAPDH;
 OS Myrmotherula fulviventris.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Passeriformes; Thamnophilidae;
 OC Myrmotherula.
 OX NCBI_TaxID=288045;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Irestedt M., Fjeldsa J., Nylander J.A., Ericson P.G.;
 RT "Phylogenetic relationships of typical antbirds (Thamnophilidae) and
 RT test of incongruence based on Bayes factors."
 RL BMC Evol. Biol. 4:23-23(2004).
 DR EMBL; AY677047; AAT96972.1; -.
 FT NON_TER
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 11 AA; 1242 MW; 9D0AEB2622C9C1EA CRC64;

Query Match 26.3%; Score 20; DB 2; Length 11;
 Best Local Similarity 75.0%; Pred. No. 1.2e+04;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 HFVR 9
 DB 5 HFVK 8

RESULT 15

Q6TKD3 Q6TKD3 PRELIMINARY; PRT; 13 AA.
 AC Q6TKD3;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Photosystem II protein (Fragment).
 GN Name=psbC;
 OS Praecitrullus fistulosus.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Cucurbitales; Cucurbitaceae; Praecitrullus.
 OX NCBI_TaxID=252558;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Decker-Walters D.S., Chung S.-M., Staub J.E.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY396191; AAR07576.1; -;
 DR GO; GO:0009507; C:Chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER 1 1
 SQ SEQUENCE 13 AA; 1579 MW; CF0270FB8503C732 CRC64;

Query Match 26.3%; Score 20; DB 2; Length 13;
 Best Local Similarity 57.1%; Pred. No. 1.4e+04;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 RDEAQLL 15
 DB 1 RDEFPVL 7

Search completed: February 22, 2005, 09:37:57
 Job time : 53.6667 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 22, 2005, 08:52:23 ; Search time 65.6667 Seconds
(without alignments)
88.346 Million cell updates/sec

Title: US-08-991-628-8
Perfect score: 76
Sequence: 1 FRQLVHFVRDFAQLL 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 632537

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	76	100.0	15	2 AAW04848	Aaw04848 Internal
2	35	46.1	15	3 AAB08960	Aab08960 Human sec
3	33	43.4	12	8 AD006895	Ado06895 Porcine r
4	31	40.8	14	8 ADG98090	Adg98090 Apoptosis
5	31	40.8	15	6 ABP71311	Abp71311 Drosophil
6	31	40.8	15	6 ADA10648	Ada10648 Drosophil
7	30	39.5	14	2 AAY06719	Aay06719 Peptide f
8	29	38.2	9	7 ADC21478	Adc21478 Human PRD
9	29	38.2	10	7 ADC21483	Adc21483 Human PRD
10	28	36.8	9	4 AAG84689	Aag84689 MAGE3 cro
11	28	36.8	9	4 AAG84688	Aag84688 MAGE3 cro
12	28	36.8	9	4 AAU27075	Aau27075 Human Leu
13	28	36.8	9	4 AAU27076	Aau27076 Human Leu
14	28	36.8	9	4 AAU26742	Aau26742 Human Leu
15	28	36.8	9	4 AAU26743	Aau26743 Human Leu
16	28	36.8	9	4 AAB75861	Aab75861 Tumour as
17	28	36.8	9	8 ADP26069	Adp26069 Plasmodiu
18	28	36.8	11	3 AAB12656	Aab12656 Protein k
19	28	36.8	15	4 AAM99415	Aam99415 Vaccine r
20	28	36.8	15	4 AAU69222	Aau69222 Human tra
21	28	36.8	15	8 ADK69557	Adk69557 Epitope l
22	27	35.5	6	2 AAY24297	Aay24297 Somatosta
23	27	35.5	8	7 ADD57458	Add57458 HLA bindi
24	27	35.5	8	7 ADD56995	Add56995 HLA bindi
25	27	35.5	8	7 ADD57770	Add57770 HLA bindi

26	27	35.5	10	4 AAM42696	Aam42696 Mycoplasma
27	27	35.5	10	6 ABJ67822	Abj67822 184P1E2-r
28	27	35.5	10	6 ABJ69045	Abj69045 184P1E2-r
29	27	35.5	10	6 ABJ68535	Abj68535 184P1E2-r
30	27	35.5	10	6 ABJ66708	Abj66708 184P1E2-r
31	27	35.5	10	6 ABJ66180	Abj66180 184P1E2-r
32	27	35.5	10	6 ABJ67345	Abj67345 184P1E2-r
33	27	35.5	10	7 ADI20156	Adi20156 Anchor mo
34	27	35.5	10	7 ADI20288	Adi20288 Anchor mo
35	27	35.5	10	7 ADI20467	Adi20467 Anchor mo
36	27	35.5	10	7 ADI20298	Adi20298 Anchor mo
37	27	35.5	10	8 ADI53583	Adi53583 Non oncog
38	27	35.5	10	8 ADM33674	Adm33674 HPV E6 PD
39	27	35.5	10	8 ADR82734	Adr82734 Human pap
40	27	35.5	10	8 ADR82804	Adr82804 Human pap
41	27	35.5	12	2 AAY21356	Aay21356 Human HUP
42	27	35.5	14	2 AAW64250	Aaw64250 Mouse mas
43	27	35.5	15	2 AAW04851	Aaw04851 Internal
44	27	35.5	15	5 ABP63564	Abp63564 Human pap
45	27	35.5	15	6 ABR37049	Abr37049 Human can

ALIGNMENTS

RESULT 1
AAW04848
ID AAW04848 standard; peptide; 15 AA.
XX
AC AAW04848;
XX
DT 18-FEB-1997 (first entry)
XX
DE Internal fragment of herpes simplex virus UL15 protein.
XX
KW Tolerisation; self-epitope; antigen; autoimmune disease; autoantigen;
KW HLA; human leukocyte antigen; T-cell; thymocyte; pemphigus vulgaris;
KW desmoglein; multiple sclerosis; herpes simplex virus; adenovirus;
KW phosphonannomutase; human papillomavirus; Epstein-Barr virus;
KW DNA polymerase; influenza; haemagglutinin; reovirus; sigma protein.
XX
OS Herpes simplex virus.
XX
PN WO9627387-A1.
XX
PD 12-SEP-1996.
XX
PF 07-MAR-1996; 96WO-US003182.
XX
PR 07-MAR-1995; 95US-00400796.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Strominger JL, Wucherpfennig KW;
XX
DR WPI; 1996-425218/42.
XX
PT Pemphigus vulgaris auto-antigens and multiple sclerosis non-self antigens
PT - useful in disease treatment, and method for identification of other
PT self and non-self antigens implicated in auto-immune disease.
XX
PS Claim 2; Page 42; 58pp; English.
XX
CC Pharmaceutical preparations for tolerisation to antigens comprise either
CC an isolated human non-collagen or non-myalin basic protein (MBP)
CC polypeptide which is capable of tolerising an individual to an
CC autoantigen; or an isolated human pathogen polypeptide capable of
CC tolerising an individual to that polypeptide. In both cases, the
CC polypeptide (whether self or non-self) includes an amino acid sequence
CC corresponding to a sequence motif for a MHC class II protein, such as HLA
CC -DR, which is associated with a human autoimmune disease and which binds
CC to the polypeptide to activate autoreactive T-cells in individuals with
CC the autoimmune disease. This peptide is an internal peptide of herpes

```
CC simplex virus UL15 protein and is implicated as a foreign epitope
CC involved in the aetiology or in remissions of multiple sclerosis. It has
CC been shown capable of inducing the proliferation of autoreactive T-cell
CC clones isolated from multiple sclerosis patients
XX
SQ Sequence 15 AA;
  Query Match      100.0%; Score 76; DB 2; Length 15;
  Best Local Similarity 100.0%; Pred. No. 4.6e-06;
  Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FRQLVHFVRDFAQLL 15
  |||||
DB 1 FRQLVHFVRDFAQLL 15
  |||||

RESULT 2
AAB08960
ID AAB08960 standard; protein; 15 AA.
XX
AC AAB08960;
XX
DT 30-AUG-2000 (first entry)
XX
DE Human secreted protein sequence encoded by gene 24 SEQ ID NO:117.
XX
KW Human; secreted protein; cytotatic; anti-proliferative; vulnery;
KW immunosuppressive; antibacterial; diagnosis; immune system; chemotaxis;
KW hyperproliferative disorder; infectious disease; tissue regeneration;
KW screening; food additive; preservative; wound healing;
KW hyper-vascular disease.
XX
OS Homo sapiens.
XX
PN WO200017222-A1.
XX
PD 30-MAR-2000.
XX
PF 22-SEP-1999; 99WO-US022012.
XX
PR 23-SEP-1998; 98US-0101546P.
XX
PR 02-OCT-1998; 98US-0102895P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Rosen CA, Duan RD, Shi Y, Lafleur DW, Young PE, Ni J;
PI Komatsoulis G, Endress GA, Soppet DR;
XX WPI; 2000-283538/24.
XX
XX Human secreted proteins and coding sequences useful in diagnostic and
PT therapeutic methods for disorders such as immune system or proliferative
PT disorders, related to the proteins.
XX
PS Disclosure; Page 69; 416pp; English.
XX
CC The polynucleotide sequences given in AAA39052 to AAA39088 encode the
CC human secreted proteins given in AAB08891 to AAB08984. The human secreted
CC proteins can have activities based on the tissues and cells they are
CC expressed in. Examples of the activities are: cytostatic; anti-
CC proliferative; immunosuppressive; antibacterial; and vulnery. The
CC secreted proteins and their related polynucleotide sequences are useful
CC for diagnostic and therapeutic methods useful for diagnosing and treating
CC disorders related to the secreted proteins. The proteins, and
CC polynucleotide sequences may be useful for treating disorders of the
CC immune system, hyperproliferative disorders, infectious disease,
CC regeneration of tissues, for chemotaxis and for screening molecules that
CC bind to the proteins. The proteins or polynucleotide sequences may be
CC used as food additives or preservatives, to increase or decrease storage
CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,
CC minerals, co-factors or other nutritional components. Agonists or
CC antagonists of the proteins may be used to prevent scar tissue growth
CC during wound healing, and hyper-vascular diseases. AAA39043 to AAA39051
CC
```

```
CC and AAB08890 are sequences used in the exemplification of the present
CC invention
XX
SQ Sequence 15 AA;
  Query Match      46.1%; Score 35; DB 3; Length 15;
  Best Local Similarity 50.0%; Pred. No. 47;
  Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY 4 LVHFVRDFAQLL 15
  |||:|:|:|
DB 3 LFHFLIDYAEIV 14
  |||:|:|:|

RESULT 3
ADO06895
ID ADO06895 standard; peptide; 12 AA.
XX
AC ADO06895;
XX
DT 01-JUL-2004 (first entry)
XX
DE Porcine reproductive and respiratory syndrome virus gp5 peptide #14.
XX
KW virucide; gene therapy; vaccine; neutralising epitope; mimotopes;
KW Porcine reproductive and respiratory syndrome virus; PRRSV; epitope B;
KW gp5.
XX
OS Porcine reproductive and respiratory syndrome virus.
XX
PN US2004014028-A1.
XX
PD 22-JAN-2004.
XX
PF 19-JUL-2002; 2002US-00199545.
XX
PR 19-JUL-2002; 2002US-00199545.
XX
XX (WOLF-) WOLF BIOTECH.
XX
PI Lopez OJ, Ostrowski M;
XX WPI; 2004-121549/12.
XX
XX Isolating neutralizing epitopes of a pathogen for vaccination purposes
PT comprises obtaining sera with and without neutralizing antibodies from a
PT species and using the difference between the sera to isolate neutralizing
PT epitopes.
XX
PS Example 2; Fig 3; 28pp; English.
XX
CC The invention describes isolating neutralising epitopes of a pathogen
CC comprising obtaining sera with and without neutralising antibodies from a
CC species, and using the difference between the serum with neutralising
CC antibodies and the serum without neutralising antibodies to isolate
CC neutralising epitopes and/or mimotopes. The composition and methods are
CC useful in diagnosing, preventing or treating Porcine reproductive and
CC respiratory syndrome virus (PRRSV) infection. The polyclonal or
CC monoclonal antibodies specific to epitope B, or the monospecific chimeric
CC mouse/porcine antibodies obtained by recombinant DNA technology specific
CC to epitope B, are used to facilitate cure of infected animals or
CC prevention of animals at risk of infection with PRRSV. This is the amino
CC acid sequence of a porcine reproductive and respiratory syndrome virus
CC (PRRSV) gp5 peptide screened using anti-PRRSV specific swine-antibodies
CC to identify protective epitopes.
XX
SQ Sequence 12 AA;
  Query Match      43.4%; Score 33; DB 8; Length 12;
  Best Local Similarity 66.7%; Pred. No. 84;
  Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 5 VHFVRDFAQ 13
```

```
Db      ||| |||
4 VHFQRFQSQ 12

RESULT 4
ADG98090
ID ADG98090 standard; peptide; 14 AA.
XX
AC ADG98090;
XX
DT 11-MAR-2004 (first entry)
XX
DE Apoptosis induction-related Drosophila melanogaster IAP1 peptide SeqID3.
XX
KW inhibitor of apoptosis protein; IAP; anti-HIV; neurotropic;
KW neuroprotective; vasotropic; cytosstatic; immunosuppressive; caspase;
KW inducing apoptosis; AIDS; IAP1; neurodegenerative disease;
KW ischaemic injury; cancer; autoimmune disease; fruit fly.
XX
OS Drosophila melanogaster.
XX
PN WO2003095473-A2.
XX
PD 20-NOV-2003.
XX
PF 08-MAY-2003; 2003WO-US012125.
XX
PR 09-MAY-2002; 2002US-0378668P.
XX
PR 24-FEB-2003; 2003US-0448869P.
XX
PA (ROCK-) ROCKEFELLER INST.
PA (RAPA-) RAPAPORT FAMILY INST RES IN MEDICAL SCI.
XX
PI Steller H, Don Ryo H, Ciechanover A, Gonen H;
XX
DR WPI; 2004-012082/01.
XX
DR N-PSDB; ADG98101.
XX
PT New nucleic acid molecules encoding a peptide or polypeptide that binds
PT to a portion of an inhibitor of apoptosis protein, useful for inducing
PT apoptosis and identifying inhibitors or enhancers of apoptosis for
PT treating AIDS, or cancer.
XX
PS Claim 46; SEQ ID NO 3; 101pp; English.
XX
CC This invention relates to a novel isolated nucleic acid molecule which
CC encodes a polypeptide that specifically binds to at least a portion of an
CC inhibitor of apoptosis protein (IAP). The invention may be useful for the
CC development of compounds with an anti-HIV, neurotropic, neuroprotective,
CC vasotropic, cytosstatic or immunosuppressive activity through the
CC inhibition or stimulation of caspase. The nucleic acid molecules and
CC peptides or polypeptides are useful for inducing apoptosis and
CC identifying inhibitors or enhancers of apoptosis for treating AIDS,
CC neurodegenerative diseases, ischaemic injury, cancer or autoimmune
CC diseases. The present sequence is that of a fruit fly (D melanogaster) -
CC derived IAP1 (IAP inhibitor) peptide of the invention.
XX
SQ Sequence 14 AA;

Query Match 40.8%; Score 31; DB 8; Length 14;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 LVHFVRDFAQLL 15
: : : :
Db 2 IAVFIPDQAQLL 13

RESULT 5
ABP71311
ID ABP71311 standard; peptide; 15 AA.
XX
AC ABP71311;

XX
DT 28-APR-2003 (first entry)
XX
DE Drosophila grim protein N-terminal fragment.
XX
KW Omi; HtrA2; serine protease; inhibitor of apoptosis protein; IAP;
KW caspase; apoptosis; cytosstatic; immunosuppressive; neuroprotective;
KW vasotropic; Gene therapy; grim.
XX
OS Drosophila sp.
XX
PN WO2003006680-A2.
XX
PD 23-JAN-2003.
XX
PF 15-JUL-2002; 2002WO-US022658.
XX
PR 13-JUL-2001; 2001US-0305378P.
XX
PR 14-DEC-2001; 2001US-0340163P.
XX
PA (UYJE-) UNIV JEFFERSON THOMAS.
XX
PI Alnemri ES;
XX
DR WPI; 2003-221760/21.
XX
PT New Omi nucleic acids and peptides that bind to an inhibitor of apoptosis
PT proteins, useful for regulating or altering caspase-mediated apoptosis
PT and for treating cancer, tumor, or autoimmune diseases.
XX
PS Example 2; Fig 6; 83pp; English.
XX
CC The invention relates to polynucleotides encoding an Omi (serine
CC protease) peptide or polypeptide. The Omi peptide specifically binds to a
CC portion of an inhibitor of Apoptosis Protein (IAP). The Omi polypeptide
CC induces caspase-independent apoptosis, or fails to have serine protease
CC activity. The Omi peptides are useful for regulating or altering
CC apoptosis, specifically caspase-mediated apoptosis, and as immunogens for
CC raising antibodies. Enhancers of apoptosis are useful for treating
CC cancers, tumors or for destroying cells that mediate autoimmune
CC diseases. Compositions may also be used for the treatment of diseases
CC associated with inappropriate activation of apoptosis such as
CC neurodegenerative diseases and ischaemic injury. The antibodies can be
CC used in isolating Omi peptides, polypeptides and their variants, in
CC identifying molecules that interact with Omi peptides and polypeptides,
CC and in inhibiting or enhancing the biological activity of Omi peptides,
CC and polypeptides. Sequences ABP71310-315 represent fragments of various
CC IAP-binding proteins, used to determine Omi as a IAP-binding protein
XX
SQ Sequence 15 AA;

Query Match 40.8%; Score 31; DB 6; Length 15;
Best Local Similarity 50.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 LVHFVRDFAQLL 15
: : : :
Db 2 IAVFIPDQAQLL 13

RESULT 6
ADA10648
ID ADA10648 standard; peptide; 15 AA.
XX
AC ADA10648;
XX
DT 06-NOV-2003 (first entry)
XX
DE Drosophila Grim protein N-terminus #1.
XX
KW caspase-9; anti-HIV; neurotropic; neuroprotective; vasotropic; cytosstatic;
KW immunosuppressive; inhibitor of apoptosis protein; IAP;
KW caspase-9 N-terminal linker; procaspase-9; cysteine protease; caspase-3;
```

```
KW Bir3 domain; apoptosis; AIDS; neurodegenerative disease;
KW ischaemic injury; cancer; autoimmune disease; Fruitfly; Grim.
XX
OS Drosophila melanogaster.
XX
PN US2002160975-A1.
XX
PD 31-OCT-2002.
XX
PF 06-FEB-2002; 2002US-00068569.
XX
XX 08-FEB-2001; 2001US-0267966P.
PR 24-AUG-2001; 2001US-00939293.
XX
XX (UYJE-) UNIV JEFFERSON THOMAS.
XX
PI Alnemri ES;
XX
DR WPI; 2003-219992/21.
XX
XX New nucleic acid molecules encoding a peptide or polypeptide that binds
PT to a portion of an inhibitor of apoptosis protein, useful for inducing
PT apoptosis and identifying inhibitors or enhancers of apoptosis for
PT treating AIDS, or cancer.
XX
XX Claim 27; Fig 9; 52pp; English.
PS
XX
CC The invention relates to an isolated nucleic acid molecule comprising a
CC polynucleotide that encodes a polypeptide or peptide, or its variants
CC that specifically binds to at least a portion of an inhibitor of
CC apoptosis protein (IAP). Also included are a peptide or a polypeptide
CC (comprising at least an N terminus sequence of caspase-9 N-terminal
CC linker sequence, a first portion of a procaspase-9 that specifically
CC binds at least a portion of an IAP and a second portion of a procaspase-9
CC containing a mutated active site, where the peptide or polypeptide
CC specifically binds at least a portion of an IAP and lacks cysteine
CC protease activity, and at least a portion of caspase-3, where the peptide
CC or polypeptide exhibits caspase-3 enzymatic activity that is inhibited by
CC an IAP or an IAP Bir3 domain) or at least a portion of a mutated
CC procaspase-9, which fails to undergo normal processing and possesses wild
CC type caspase-9 enzymatic activity, a nucleic acid molecule comprising a
CC polynucleotide sequence that encodes the caspase-9 N-terminal linker), an
CC expression vector comprising any of the nucleic acids, a host cell
CC containing the expression vector, an antibody that specifically binds to
CC the peptide or polypeptide, an antibody that specifically binds to an
CC epitope located on the N-terminus of a caspase-9-p12, inducing apoptosis
CC in a cell or stimulating apoptosis in a neoplastic or tumour cell,
CC identifying an inhibitor or enhancer of caspase-mediated apoptosis,
CC identifying a compound that inhibits the peptide or polypeptide,
CC producing a compound for inhibiting or enhancing apoptosis in a cell, and
CC a process for the manufacture of a compound for inhibiting or enhancing
CC apoptosis in a cell. The nucleic acid molecules and peptides or
CC polypeptides are useful for inducing apoptosis and identifying inhibitors
CC or enhancers of apoptosis for treating AIDS, neurodegenerative diseases,
CC ischaemic injury, cancer, autoimmune diseases. The present sequence
CC represents the N-terminus of an IAP protein containing a Bir3 domain.
XX
XX Sequence 15 AA;
XX
Query Match 40.8%; Score 31; DB 6; Length 15;
Best Local Similarity 50.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 4 LVHFVRDFAQLL 15
DB : : : : :
2 IAYFIPDQALL 13
RESULT 7
RAY06719
ID AAY06719 standard; peptide; 14 AA.
XX
XX AAY06719;
XX
AC
```

```
XX 18-JUN-1999 (first entry)
XX
DE Peptide fragment from bovine prion protein (residues 146-159).
XX
KW Prion; PrP-Sc protein; transmissible spongiform encephalopathy; TSE;
KW ruminant; immunoassay; third eyelid-associated lymphoid tissue; epitope;
KW neurodegenerative disorder; scrapie; bovine prion protein.
XX
OS Synthetic.
OS Bos sp.
XX
PN WO9919360-A1.
XX
PD 22-APR-1999.
XX
PF 14-OCT-1998; 98WO-US021704.
XX
PR 14-OCT-1997; 97US-00950271.
XX
XX (USDA ) US SEC OF AGRIC.
PA (UNIW ) UNIV WASHINGTON STATE RES FOUND.
XX
XX O'rourke KI, Knowles DP, Baezler TV, Parish SM;
PI WPI; 1999-277597/23.
XX
DR Assay for detecting prion (PrP-Sc) protein - as indicator for
XX transmissible spongiform encephalopathy.
XX
XX Example 2; Page 15; 33pp; English.
XX
CC The invention relates to immunoassay for detecting the presence of PrP-Sc
CC (prion) protein as an indication of transmissible spongiform
CC encephalopathy (TSE) in a ruminant. The assay comprises (a) obtaining
CC third eyelid-associated lymphoid tissue from a ruminant to be tested; (b)
CC treating the tissue to unmask an epitope to PrP-Sc protein and eliminate
CC availability of a corresponding epitope of PrP-C which is expressed in
CC tissues from normal animals; (c) contacting said treated tissue with an
CC antibody which specifically binds said PrP-Sc epitope under conditions
CC such that said antibody binds PrP-Sc protein if said protein is present
CC in the tissue, and (d) detecting the presence of said bound antibody. The
CC methods are used for the detection of transmissible spongiform
CC encephalopathies which are a heterogeneous group of fatal
CC neurodegenerative disorders occurring in humans, ruminants, herbivores,
CC mink and cats, sheep scrapie being a representative of this group. The
CC methods are non-invasive and pre-clinical. The present sequence
CC represents a peptide fragment from the bovine prion protein
XX
XX Sequence 14 AA;
XX
Query Match 39.5%; Score 30; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 2 ROLVHFVRDF 11
DB : : : : :
2 RPLHFPGSDY 11
RESULT 8
ADC21478
ID ADC21478 standard; peptide; 9 AA.
XX
XX ADC21478;
AC
XX
XX 18-DEC-2003 (first entry)
XX
XX Human PRDI-BF1 peptide fragment SEQ ID 15.
DE
XX tumor; antigen; CD8+ cytotoxic T lymphocyte; CTL; CTL-induced lysis;
KW multiple myeloma cell; human; PRDI-BF1;
KW positive regulatory domain I-binding factor-1; MHC;
```


KW major histocompatibility complex Class I; cytostatic; vaccine.
 OS Homo sapiens.
 XX WO2003029282-A2.
 PN 10-APR-2003.
 PD
 XX 24-SEP-2002; 2002WO-EP010701.
 XX 29-SEP-2001; 2001DE-01048236.
 XX (IMMU-) IMMUGENICS AG.
 XX Theobald M, Lotz C;
 PI WPI; 2003-354724/33.
 DR
 XX New tumor-associated oligopeptide, useful particularly for treating
 PT multiple myeloma, is recognized by CD8 cytotoxic T cells, also
 PT derivatives and related nucleic acid.
 XX
 XX Claim 1; SEQ ID NO 15; 64pp; German.
 PS
 CC This invention describes a novel tumor-associated oligopeptide that is
 CC recognized as an antigen by CD8+ cytotoxic T lymphocytes (CTL) and causes
 CC CTL-induced lysis and/or apoptosis of tumor cells, especially multiple
 CC myeloma cells. The oligopeptide is derived from human PRDI-BF1 (positive
 CC regulatory domain I-binding factor-1) which is able to induce an MHC
 CC (major histocompatibility complex) Class I allele variant A2-restricted
 CC immune response of CD8+ CTL against tumor cells. The products of the
 CC invention have cytostatic activity and can be used in a vaccine. The
 CC peptide of the invention, also related retro-inverse and pseudopeptides,
 CC fusion proteins (FP), polynucleotides, vectors, host cells and antibodies
 CC and T cell receptors specific for PRDI-BF1 peptides are useful for
 CC treating diseases associated with PRDI-BF1, particularly tumors. The
 CC products of the invention are also useful as diagnostic, therapeutic and
 CC prophylactic agents for detecting, modifying, generating, expanding
 CC and/or regulating activation and functional status of T cells, and for
 CC preparation of poly- or mono-clonal or recombinant A2-restricted T cell
 CC receptors and their functional equivalents.
 XX
 SQ Sequence 9 AA;
 Query Match 38.2%; Score 29; DB 7; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.8e+06;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 4 LVHFVRDFA 12
 Db || : ||||
 1 LVWYCRDFA 9
 RESULT 9
 ADC21483
 ID ADC21483 standard; peptide; 10 AA.
 AC
 XX ADC21483;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Human PRDI-BF1 peptide fragment SEQ ID 20.
 XX
 KW tumor; antigen; CD8+ cytotoxic T lymphocyte; CTL; CTL-induced lysis;
 KW multiple myeloma cell; human; PRDI-BF1;
 KW positive regulatory domain I-binding factor-1; MHC;
 KW major histocompatibility complex Class I; cytostatic; vaccine.
 XX
 XX Homo sapiens.
 OS
 XX WO2003029282-A2.
 PN 10-APR-2003.
 PD
 XX

XX 24-SEP-2002; 2002WO-EP010701.
 XX 29-SEP-2001; 2001DE-01048236.
 XX (IMMU-) IMMUGENICS AG.
 XX Theobald M, Lotz C;
 PI WPI; 2003-354724/33.
 DR
 XX New tumor-associated oligopeptide, useful particularly for treating
 PT multiple myeloma, is recognized by CD8 cytotoxic T cells, also
 PT derivatives and related nucleic acid.
 XX
 XX Claim 1; SEQ ID NO 20; 64pp; German.
 PS
 CC This invention describes a novel tumor-associated oligopeptide that is
 CC recognized as an antigen by CD8+ cytotoxic T lymphocytes (CTL) and causes
 CC CTL-induced lysis and/or apoptosis of tumor cells, especially multiple
 CC myeloma cells. The oligopeptide is derived from human PRDI-BF1 (positive
 CC regulatory domain I-binding factor-1) which is able to induce an MHC
 CC (major histocompatibility complex) Class I allele variant A2-restricted
 CC immune response of CD8+ CTL against tumor cells. The products of the
 CC invention have cytostatic activity and can be used in a vaccine. The
 CC peptide of the invention, also related retro-inverse and pseudopeptides,
 CC fusion proteins (FP), polynucleotides, vectors, host cells and antibodies
 CC and T cell receptors specific for PRDI-BF1 peptides are useful for
 CC treating diseases associated with PRDI-BF1, particularly tumors. The
 CC products of the invention are also useful as diagnostic, therapeutic and
 CC prophylactic agents for detecting, modifying, generating, expanding
 CC and/or regulating activation and functional status of T cells, and for
 CC preparation of poly- or mono-clonal or recombinant A2-restricted T cell
 CC receptors and their functional equivalents.
 XX
 SQ Sequence 10 AA;
 Query Match 38.2%; Score 29; DB 7; Length 10;
 Best Local Similarity 66.7%; Pred. No. 3.4e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 4 LVHFVRDFA 12
 Db || : ||||
 2 LVWYCRDFA 10
 RESULT 10
 AAG84689
 ID AAG84689 standard; peptide; 9 AA.
 AC
 XX AAG84689;
 XX
 DT 10-SEP-2001 (first entry)
 XX
 DE MAGE3 crossbinding data A2 supermotif peptide #13.
 XX
 KW Human; human leukocyte antigen; HLA epitope; cytotoxic T lymphocyte; CTL;
 KW MAGE2; MAGE3; melanoma antigen gene; immune response; vaccine; cancer;
 KW cytostatic; immunostimulant.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX WO200142267-A1.
 PN 14-JUN-2001.
 PD
 XX 11-DEC-2000; 2000WO-US033545.
 XX
 XX 10-DEC-1999; 99US-00458298.
 XX
 XX (EPIM-) EPIMUNE INC.
 XX

CC human leukocyte antigen A2.1 (HLA-A2.1) binding motif. The peptides of
 CC the invention are capable of specifically binding glycoproteins encoded
 CC by HLA alleles and inducing a cytotoxic T cell response against an
 CC antigen in a patient expressing HLA-A2.1. This method is useful for the
 CC treatment, prevention and diagnosis of pathological states such as viral
 CC diseases and cancers, including prostate cancer, hepatitis B, hepatitis
 CC C, AIDS, renal carcinoma, cervical carcinoma, lymphoma, and condyloma
 CC acuminatum. The peptides are used for treatment of chronic infection and
 CC for stimulating the immune system to eliminate virus-infected cells
 XX
 SQ Sequence 9 AA;

Query Match 36.8%; Score 28; DB 4; Length 9;
 Best Local Similarity 83.3%; Pred. No. 1.8e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 QLVHVF 8
 :|||||
 Db 4 ELVHVF 9

RESULT 13

AAU27076
 ID AAU27076 standard; peptide; 9 AA.

XX
 AC AAU27076;

XX
 DT 18-DEC-2001 (first entry)

XX Human Leukocyte Antigen (HLA) HLA-A2.1 immunogenic binding peptide #360.
 XX Immunogenic peptide; human leukocyte antigen; HLA-A2.1 binding motif;
 XX immunostimulant; cytostatic; antiviral; glycoprotein; cytotoxic T cell;
 KW viral disease; prostate cancer; hepatitis B; hepatitis C; lymphoma; AIDS;
 KW renal carcinoma; cervical carcinoma; condyloma acuminatum.
 XX
 OS Homo sapiens.

XX
 PN WO200162776-A1.

XX
 PD 30-AUG-2001.

XX
 PF 23-FEB-2000; 2000WO-US004655.

XX
 PR 23-FEB-2000; 2000WO-US004655.

XX
 PA (EPIM-) EPIMMUNE INC.

XX
 PI Sette A, Sidney J, Kast WM, Southwood S;

XX
 DR WPI; 2001-582039/65.

XX Composition for treating viral diseases and cancer comprises an
 PT immunogenic peptide having an HLA-A2.1 binding motif.
 PS Claim 1; Page 71; 85pp; English.

XX Sequences AAU26558-AAU27161 represent immunogenic peptides containing a
 CC human leukocyte antigen A2.1 (HLA-A2.1) binding motif. The peptides of
 CC the invention are capable of specifically binding glycoproteins encoded
 CC by HLA alleles and inducing a cytotoxic T cell response against an
 CC antigen in a patient expressing HLA-A2.1. This method is useful for the
 CC treatment, prevention and diagnosis of pathological states such as viral
 CC diseases and cancers, including prostate cancer, hepatitis B, hepatitis
 CC C, AIDS, renal carcinoma, cervical carcinoma, lymphoma, and condyloma
 CC acuminatum. The peptides are used for treatment of chronic infection and
 CC for stimulating the immune system to eliminate virus-infected cells
 XX
 SQ Sequence 9 AA;

Query Match 36.8%; Score 28; DB 4; Length 9;
 Best Local Similarity 83.3%; Pred. No. 1.8e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 QLVHVF 8
 :|||||
 Db 4 ELVHVF 9

RESULT 14

AAU26742
 ID AAU26742 standard; peptide; 9 AA.

XX
 AC AAU26742;

XX
 DT 18-DEC-2001 (first entry)

XX Human Leukocyte Antigen (HLA) HLA-A2.1 immunogenic binding peptide #185.

XX Immunogenic peptide; human leukocyte antigen; HLA-A2.1 binding motif;
 KW immunostimulant; cytostatic; antiviral; glycoprotein; cytotoxic T cell;
 KW viral disease; prostate cancer; hepatitis B; hepatitis C; lymphoma; AIDS;
 KW renal carcinoma; cervical carcinoma; condyloma acuminatum.
 XX
 OS Homo sapiens.

XX
 PN WO200162776-A1.

XX
 PD 30-AUG-2001.

XX
 PF 23-FEB-2000; 2000WO-US004655.

XX
 PR 23-FEB-2000; 2000WO-US004655.

XX
 PA (EPIM-) EPIMMUNE INC.

XX
 PI Sette A, Sidney J, Kast WM, Southwood S;

XX
 DR WPI; 2001-582039/65.

XX Composition for treating viral diseases and cancer comprises an
 PT immunogenic peptide having an HLA-A2.1 binding motif.
 PS Example 1; Page 33; 85pp; English.

XX Sequences AAU26558-AAU27161 represent immunogenic peptides containing a
 CC human leukocyte antigen A2.1 (HLA-A2.1) binding motif. The peptides of
 CC the invention are capable of specifically binding glycoproteins encoded
 CC by HLA alleles and inducing a cytotoxic T cell response against an
 CC antigen in a patient expressing HLA-A2.1. This method is useful for the
 CC treatment, prevention and diagnosis of pathological states such as viral
 CC diseases and cancers, including prostate cancer, hepatitis B, hepatitis
 CC C, AIDS, renal carcinoma, cervical carcinoma, lymphoma, and condyloma
 CC acuminatum. The peptides are used for treatment of chronic infection and
 CC for stimulating the immune system to eliminate virus-infected cells
 XX
 SQ Sequence 9 AA;

Query Match 36.8%; Score 28; DB 4; Length 9;
 Best Local Similarity 83.3%; Pred. No. 1.8e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 QLVHVF 8
 :|||||
 Db 4 ELVHVF 9

RESULT 15

AAU26743
 ID AAU26743 standard; peptide; 9 AA.

XX
 AC AAU26743;

XX
 DT 18-DEC-2001 (first entry)

XX Human Leukocyte Antigen (HLA) HLA-A2.1 immunogenic binding peptide #186.

XX Immunogenic peptide; human leukocyte antigen; HLA-A2.1 binding motif;
KW immunostimulant; cytostatic; antiviral; glycoprotein; cytotoxic T cell;
KW viral disease; prostate cancer; hepatitis B; hepatitis C; lymphoma; AIDS;
KW renal carcinoma; cervical carcinoma; condyloma acuminatum.
XX
XX Homo sapiens.
XX OS
XX WO200162776-A1.
XX PN
XX
XX 30-AUG-2001.
XX PD
XX
XX 23-FEB-2000; 2000WO-US004655.
XX PF
XX 23-FEB-2000; 2000WO-US004655.
XX PR
XX (EPIM-) EPIMUNE INC.
XX PA
XX
XX Sette A, Sidney J, Kast WM, Southwood S;
XX PI
XX WPI; 2001-582039/65.
XX DR
XX Composition for treating viral diseases and cancer comprises an
PT immunogenic peptide having an HLA-A2.1 binding motif.
PT
XX
XX Example 1; Page 33; 85pp; English.
XX
XX Sequences AAU26558-AAU27161 represent immunogenic peptides containing a
CC human leukocyte antigen A2.1 (HLA-A2.1) binding motif. The peptides of
CC the invention are capable of specifically binding glycoproteins encoded
CC by HLA alleles and inducing a cytotoxic T cell response against an
CC antigen in a patient expressing HLA-A2.1. This method is useful for the
CC treatment, prevention and diagnosis of pathological states such as viral
CC diseases and cancers, including prostate cancer, hepatitis B, hepatitis
CC C, AIDS, renal carcinoma, cervical carcinoma, lymphoma, and condyloma
CC acuminatum. The peptides are used for treatment of chronic infection and
CC for stimulating the immune system to eliminate virus-infected cells
XX
XX Sequence 9 AA;
XX
XX Query Match 36.8%; Score 28; DB 4; Length 9;
XX Best Local Similarity 83.3%; Pred. NO. 1.8e+06;
XX Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 3 QLVHVV 8
XX :|||
XX Db 4 ELVHVV 9

Search completed: February 22, 2005, 09:24:44
Job time : 67.6667 secs

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OM protein - protein search, using sw model

Run on: February 22, 2005, 09:08:09 ; Search time 11.1333 Seconds
(without alignments)
129.633 Million cell updates/sec

Title: US-08-991-628-9
Perfect score: 77 DFEVTFKDVLPF 15
Sequence: 1 DFEVTFKDVLPF 15
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 2523

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23	29.9	15	2 G49732	NADH2 dehydrogenas
2	22	28.6	14	2 E33098	214K exoantigen (v
3	22	28.6	15	2 A36315	recycling receptor
4	22	28.6	15	2 PN0662	dystrophin-associa
5	22	28.6	15	2 PA0061	protein QF200039 -
6	21	27.3	8	2 S66296	Na+-transporting A
7	21	27.3	15	2 PS0185	27K protein A 3.4/
8	20	26.0	9	2 S78426	52.5K protein - sp
9	20	26.0	11	2 S41747	chaperonin 10 homo
10	20	26.0	12	2 PT0228	Ig heavy chain CDR
11	20	26.0	14	2 I54945	Gene C protein - E
12	20	26.0	14	2 S14336	mastoparan B - hor
13	20	26.0	15	2 B61457	alpha-glucosidase
14	19	24.7	7	2 B39127	phosphotransferase
15	19	24.7	14	2 PS0249	porin - rice (stra
16	19	24.7	15	2 T09463	ribosomal protein
17	19	24.7	15	2 S62675	collagen type I -
18	18	23.4	9	2 B30572	T-cell receptor be
19	18	23.4	9	2 S77984	cytochrome-c oxida
20	18	23.4	10	2 C30572	T-cell receptor be
21	18	23.4	12	2 PS0213	28K protein 4412 -
22	18	23.4	13	2 PN0122	Oil protein - vacc
23	18	23.4	14	2 S29789	hypothetical prote
24	18	23.4	14	2 A60737	pollen allergen Lo
25	18	23.4	14	2 PC4382	dehydrin 4.5K poly
26	18	23.4	14	2 A4920	2-halobenzoate 1.2
27	18	23.4	14	2 PC4376	telomeric and tetr
28	18	23.4	15	2 PH1807	T cell receptor al
29	18	23.4	15	2 A26228	spot 42 protein -

30	17.5	22.7	15	2 PQ0195	Sf11-glycoprotein
31	17	22.1	10	2 S48182	bacterioferritin -
32	17	22.1	10	2 A44646	neurotoxin-associa
33	17	22.1	11	2 PT0229	Ig heavy chain CDR
34	17	22.1	11	2 PT0249	Ig heavy chain CDR
35	17	22.1	11	2 PD0441	translation elonga
36	17	22.1	12	2 PA0047	protein QA100045 -
37	17	22.1	12	2 I58273	thyroglobulin - ra
38	17	22.1	13	2 PH1599	Ig H chain V-D-J r
39	17	22.1	14	2 S23369	T-cell receptor al
40	17	22.1	14	2 A61032	troponin T, cardia
41	17	22.1	14	2 A41589	25K elastin-bindin
42	17	22.1	14	2 PC7075	guanylate cyclase
43	17	22.1	15	2 S29485	GTP-binding protei
44	17	22.1	15	2 PH1612	Ig H chain V-D-J r
45	17	22.1	15	2 PA0093	ennatiatin synthetas

ALIGNMENTS

RESULT 1

G49732
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) 20K chain - potato mitochondrion (fragment)
N;Alternate names: complex 1 hydrogenase 20K chain; NADH-ubiquinone oxidoreductase 20K ch
C;Species: mitochondrion Solanum tuberosum (potato)
C;Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 09-Jul-2004
C;Accession: G49732
R;Herz, U.; Schroeder, W.; Liddell, A.; Leaver, C.J.; Brennicke, A.; Grohmann, L.
J. Biol. Chem. 269, 2263-2269, 1994
A;Title: Purification of the NADH:ubiquinone oxidoreductase (complex I) of the respirato
A;Reference number: A49732; MUID:94124587; PMID:8294484
A;Accession: G49732
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-15 <HER>
A;Cross-references: UNIPROT:P80263
C;Genetics:
A;Genome: mitochondrion
C;Keywords: electron transfer; hydrogen ion transport; mitochondrial inner membrane; mitr

Query Match 29.9%; Score 23; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 1.4e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 TELKDV 11
| | | | |
DB 8 TYLKDV 13

RESULT 2

E33098
214K exoantigen (version 2) - malaria parasite (Plasmodium falciparum) (fragments)
C;Species: Plasmodium falciparum
C;Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000
C;Accession: E33098
R;Nichols, J.H.; Hager, L.P.
submitted to the Protein Sequence Database, May 1990
A;Reference number: A33098
A;Accession: E33098
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-14 <NIC>

Query Match 28.6%; Score 22; DB 2; Length 14;
Best Local Similarity 66.7%; Pred. No. 1.9e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 EVVTF 8
: | | | :
DB 5 DVVTYL 10

RESULT 3

A36315
recycling receptor p180 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 25-Jan-1991 #sequence_revision 25-Jan-1991 #text_change 30-Sep-1993
C:Accession: A36315
R:Tsacke, C.M.; van der Geer, P.; Hunter, T.; Trowbridge, I.S.
Mol. Cell. Biol. 10, 2606-2618, 1990
A:Title: p180, a novel recycling transmembrane glycoprotein with restricted cell type expression
A:Reference number: A36315; MUID:90258846; PMID:2188094
A:Accession: A36315
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <ISA>

Query Match 28.6%; Score 22; DB 2; Length 15;
Best Local Similarity 80.0%; Pred. No. 2e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 DVLPE 14
| | | |
Db 5 DALPE 9

RESULT 4

PN0662
dytrophin-associated glycoprotein A3a-I - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 07-May-1999
C:Accession: PN0662
R:Yoshida, M.; Mizuno, Y.; Nonaka, I.; Ozawa, E.
J. Biochem. 114, 634-639, 1993
A:Title: A dystrophin-associated glycoprotein, A3a (one of 43DAG doublets), is retained in the trans Golgi apparatus
A:Reference number: PN0662; MUID:94156881; PMID:8113213
A:Accession: PN0662
A:Molecule type: protein
A:Residues: 1-15 <YOS>
C:Comment: This protein is retained in Duchenne type muscular dystrophy muscle.
C:Keywords: glycoprotein; skeletal muscle

Query Match 28.6%; Score 22; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 2e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 TFLKDVLP 13
| | | | |
Db 4 TFIKGVLP 11

RESULT 5

PA0061
protein QP200039 - fungus (Fusarium sporotrichioides) (fragment)
C:Species: Fusarium sporotrichioides
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: PA0061
R:Chow, L.P.; Fukaya, N.; Sugiyura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JIPID, October 1994
A:Description: two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichioides
A:Reference number: PA0051
A:Accession: PA0061
A:Molecule type: protein
A:Residues: 1-15 <CHO>
A:Cross-references: UNIPROT:Q7M4Y2

Query Match 28.6%; Score 22; DB 2; Length 15;
Best Local Similarity 44.4%; Pred. No. 2e+03;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 VTFLKDVLP 13
| | | | |
Db 7 VAIVKDTAP 15

RESULT 6

S66296
Na+-transporting ATP synthase (EC 3.6.1.-) chain c - Acetobacterium woodii (fragment)
N:Alternate names: ATPase chain c
C:Species: Acetobacterium woodii
C:Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 07-May-1999
C:Accession: S66296
R:Reidlinger, J.; Mueller, V.
Eur. J. Biochem. 223, 275-283, 1994
A:Title: Purification of ATP synthase from Acetobacterium woodii and identification as a Na+-driven proton pump
A:Reference number: S45648; MUID:94307271; PMID:8033902
A:Accession: S66296
A:Molecule type: protein
A:Residues: 1-8 <REI>
A:Experimental source: DSM 1030
C:Keywords: hydrolase

Query Match 27.3%; Score 21; DB 2; Length 8;
Best Local Similarity 42.9%; Pred. No. 2.8e+05;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 EVVTFLK 9
| : : | : |
Db 2 EILDEIK 8

RESULT 7

PS0185
27K protein A 3.4/5 - rice (fragment)
C:Species: Oryza sativa (rice)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 24-Feb-1995
C:Accession: PS0185
R:Kamo, M.; Tsugita, A.
submitted to JIPID, June 1991
A:Reference number: PS0184
A:Accession: PS0185
A:Molecule type: protein
A:Residues: 1-15 <KAM>

Query Match 27.3%; Score 21; DB 2; Length 15;
Best Local Similarity 37.5%; Pred. No. 2.9e+03;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 7 FLKDVLP 14
| : : | : |
Db 4 YIVDVAPD 11

RESULT 8

S78426
52.5K protein - spiny lobster (fragment)
C:Species: Panulirus argus (spiny lobster)
C:Date: 14-Apr-1998 #sequence_revision 24-Apr-1998 #text_change 19-May-2000
C:Accession: S78426
R:James, M.O.; Boyle, S.M.; Trapido-Rosenthal, H.G.; Smith, W.C.; Greenberg, R.M.; Shiver, A.R.
Arch. Biochem. Biophys. 329, 31-38, 1996
A:Title: cDNA and protein sequence of a major form of P450, CYP2L, in the hepatopancreas of the spiny lobster
A:Reference number: S68856; MUID:96201120; PMID:8619632
A:Accession: S78426
A:Molecule type: protein
A:Residues: 1-9 <JAM>
A:Experimental source: hepatopancreas microsomes

Query Match 26.0%; Score 20; DB 2; Length 9;
Best Local Similarity 57.1%; Pred. No. 2.8e+05;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 TFLKDVLP 12
| : : | : |
Db 1 TWIKVLP 7

RESULT 9

S41747
chaperonin 10 homolog - potato (fragment)
C:Species: Solanum tuberosum (potato)
C>Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 09-Jul-2004
C:Accession: S41747
R:Burt, W.J.E.; Leaver, C.J.
FEBS Lett. 339, 139-141, 1994
A:Title: Identification of a chaperonin-10 homologue in plant mitochondria.
A:Reference number: S41747; MUID:94148071; PMID:7906228
A:Accession: S41747
A:Molecule type: protein
A:Residues: 1-11 <BUR>
A:Cross-references: UNIPROT:Q7M1H1
A:Experimental source: mitochondrial
C:Keywords: mitochondrion; molecular chaperone

Query Match 26.0%; Score 20; DB 2; Length 11;
Best Local Similarity 60.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 11 VLPEP 15
:|:|:
Db 2 LKPEY 6

RESULT 10
PT0228
IG heavy chain CDR3 region (clone 1-112) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0228
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0228
A:Molecule type: DNA
A:Residues: 1-12 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotrimer; immunoglobulin

Query Match 26.0%; Score 20; DB 2; Length 12;
Best Local Similarity 37.5%; Pred. No. 3.4e+03;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 7 FLKDVLP 14
:|:|:
Db 3 YVRDSSPE 10

RESULT 11
I54945
gene C protein - Escherichia coli (fragment)
C:Species: Escherichia coli
C>Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
C:Accession: I54945
R:Tao, T.; Bourne, J.C.; Blumenthal, R.M.
J. Bacteriol. 173, 1367-1375, 1991
A:Title: A family of regulatory genes associated with type II restriction-modification
A:Reference number: I54945; MUID:91139577; PMID:1995588
A:Accession: I54945
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-14 <RES>
A:Cross-references: UNIPROT:Q47599; GB:M63619; NID:g147664; PIDN:AAA24555.1; PID:g147665

Query Match 26.0%; Score 20; DB 2; Length 14;
Best Local Similarity 57.1%; Pred. No. 4e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 LKDVLP 14
:|:|:
Db 1 LKEVIME 7

RESULT 12
S14336
mastoparan B - hornet (Vespa basalis)
C:Species: Vespa basalis
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S14336
R:Ho, C.L.; Hwang, L.L.
Biochem. J. 274, 453-456, 1991
A:Title: Structure and biological activities of a new mastoparan isolated from the venom
A:Reference number: S14336; MUID:91174755; PMID:2006909
A:Accession: S14336
A:Molecule type: protein
A:Residues: 1-14 <HOC>
A:Cross-references: UNIPROT:P21654
A:Experimental source: venom
C:Function:
A:Description: possesses a potent hemolytic activity which acts in synergy with the lethal
C:Keywords: amidated carboxyl end; mast cell; venom
F:14/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 26.0%; Score 20; DB 2; Length 14;
Best Local Similarity 44.4%; Pred. No. 4e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 VVTFLKDV 12
:|:|:
Db 6 IVSMACKVL 14

RESULT 13
B61457
alpha-glucosidase (EC 3.2.1.20) - Tetrahymena pyriformis (strain W) (fragment)
C:Species: Tetrahymena pyriformis
C>Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 07-Dec-1999
C:Accession: B61457
R:Banno, Y.; Sasaki, N.; Yoshino, T.; Mochizuki, J.I.; Hirata, H.; Nozawa, Y.
J. Protozool. 36, 562-567, 1989
A:Title: A thermostable acid alpha-glucosidase from Tetrahymena thermophila: purification
A:Reference number: A61457; MUID:90095988; PMID:2689637
A:Accession: B61457
A:Molecule type: protein
A:Residues: 1-15 <BAN>
C:Genetics:
A:Genetic code: SGCS
C:Keywords: extracellular protein; glycoprotein; glycosidase; hydrolase; lysosome; monome

Query Match 26.0%; Score 20; DB 2; Length 15;
Best Local Similarity 80.0%; Pred. No. 4.3e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 VLPEP 15
:|:|:
Db 1 VLPPF 5

RESULT 14
B39127
phosphotransferase system enzyme II (EC 2.7.1.69) - Escherichia coli (fragment)
C:Species: Escherichia coli
C>Date: 27-Nov-1991 #sequence_revision 27-Nov-1991 #text_change 08-Oct-1999
C:Accession: B39127
R:Hardesty, C.; Ferran, C.; DiRienzo, J.M.
J. Bacteriol. 173, 449-456, 1991
A:Title: Plasmid-mediated sucrose metabolism in Escherichia coli: characterization of sc
rin.
A:Reference number: A39127; MUID:91100329; PMID:1846143
A:Accession: B39127
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-7 <HAR>
A:Cross-references: GB:M38416; NID:g155142; PIDN:AAA98418.1; PID:g155144

C:Keywords: phosphotransferase

Query Match 24.7%; Score 19; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DFEVVT 6
||| :
Db 2 DFEQIS 7

RESULT 15

PS0249
porin - rice (strain Nihonbare) (fragment)
C:Species: Oryza sativa (rice)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C:Accession: PS0249
R.Tsugita, A.
submitted to JIPID, April 1993
A:Reference number: PS0206
A:Accession: PS0249
A:Molecule type: protein
A:Residues: 1-14 <TSU>
A:Cross-references: UNIPROT:Q7M1U8
A:Experimental source: callus

Query Match 24.7%; Score 19; DB 2; Length 14;
Best Local Similarity 66.7%; Pred. No. 5.8e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 VTFLKD 10
||| |
Db 2 VTFTDD 7

Search completed: February 22, 2005, 09:46:27
Job time : 11.1333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 22, 2005, 08:53:13 ; Search time 52.6 Seconds
(without alignments)
146.030 Million cell updates/sec

Title: US-08-991-628-9
Perfect score: 77
Sequence: 1 DFEVTFKDLVLPF 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 6622

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	33.8	13	Q6TKD3	Q6tkd3 praecitrull
2	26	33.8	13	Q6TKD4	Q6tkd4 sechium edu
3	26	33.8	13	Q6TKD5	Q6tkd5 sicyos angu
4	26	33.8	13	Q6TKD6	Q6tkd6 trichosanth
5	26	33.8	13	Q6TKD7	Q6tkd7 luffa grave
6	26	33.8	13	Q6TKD8	Q6tkd8 luffa echin
7	26	33.8	13	Q6TKD9	Q6tkd9 cucurbita p
8	26	33.8	13	Q6TKD0	Q6tkd0 benincasa h
9	26	33.8	13	Q6TKD1	Q6tkd1 marah orega
10	26	33.8	13	Q6TKD2	Q6tkd2 cyclanthera
11	26	33.8	13	Q6TKD3	Q6tkd3 echinocysti
12	26	33.8	13	Q6TKD4	Q6tkd4 luffa quinq
13	26	33.8	13	Q6TKD5	Q6tkd5 lagenaria l
14	26	33.8	13	Q6TKD6	Q6tkd6 citrullus l
15	26	33.8	13	Q6TKD7	Q6tkd7 citrullus c
16	26	33.8	13	Q6TKD8	Q6tkd8 acanthosicy
17	26	33.8	13	Q6TKD9	Q6tkd9 bryonia dio
18	26	33.8	13	Q6TKD0	Q6tkd0 coccinia pa
19	26	33.8	13	Q6TKD1	Q6tkd1 diplocyclos
20	26	33.8	13	Q6TKD2	Q6tkd2 ecballium e
21	26	33.8	15	Q9R565	Q9r565 streptomyc
22	24	31.2	10	P82222	P82222 bombyx mori
23	24	31.2	12	P82246	P82246 spinacia ol
24	24	31.2	12	P82247	P82247 spinacia ol
25	23	29.9	10	AKHX LOCM1	P81626 locusta mig
26	23	29.9	12	Q7RH69	Q7rh69 plasmodium
27	23	29.9	14	O70599	O70599 rattus norv
28	23	29.9	15	1 NVO3	P80263 solanum tub
29	23	29.9	15	2 Q9UCJ8	Q9ucj8 homo sapien
30	23	29.9	15	2 Q9R599	Q9r599 micrococcu
31	22	28.6	14	2 Q7Z7E2	Q7z7e2 homo sapien

32	22	28.6	15	2 Q7M4Y2	Q7m4y2 fusarium sp
33	22	28.6	15	2 Q7XQX8	Q7xqx8 oryza sativ
34	21	27.3	13	2 Q8I2E2	Q8i2e2 plasmodium
35	21	27.3	14	1 RAN9 RANCA	P82824 rana catesb
36	20	26.0	9	2 Q7RSP1	Q7rsp1 plasmodium
37	20	26.0	10	2 Q6JDL6	Q6jdl6 canis famil
38	20	26.0	11	2 Q6JDL6	Q6jdl6 solanum tub
39	20	26.0	12	1 XYLA STRVN	P14405 streptomyc
40	20	26.0	13	2 Q16007	Q16007 homo sapien
41	20	26.0	13	2 Q83171	Q83171 cauliflowe
42	20	26.0	13	2 Q98VM1	Q98vm1 human immun
43	20	26.0	14	1 MAST VESBA	P21654 vespa basal
44	20	26.0	14	2 Q47599	Q47599 escherichia
45	20	26.0	15	1 UC16_MAIZE	P80622 zea mays (m

ALIGNMENTS

RESULT 1					
Q6TKD3	PRELIMINARY;	PRT;	13 AA.		
ID	Q6TKD3				
AC	Q6TKD3;				
DT	05-JUL-2004 (Tremblrel. 27, Created)				
DT	05-JUL-2004 (Tremblrel. 27, Last sequence update)				
DE	Photosystem II protein (Fragment)				
GN	Name=psbC;				
OS	Praecitrullus fistulosus.				
OG	Chloroplast.				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;				
OC	eurosid1; Cucurbitales; Cucurbitaceae; Praecitrullus.				
OX	NCBI_TaxID=252558;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Decker-Walters D.S., Chung S.-M., Staub J.E.;				
RL	Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AY396191; AAR07576.1; -				
DR	GO; GO:0009507; C:chloroplast; IEA.				
KW	Chloroplast.				
FT	NON_TER	1			
SQ	SEQUENCE	13 AA;	1579 MW;	CF0270FB503C732 CRC64;	
Query Match 33.8%; Score 26; DB 2; Length 13;					
Best Local Similarity 62.5%; Pred. No. 2e+03;					
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;					
QY	1 DFEVTFFL 8				
Db					
	2 DFEPVLFM 9				
RESULT 2					
Q6TKD4	PRELIMINARY;	PRT;	13 AA.		
ID	Q6TKD4				
AC	Q6TKD4;				
DT	05-JUL-2004 (Tremblrel. 27, Created)				
DT	05-JUL-2004 (Tremblrel. 27, Last sequence update)				
DE	Photosystem II protein (Fragment)				
GN	Name=psbC;				
OS	Sechium edule.				
OG	Chloroplast.				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;				
OC	eurosid1; Cucurbitales; Cucurbitaceae; Sechium.				
OX	NCBI_TaxID=184140;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Decker-Walters D.S., Chung S.-M., Staub J.E.;				
RL	Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AY396190; AAR07575.1; -				

DR	GO; GO:0009507; C:chloroplast; IEA.
KW	Chloroplast.
FT	NON TER
SQ	SEQUENCE 13 AA; 1579 MW; CF0270FBB503C732 CRC64;
Query Match	33.8%; Score 26; DB 2; Length 13;
Best Local Similarity	62.5%; Pred.No. 2e+03;
Matches	5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY	1 DFEVVTPL 8 : 2 DFEVLFM 9
Db	
RESULT 3	
Q6TKD5	PRELIMINARY; PRT; 13 AA.
ID Q6TKD5	
AC Q6TKD5	
DT 05-JUL-2004	(TrEMBLrel. 27, Created)
DT 05-JUL-2004	(TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004	(TrEMBLrel. 27, Last annotation update)
DE Photosystem II protein (Fragment).	
GN Name=psbC;	
OS Sicyos angulatus.	
OG Chloroplast.	
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;	
OC eurooids I; Cucurbitales; Cucurbitaceae; Sicyos.	
OX NCBI_TaxID=64232;	
RN [1]	
RP SEQUENCE FROM N.A.	
RA Decker-Walters D.S.; Chung S.-M.; Staub J.E.;	
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.	
DR EMBL; AY396189; AAR07574.1; -.	
DR GO; GO:0009507; C:chloroplast; IEA.	
KW Chloroplast.	
FT NON TER	
SQ SEQUENCE 13 AA; 1579 MW; CF0270FBB503C732 CRC64;	
Query Match	33.8%; Score 26; DB 2; Length 13;
Best Local Similarity	62.5%; Pred.No. 2e+03;
Matches	5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY	1 DFEVVTPL 8 : 2 DFEVLFM 9
Db	
RESULT 4	
Q6TKD6	PRELIMINARY; PRT; 13 AA.
ID Q6TKD6	
AC Q6TKD6	
DT 05-JUL-2004	(TrEMBLrel. 27, Created)
DT 05-JUL-2004	(TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004	(TrEMBLrel. 27, Last annotation update)
DE Photosystem II protein (Fragment).	
GN Name=psbC;	
OS Trichosanthes cucumerina.	
OG Chloroplast.	
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;	
OC eurooids I; Cucurbitales; Cucurbitaceae; Trichosanthes.	
OX NCBI_TaxID=50543;	
RN [1]	
RP SEQUENCE FROM N.A.	
RA Decker-Walters D.S.; Chung S.-M.; Staub J.E.;	
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.	
DR EMBL; AY396188; AAR07573.1; -.	
DR GO; GO:0009507; C:chloroplast; IEA.	
KW Chloroplast.	
FT NON TER	
SQ SEQUENCE 13 AA; 1579 MW; CF0270FBB503C732 CRC64;	

```

||||| |
Db 2 DFEVLFM 9

RESULT 7
Q6TKD9 PRELIMINARY; PRT; 13 AA.
ID Q6TKD9
AC Q6TKD9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Photosystem II protein (Fragment).
GN Name=psbC;
OS Cucurbita pepo (Vegetable marrow) (Summer squash).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurooids I; Cucurbitales; Cucurbitaceae; Cucurbita.
OX NCBI_TaxID=3663;
RN [1]
RP SEQUENCE FROM N.A.
RA Decker-Walters D.S., Chung S.-M., Staub J.E.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY396185; AAR07570.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 13 AA; 1579 MW; CF0270FBB503C732 CRC64;

Query Match 33.8%; Score 26; DB 2; Length 13;
Best Local Similarity 62.5%; Pred. No. 2e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DFEVVTFL 8
Db ||||| |
2 DFEVLFM 9

RESULT 8
Q6TKE0 PRELIMINARY; PRT; 13 AA.
ID Q6TKE0
AC Q6TKE0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Photosystem II protein (Fragment).
GN Name=psbC;
OS Benincasa hispida (Wax gourd).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurooids I; Cucurbitales; Cucurbitaceae; Benincasa.
OX NCBI_TaxID=102211;
RN [1]
RP SEQUENCE FROM N.A.
RA Decker-Walters D.S., Chung S.-M., Staub J.E.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY396184; AAR07569.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 13 AA; 1579 MW; CF0270FBB503C732 CRC64;

Query Match 33.8%; Score 26; DB 2; Length 13;
Best Local Similarity 62.5%; Pred. No. 2e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DFEVVTFL 8
Db ||||| |
2 DFEVLFM 9

RESULT 9
Q6TKE3 PRELIMINARY; PRT; 13 AA.
ID Q6TKE3
AC Q6TKE3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Photosystem II protein (Fragment).
GN Name=psbC;
OS Cucurbita pepo (Vegetable marrow) (Summer squash).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurooids I; Cucurbitales; Cucurbitaceae; Cucurbita.
OX NCBI_TaxID=3663;
RN [1]
RP SEQUENCE FROM N.A.
RA Decker-Walters D.S., Chung S.-M., Staub J.E.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY396185; AAR07570.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 13 AA; 1579 MW; CF0270FBB503C732 CRC64;

Query Match 33.8%; Score 26; DB 2; Length 13;
Best Local Similarity 62.5%; Pred. No. 2e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DFEVVTFL 8
Db ||||| |
2 DFEVLFM 9

RESULT 10
Q6TKE2 PRELIMINARY; PRT; 13 AA.
ID Q6TKE2
AC Q6TKE2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Photosystem II protein (Fragment).
GN Name=psbC;
OS Cyclanthera pedata (Achocha) (Caihua).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurooids I; Cucurbitales; Cucurbitaceae; Cyclanthera.
OX NCBI_TaxID=198836;
RN [1]
RP SEQUENCE FROM N.A.
RA Decker-Walters D.S., Chung S.-M., Staub J.E.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY396182; AAR07567.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 13 AA; 1579 MW; CF0270FBB503C732 CRC64;

Query Match 33.8%; Score 26; DB 2; Length 13;
Best Local Similarity 62.5%; Pred. No. 2e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DFEVVTFL 8
Db ||||| |
2 DFEVLFM 9

RESULT 11
Q6TKE3 PRELIMINARY; PRT; 13 AA.
ID Q6TKE3
AC Q6TKE3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Photosystem II protein (Fragment).
GN Name=psbC;
OS Cucurbita pepo (Vegetable marrow) (Summer squash).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurooids I; Cucurbitales; Cucurbitaceae; Cucurbita.
OX NCBI_TaxID=3663;
RN [1]
RP SEQUENCE FROM N.A.
RA Decker-Walters D.S., Chung S.-M., Staub J.E.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY396185; AAR07570.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 13 AA; 1579 MW; CF0270FBB503C732 CRC64;

Query Match 33.8%; Score 26; DB 2; Length 13;
Best Local Similarity 62.5%; Pred. No. 2e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DFEVVTFL 8
Db ||||| |
2 DFEVLFM 9

RESULT 12
Q6TKE1 PRELIMINARY; PRT; 13 AA.
ID Q6TKE1
AC Q6TKE1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Photosystem II protein (Fragment).
GN Name=psbC;
OS Cucurbita pepo (Vegetable marrow) (Summer squash).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurooids I; Cucurbitales; Cucurbitaceae; Cucurbita.
OX NCBI_TaxID=252534;
RN [1]
RP SEQUENCE FROM N.A.
RA Decker-Walters D.S., Chung S.-M., Staub J.E.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY396183; AAR07568.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 13 AA; 1579 MW; CF0270FBB503C732 CRC64;

Query Match 33.8%; Score 26; DB 2; Length 13;
Best Local Similarity 62.5%; Pred. No. 2e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DFEVVTFL 8
Db ||||| |
2 DFEVLFM 9

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DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Photosystem II protein (Fragment).
GN Name=psbC;
OS Echinocystis lobata.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Cucurbitales; Cucurbitaceae; Echinocystis.
OX NCBI_TaxID=252533;
RN [1]
RP SEQUENCE FROM N.A.
RA Decker-Walters D.S., Chung S.-M., Staub J.E.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY396181; AAR07566.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 13 AA; 1579 MW; CF0270FBB503C732 CRC64;

Query Match 33.8%; Score 26; DB 2; Length 13;
Best Local Similarity 62.5%; Pred. No. 2e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DFEVVTFL 8
Db 2 DFEPLVLFM 9

RESULT 12
Q6TKE4
ID Q6TKE4 PRELIMINARY; PRT; 13 AA.
AC Q6TKE4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Photosystem II protein (Fragment).
GN Name=psbC;
OS Luffa quinquedida.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Cucurbitales; Cucurbitaceae; Luffa.
OX NCBI_TaxID=34295;
RN [1]
RP SEQUENCE FROM N.A.
RA Decker-Walters D.S., Chung S.-M., Staub J.E.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY396180; AAR07565.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 13 AA; 1579 MW; CF0270FBB503C732 CRC64;

Query Match 33.8%; Score 26; DB 2; Length 13;
Best Local Similarity 62.5%; Pred. No. 2e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DFEVVTFL 8
Db 2 DFEPLVLFM 9

RESULT 13
Q6TKE5
ID Q6TKE5 PRELIMINARY; PRT; 13 AA.
AC Q6TKE5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Photosystem II protein (Fragment).
GN Name=psbC;
OS Lagenaria leucantha (Bottle gourd) (Lagenaria siceraria).
OG Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Cucurbitales; Cucurbitaceae; Lagenaria.
OX NCBI_TaxID=3668;
RN [1]
RP SEQUENCE FROM N.A.
RA Decker-Walters D.S., Chung S.-M., Staub J.E.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY396179; AAR07564.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 13 AA; 1579 MW; CF0270FBB503C732 CRC64;

Query Match 33.8%; Score 26; DB 2; Length 13;
Best Local Similarity 62.5%; Pred. No. 2e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DFEVVTFL 8
Db 2 DFEPLVLFM 9

RESULT 14
Q6TKE6
ID Q6TKE6 PRELIMINARY; PRT; 13 AA.
AC Q6TKE6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Photosystem II protein (Fragment).
GN Name=psbC;
OS Citrullus lanatus (Watermelon) (Citrullus vulgaris).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Cucurbitales; Cucurbitaceae; Citrullus.
OX NCBI_TaxID=3654;
RN [1]
RP SEQUENCE FROM N.A.
RA Decker-Walters D.S., Chung S.-M., Staub J.E.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY396178; AAR07563.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 13 AA; 1579 MW; CF0270FBB503C732 CRC64;

Query Match 33.8%; Score 26; DB 2; Length 13;
Best Local Similarity 62.5%; Pred. No. 2e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DFEVVTFL 8
Db 2 DFEPLVLFM 9

RESULT 15
Q6TKE7
ID Q6TKE7 PRELIMINARY; PRT; 13 AA.
AC Q6TKE7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Photosystem II protein (Fragment).
GN Name=psbC;
OS Citrullus colocynthis.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Cucurbitales; Cucurbitaceae; Citrullus.
OX NCBI_TaxID=252529;
RN [1]

```

RP SEQUENCE FROM N.A.
RA Decker-Walters D.S., Chung S.-M., Staub J.E.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY396177; AAR07562.1; -
DR GO; GO:0009507; C:Chloroplast; IEA.
KW Chloroplast.
FT NON_TER 1 1
SQ SEQUENCE 13 AA; 1579 MW; CF0270FBB503C732 CRC64;
Query Match 33.8%; Score 26; DB 2; Length 13;
Best Local Similarity 62.5%; Pred. No. 2e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DFEVVTFL 8
||| | :
Db 2 DFEFVLFM 9

Search completed: February 22, 2005, 09:37:58
Job time : 53.6667 secs

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OM protein - protein search, using sw model

Run on: February 22, 2005, 08:52:23 ; Search time 65.6667 Seconds
(without alignments)
88.346 Million cell updates/sec

Title: US-08-991-628-9
Perfect score: 77
Sequence: 1 DFEVTFKDLVPEF 15
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 632537

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:.*
1: Geneseqp1980s:.*
2: Geneseqp1990s:.*
3: Geneseqp2000s:.*
4: Geneseqp2001s:.*
5: Geneseqp2002s:.*
6: Geneseqp2003as:.*
7: Geneseqp2003bs:.*
8: Geneseqp2004s:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	62.5	81.2	14	2 AAW04849	AAW04849 Internal
2	35	45.5	15	1 AAP82806	AAP82806 Von Wille
3	35	45.5	15	2 AAR40254	AAR40254 von Wille
4	33	42.9	14	2 AAW90258	AAW90258 Human NBC
5	29	37.7	14	4 AAU69166	AAU69166 Human Ace
6	29	37.7	15	5 AAM47974	AAM47974 Human cyt
7	28	36.4	9	3 AAB06739	AAB06739 Claudin-5
8	28	36.4	9	4 AAB75878	AAB75878 Influenza
9	28	36.4	10	7 ADD23785	Add23785 Breast ca
10	28	36.4	10	8 ADK08674	ADK08674 Human pap
11	28	36.4	14	2 AAW74950	AAW74950 Human sec
12	28	36.4	14	5 ABG95408	ABG95408 Human nov
13	28	36.4	14	6 ABO34602	ABO34602 Region of
14	28	36.4	14	7 ADI23263	ADI23263 Novel hum
15	28	36.4	14	8 ADH74265	ADH74265 Human sec
16	28	36.4	14	8 ADN65356	ADN65356 HLA bindi
17	28	36.4	15	2 AAW61167	AAW61167 HLA-A1
18	27	35.1	9	5 ABG32317	ABG32317 HLA-A1/A2
19	27	35.1	10	4 AAM42905	AAM42905 Mycoplasma
20	27	35.1	13	2 AAR54969	AAR54969 Sorhi gra
21	27	35.1	13	2 AAR54970	AAR54970 Sorhi gra
22	27	35.1	13	2 AAW72553	AAW72553 Pertussis
23	27	35.1	13	2 AAW29757	AAW29757 Malassezi
24	27	35.1	13	2 AAY41824	AAY41824 Pertussis
25	27	35.1	13	2 AAW95234	AAW95234 PT toxin

ALIGNMENTS

RESULT 1
AAW04849
ID AAW04849 standard; peptide; 14 AA.
XX
AC AAW04849;
XX
DT 16-OCT-2003 (revised)
DT 18-FEB-1997 (first entry)
XX
DE Internal fragment of adenovirus type 12 ORF.

XX Tolerisation; self-epitope; antigen; autoimmune disease; autoantigen;
KW HLA; human leukocyte antigen; T-cell; thymocyte; pemphigus vulgaris;
KW desmoglein; multiple sclerosis; herpes simplex virus; adenovirus;
KW phosphonannomutase; human papillomavirus; Epstein-Barr virus;
KW DNA polymerase; influenza; haemagglutinin; reovirus; sigma protein.
XX Human adenovirus type 12.
OS
XX WO9627387-A1.
PN
XX 12-SEP-1996.
PD
XX 07-MAR-1996; 96WO-US003182.
PF
XX 07-MAR-1995; 95US-00400796.
PR
XX (HARD) HARVARD COLLEGE.
PA
XX Strominger JL, Wucherpfennig KW;
PI WPI; 1996-425218/42.
DR
XX Pemphigus vulgaris auto-antigens and multiple sclerosis non-self antigens
XX - useful in disease treatment, and method for identification of other
XX self and non-self antigens implicated in auto-immune disease.

Claim 2; Page 43; 58pp; English.

CC Pharmaceutical preparations for tolerisation to antigens comprise either
CC an isolated human non-collagen or non-mysin basic protein (MBP)
CC polypeptide which is capable of tolerising an individual to an
CC autoantigen; or an isolated human pathogen polypeptide capable of
CC tolerising an individual to that polypeptide. In both cases, the
CC polypeptide (whether self or non-self) includes an amino acid sequence
CC corresponding to a sequence motif for a MHC class II protein, such as HLA
CC -DR, which is associated with a human autoimmune disease and which binds
CC to the polypeptide to activate autoreactive T-cells in individuals with

Aay43371 Pertussis
Aay68373 Pertussis
Aab66247 B pertuss
Aau25795 Breast ca
Aau96084 Peptide e
Aar97502 Mycobacte
Aaw04851 Internal
Aaw08922 Tumour as
Aaw59078 FMDV non-
Aay29716 Mycobacte
Abp30998 Peptide #
Ada08661 Human O77
Adf09004 Secreted
Adn71486 Human 273
Adn70576 Human 273
Adn71729 Human 273
Adn70668 Human 273
Adn71020 Human 273
Adn71487 Human 273
Adn71526 Human 273

CC the autoimmune disease. This peptide is an internal peptide of the
 CC adenovirus type 12 ORF and is implicated as a foreign epitope involved in
 CC the aetiology or in remissions of multiple sclerosis. It has been shown
 CC capable of inducing the proliferation of autoreactive T-cell clones
 CC isolated from multiple sclerosis patients. (Updated on 16-OCT-2003 to
 CC standardise OS field)
 XX
 XX Sequence 14 AA;

Query Match 81.2%; Score 62.5; DB 2; Length 14;
 Best Local Similarity 93.3%; Pred. No. 0.0012; Indels 1; Gaps 1;
 Matches 14; Conservative 0; Mismatches 0;

QY 1 DFEVTFKDVLPPEF 15
 |||||
 DB 1 DFEVTFKDV-PEF 14

RESULT 2
 AAP82806
 ID AAP82806 standard; protein; 15 AA.
 XX
 AC AAP82806;
 XX
 DT 25-MAR-2003 (revised)
 DT 12-DEC-1990 (first entry)
 XX
 DE Von Willebrand Factor-inhibiting peptide #46.

XX Von Willebrand Factor; thrombosis; platelet binding inhibitor.
 KW
 XX Synthetic.
 OS
 XX AU8773715-A.

XX
 PD 03-DEC-1987.
 XX
 PF 01-JUN-1987; 87AU-00073715.
 XX
 PR 30-MAY-1986; 86US-00869188.
 XX
 PA (SCRI) SCRIPPS CLINIC & RE.

XX WPI; 1988-021781/04.
 DR
 XX New peptide fragments of Von Willebrand factor - inhibit binding of Von
 PT Willebrand factor to platelets, heparin and collagen, used for treating
 PT thrombosis.

XX Claim 2; Page 22; 29pp; English.

XX This 15 residue inhibitory peptide is based on part of the sequence of a
 CC 52/48kD polypeptide fragment from Von Willebrand factor. The polypeptide
 CC corresponds to residues 449-729 of vWF. Other 15 residue peptide based on
 CC other regions of the same fragment of vWF are also found to inhibit
 CC binding to platelets and heparin. A more potent inhibitor could be
 CC produced by linking two or more of these peptides. On its own this
 CC peptide reduces vWF binding to platelets to 20% (c.f. 52/48kD fragment
 CC reduces binding to 0%). See also AAP82761-P82805 and AAP82807-P82810.
 CC (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 15 AA;

Query Match 45.5%; Score 35; DB 1; Length 15;
 Best Local Similarity 50.0%; Pred. No. 60;
 Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 EVVTFKDVLPPE 14
 |||||
 DB 1 EIVSYLCDLAPE 12

RESULT 3

AAR40254
 ID AAR40254 standard; protein; 15 AA.
 XX
 AC AAR40254;
 XX
 DT 25-MAR-2003 (revised)
 DT 15-FEB-1994 (first entry)
 XX
 DE von Willebrand Factor/platelet binding inhibitor peptide.

XX vWF; pMWB3; expression; binding inhibition; inhibiting; prevention;
 KW treatment; cardiovascular disorders; thrombosis.

XX Synthetic.
 OS
 XX US5238919-A.

XX 24-AUG-1993.

XX 07-MAY-1990; 90US-00519606.

XX 30-MAY-1986; 86US-00869188.

XX 04-NOV-1988; 88US-00270488.

XX (SCRI) SCRIPPS CLINIC & RES FOUND.

XX Zimmerman TS, Fujimura Y, Houghten RA, Ruggeri ZM;

XX WPI; 1993-280681/35.

XX Use of Von-Willebrand Factor fragment peptide(s) - for inhibiting binding
 PT of factor to platelets, heparin and collagen, partic. for treating
 PT thrombosis.

XX Claim 3; Page 26; 26pp; English.

XX The sequence is that of a peptide which is capable of inhibiting the
 CC binding of von Willebrand factor (vWF) to platelets. As such it can be
 CC used for the prevention and treatment of cardiovascular disorders such as
 CC thrombosis. (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 15 AA;

Query Match 45.5%; Score 35; DB 2; Length 15;
 Best Local Similarity 50.0%; Pred. No. 60;
 Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 EVVTFKDVLPPE 14
 |||||
 DB 1 EIVSYLCDLAPE 12

RESULT 4
 AA90258
 ID AA90258 standard; peptide; 14 AA.

XX AA90258;

XX 27-APR-1999 (first entry)

XX Human NBC protein fragment #1.

XX Anion exchange; NBC; sodium bicarbonate transporter family; DIDS motif;
 KW treatment; water retention; blood pressure; acidosis; inflammation;
 KW cell proliferation; cancer; sperm activation; inactivation; epilepsy;
 KW hydrocephaly; glaucoma; colitis; pH regulation; immunoassay.

XX Homo sapiens.

XX WO9853067-A1.

XX 26-NOV-1998.

XX


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PF 20-MAY-1998; 98WO-US010297.
XX
PR 20-MAY-1997; 97US-0047131P.
XX
PA (UYUA ) UNIV YALE.
XX
PI Bevensee MO, Schmitt BM, Romero WF, Boron WF, Biemesderfer D;
PI Davis BA, Suseman CR, Choi I, Aalkjaer C, Grichtchenko II;
XX
XX WPI; 1999-059743/05.
XX
XX New nucleic acid molecules encoding proteins of the Sodium Bicarbonate
XX Cotransporter (NBC) family - useful for identifying agents that agonise
XX or antagonise NBC activity and treating disorders mediated by NBC.
XX
XX Example 3; Page 44; 138pp; English.
XX
XX This peptide fragment represents an anion exchange DIDS binding motif
XX which is found in a novel sodium bicarbonate transporter (NBC). The novel
XX NBC proteins and nucleic acid sequences may be used to treat pathological
XX processes including water retention, increased blood pressure, chronic
XX respiratory and metabolic acidosis, inflammation, cell proliferation,
XX cancer, sperm activation/inactivation, hydroencephaly, epilepsy, glaucoma
XX and colitis. Members of the NBC family of proteins can be used (i) as a
XX target to identify agents that block or stimulate NBC mediated pH
XX regulation, (ii) as a target or bait to identify and isolate binding
XX partners that bind NBC, (iii) in methods to identify agents that block or
XX stimulate activity of an NBC protein, and (iv) as a target to assay for
XX NBC-mediated activity. Anti-NBC antibodies are also useful as modulators
XX of NBC activity, useful in the immunoassays for detecting NBC
XX expression/activity and for purifying an NBC protein
XX
XX Sequence 14 AA;
XX
XX Query Match 42.9%; Score 33; DB 2; Length 14;
XX Best Local Similarity 75.0%; Pred. No. 1.2e+02;
XX Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 7 FLKDLVLP 14
XX |||||
XX 1 FLDDVIPE 8
XX
XX
XX RESULT 5
XX AAU69166
XX ID AAU69166 standard; peptide; 14 AA.
XX
XX AC AAU69166;
XX
XX DT 29-JAN-2002 (first entry)
XX
XX DE Human Acetylcholine receptor alpha subunit peptide AChR 99-112.
XX
XX DX Human; epitope; autoimmune disease; myasthenia gravis;
XX KW Human leukocyte antigen; acetylcholine receptor; HLA DR3; HLA DR2; AChR;
XX KW antigen; immunosuppressive; major histocompatibility complex; MHC.
XX
XX OS Homo sapiens.
XX
XX PN WO200174848-A2.
XX
XX PD 11-OCT-2001.
XX
XX PF 30-MAR-2001; 2001WO-US010450.
XX
XX PR 31-MAR-2000; 2000US-0193745P.
XX
XX PA (CORI-) CORIXA CORP.
XX
XX PI Deshpande S, Spack E, Wehner N, Arimilli S;
XX
XX DR WPI; 2001-648547/74.
XX
XX
XX Peptide epitopes of the acetylcholine receptor target helper T cells
XX recognize an antigen in association with an MHC component and are useful
XX to treat autoimmune disease particularly myasthenia gravis.
XX
XX Example 1; Fig 2; 46pp; English.
XX
XX The invention relates to a composition comprising an isolated
XX acetylcholine receptor (AChR) oligopeptide of about 12 to 20 amino acids.
XX The peptides form a set of 69 overlapping antigenic peptide epitopes
XX which show various affinities for human leukocyte antigens (HLA) HLA-DR2
XX and DR3. Also included is a composition comprising an antigenic peptide
XX and a Major histocompatibility complex (MHC) component having an
XX antigenic binding site, where binding of the peptide to the binding site
XX induces non-responsiveness in a target T cell in a mammal, where the MHC
XX component is an MHC class II component. Peptides with affinity for HLA-
XX DR2 and DR-3 from proteins other than AChR are also included. The
XX composition is used to treat myasthenia gravis and other autoimmune
XX diseases. The present sequence is an antigenic peptide epitope
XX
XX Sequence 14 AA;
XX
XX Query Match 37.7%; Score 29; DB 4; Length 14;
XX Best Local Similarity 50.0%; Pred. No. 5.8e+02;
XX Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 1 DFEWTFKLKDLV 12
XX |||||
XX 1 DPAIVKFTKVL 12
XX
XX
XX RESULT 6
XX AAU47974
XX ID AAU47974 standard; peptide; 15 AA.
XX
XX AC AAU47974;
XX
XX DT 06-MAR-2002 (first entry)
XX
XX DE Human cytokinesis regulatory protein 55 peptide SEQ ID NO 7.
XX
XX DX Human; cytokinesis regulatory protein 55; cancer; haemopathy; HIV;
XX KW human immunodeficiency virus; infection.
XX
XX OS Homo sapiens.
XX
XX PN CN1315368-A.
XX
XX PD 03-OCT-2001.
XX
XX PF 27-MAR-2000; 2000CN-00115139.
XX
XX PR 27-MAR-2000; 2000CN-00115139.
XX
XX PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
XX
XX PI Mao Y, Xie Y;
XX
XX DR WPI; 2002-056314/08.
XX
XX PT Polypeptide-human cytokinesis regulating protein 55 and polynucleotide
XX for coding it.
XX
XX PS Example 6; Page 19 (Disclosure); 32pp; Chinese.
XX
XX CC The invention relates to human cytokinesis regulatory protein 55, the
XX polynucleotide encoding it, the process for preparing the polypeptide by
XX DNA recombinant technology, the application of the polypeptide in
XX CC treating several diseases such as cancer, haemopathy, HIV infection. The
XX present sequence is that of a peptide, useful to the invention
XX
XX Sequence 15 AA;
XX
XX Query Match 37.7%; Score 29; DB 5; Length 15;

```

```

Best Local Similarity 50.0%; Pred. No. 6.2e+02;
Matches 4; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 8 LKDVLPFP 15
Db 4 VXEIIPFP 11

RESULT 7
AAB06739
ID AAB06739 standard; peptide; 9 AA.
XX
XX AAB06739;
XX
XX 28-SEP-2000 (first entry)
XX
XX Claudin-5 cyclic cell adhesion recognition sequence SEQ ID NO: 310.
XX
XX Claudin-5 modulating agent; cell adhesion recognition sequence;
KW CAR sequence; autoimmune disease; inflammatory disease; cancer;
KW graft rejection; cyclic.
XX
XX Mammalia.
OS
XX
XX WO200026360-A1.
PN
XX
XX 11-MAY-2000.
PD
XX
XX 03-NOV-1999; 99WO-CA001029.
PF
XX
XX 03-NOV-1998; 98US-00185908.
PR
XX
XX 30-MAR-1999; 99US-00283029.
PA
XX (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
XX Blaschuck OW, Symonds JM, Gour BU;
PI
XX
XX WPI; 2000-365610/31.
DR
XX
XX Antibody modulation of claudin-mediated cell adhesion for increasing
PT vasopermeability, for delivering drugs to tumors and the nervous system
PT and across the skin.
XX
XX Claim 67; Page 102; 121pp; English.
PS
XX
XX The present invention relates to the use of peptides as claudin-mediated
CC cell adhesion modulators. The claudin-5 group of proteins are cadherins,
CC which are membrane glycoproteins involved in cell adhesion. In some
CC situations, cell adhesion occurs at abnormal levels, and these peptides
CC can be used to modulate these levels, and thus treat autoimmune diseases,
CC inflammatory diseases and cancer, and aid wound healing and implant
CC adhesion. In addition, they can also be used to facilitate drug delivery
CC to the desired target site. The present sequence has a cyclic
CC conformation
XX
XX Sequence 9 AA;

Query Match 36.4%; Score 28; DB 3; Length 9;
Best Local Similarity 55.6%; Pred. No. 1.8e+06;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DPEVVTFLK 9
Db 1 DWQVTAFLK 9

RESULT 8
AAB75878
ID AAB75878 standard; peptide; 9 AA.
XX
XX AAB75878;
AC
XX
XX 10-APR-2001 (first entry)
,DT

```

```

XX
DE
XX
XX Influenza virus HLA-A2 binding peptide.
KW
XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW cytotoxic T lymphocyte; CTL; human class I MHC; immunogenic;
KW HLA binding peptide; immune response; glycoprotein; cytostatic; virucide;
KW hepatotropic; antiinflammatory; anti-HIV; vaccine;
KW human immunodeficiency virus; protozoacide; viral infection; cancer;
KW prostate cancer; hepatitis B; hepatitis C; human papilloma virus; HPV;
KW cytomegalovirus; CMV; acquired immunodeficiency syndrome; AIDS;
KW renal carcinoma; cervical carcinoma; lymphoma; malaria;
KW condyloma acuminatum.
XX
XX Influenza virus.
OS
XX WO200100225-A1.
PN
XX
XX 04-JAN-2001.
PD
XX
XX 28-JUN-2000; 2000WO-US017842.
PF
XX
XX 29-JUN-1999; 99US-0141422P.
PR
XX
XX (EPIM-) EPIMUNE INC.
PA
XX
XX Sette A, Sidney J, Southwood S;
PI
XX
XX WPI; 2001-112389/12.
DR
XX
XX Composition comprising human leukocyte antigen binding peptide which
PT comprises isolated, prepared epitope useful for treating viral infections
PT such as acquired immunodeficiency syndrome, and cancer.
XX
XX Claim 1; Page 42; 58pp; English.
PS
XX
XX The present invention describes a composition (I) which comprises at
CC least one human leukocyte antigen (HLA) binding peptide comprising an
CC isolated, prepared epitope comprising one of 547 8-11 residue amino acid
CC sequences (S1), given in AAB75803 to AAB76349. (I) has cytostatic,
CC virucide, hepatotropic, antiinflammatory, anti-HIV (human
CC immunodeficiency virus) and protozoacide activities, which can be used in
CC vaccine production and is an inducer of cytotoxic T-cell response. (I) is
CC useful for inducing a cytotoxic T cell response against a preselected
CC antigen in a patient expressing a specific major histocompatibility
CC complex (MHC) class I allele, by contacting cytotoxic T cells (CTLs) from
CC the patient with (I). (I) is useful as a vaccine to treat and/or prevent
CC viral infection and cancer such as prostate cancer, hepatitis B,
CC hepatitis C, human papilloma virus (HPV) infection, cytomegalovirus
CC (CMV), acquired immunodeficiency syndrome (AIDS), renal carcinoma,
CC cervical carcinoma, lymphoma, malaria, and condyloma acuminatum
XX
XX Sequence 9 AA;

Query Match 36.4%; Score 28; DB 4; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.8e+06;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 VVTFKDV 11
Db 2 LIDFLKDV 9

RESULT 9
ADD23785
ID ADD23785 standard; peptide; 10 AA.
XX
XX ADD23785;
AC
XX
XX 15-JAN-2004 (first entry)
DT
XX
XX Breast cancer membrane protein (BCMP) peptide SEQ ID NO:368.
DE
XX
XX breast cancer; screening; diagnosis; breast cancer therapy;
KW

```

KW breast cancer membrane protein; BCMP; cytostatic; vaccine; human.
 OS Homo sapiens.
 XX WO2003087831-A2.
 XX 23-OCT-2003.
 XX 10-APR-2003; 2003WO-GB001559.
 XX 11-APR-2002; 2002GB-00008331.
 XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 XX Hudson LJ, Stamps AC, Terrett JA;
 XX WPI; 2003-845381/78.
 XX Screening, diagnosing and/or treating breast cancer by detecting a change
 PT in expression or activity of a breast cancer membrane protein (BCMP)
 PT polypeptide or encoding nucleic acid molecule.
 XX Claim 1; SEQ ID NO 368; 81pp; English.
 XX The present invention describes a method of screening for and/or
 CC diagnosing breast cancer in a subject, and/or monitoring the
 CC effectiveness of breast cancer therapy. The method comprises detecting
 CC and/or quantifying in a biological sample obtained from the subject a
 CC breast cancer membrane protein (BCMP) polypeptide and a nucleic acid
 CC molecule. Also described: (1) an antibody, its functionally-active
 CC fragment, derivative or analogue, that specifically binds to one or more
 CC of the BCMP polypeptide; (2) a diagnostic kit comprising a capture
 CC reagent specific for an BCMP polypeptide, reagents and instructions for
 CC use; (3) a method for screening for anti-breast cancer agents that
 CC interact with the BCMP polypeptide, comprising contacting the polypeptide
 CC with a candidate agent, and determining whether or not the candidate
 CC agent interacts with the polypeptide; (4) a method for screening for anti
 CC -breast cancer agents that modulate the expression or activity of an BCMP
 CC polypeptide or the nucleic acid molecule cited above, comprising
 CC comparing the expression or activity of the polypeptide or nucleic acid
 CC molecule, in the presence and absence of a candidate agent or in the
 CC presence of a control agent, and determining whether the candidate agent
 CC causes the expression or activity of the polypeptide or nucleic acid
 CC molecule to change; and (5) an agent identified by the method of (3) or
 CC (4), which interacts with the polypeptide or causes the expression or
 CC activity of the polypeptide, or the expression of the nucleic acid
 CC molecule to change. BCMPs have cytostatic activities, and can be used in
 CC vaccines. The BCMP polypeptide, nucleic acid molecule, antibody, agent or
 CC their derivatives, are useful in the manufacture of a medicament for the
 CC treatment of breast cancer, where the composition is a vaccine. The
 CC present sequence represents a BCMP peptide which is used in the
 CC exemplification of the present invention.
 XX Sequence 10 AA;
 SQ

Query Match 36.4%; Score 28; DB 7; Length 10;
 Best Local Similarity 62.5%; Pred. No. 6e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 8 LKDVLPFF 15
 Db 1 LEDYFFPF 8

RESULT 10
 ADK08674
 ID ADK08674 standard; peptide; 10 AA.
 XX AC ADK08674;
 XX 06-MAY-2004 (first entry)
 XX Human papillomavirus peptide #729.
 DE

Query Match 36.4%; Score 28; DB 8; Length 10;
 Best Local Similarity 62.5%; Pred. No. 6e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 5 VTFLKDVVL 12
 Db 1 ILFLKDVV 8

RESULT 11
 AAW74950
 ID AAW74950 standard; protein; 14 AA.
 XX AC AAW74950;
 XX 19-JAN-1999 (first entry)
 XX Human secreted protein encoded by gene 66 clone HTOCD52.
 DE
 XX Human; secreted protein; testis; tumour; foetal brain tissue;
 KW fusion protein; cancer; central nervous system; seizure; diagnosis;
 KW neurodegenerative disease.
 XX Homo sapiens.
 XX WO9839448-A2.
 XX 11-SEP-1998.
 XX 06-MAR-1998; 98WO-US0004493.
 XX 07-MAR-1997; 97US-0038621P.
 PR 07-MAR-1997; 97US-0040161P.

XX pathogenic virus; alternative reading frame; antigenic determinant;
 KW virucide; vaccine; therapeutic agent; infection; HPV.
 XX Human papillomavirus.
 XX WO2004011650-A2.
 XX 05-FEB-2004.
 XX 24-JUL-2003; 2003WO-EP008112.
 XX 24-JUL-2002; 2002AT-00001124.
 PR 11-JUL-2003; 2003EP-00450171.
 XX (INTE-) INTERCELL AG.
 XX Mattner F, Schmidt W, Habel A;
 XX WPI; 2004-169243/16.
 DR New polypeptide encoded by an alternative reading frame of a pathogenic
 XX virus comprising an antigenic determinant, useful for treating or
 PT preventing an infection with the pathogenic virus.
 XX Claim 18; Page 181; 220pp; English.
 XX This invention relates to a novel polypeptide encoded by an alternative
 CC reading frame of a pathogenic virus, where the polypeptide starts with a
 CC methionine amino acid residue, which comprises an antigenic determinant
 CC and more than 7 amino acid residues. The invention may be useful for the
 CC production of compounds with a virucide activity or the development of a
 CC vaccine. The polypeptide or its fragments may be useful as a therapeutic
 CC agent. It is also useful for the manufacture of a medicament for treating
 CC or preventing an infection with the pathogenic virus. The present
 CC sequence is that of a human papillomavirus (HPV) epitope peptide of the
 CC invention.
 XX Sequence 10 AA;
 SQ

Query Match 36.4%; Score 28; DB 8; Length 10;
 Best Local Similarity 62.5%; Pred. No. 6e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 5 VTFLKDVVL 12
 Db 1 ILFLKDVV 8

RESULT 11
 AAW74950
 ID AAW74950 standard; protein; 14 AA.
 XX AC AAW74950;
 XX 19-JAN-1999 (first entry)
 XX Human secreted protein encoded by gene 66 clone HTOCD52.
 DE
 XX Human; secreted protein; testis; tumour; foetal brain tissue;
 KW fusion protein; cancer; central nervous system; seizure; diagnosis;
 KW neurodegenerative disease.
 XX Homo sapiens.
 XX WO9839448-A2.
 XX 11-SEP-1998.
 XX 06-MAR-1998; 98WO-US0004493.
 XX 07-MAR-1997; 97US-0038621P.
 PR 07-MAR-1997; 97US-0040161P.

PR 07-MAR-1997; 97US-0040162P.
PR 07-MAR-1997; 97US-0040163P.
PR 07-MAR-1997; 97US-0040333P.
PR 07-MAR-1997; 97US-0040334P.
PR 07-MAR-1997; 97US-0040336P.
PR 07-MAR-1997; 97US-0040626P.
PR 11-APR-1997; 97US-0043311P.
PR 11-APR-1997; 97US-0043312P.
PR 11-APR-1997; 97US-0043313P.
PR 11-APR-1997; 97US-0043314P.
PR 11-APR-1997; 97US-0043315P.
PR 11-APR-1997; 97US-0043568P.
PR 11-APR-1997; 97US-0043569P.
PR 11-APR-1997; 97US-0043576P.
PR 11-APR-1997; 97US-0043578P.
PR 11-APR-1997; 97US-0043580P.
PR 11-APR-1997; 97US-0043669P.
PR 11-APR-1997; 97US-0043670P.
PR 11-APR-1997; 97US-0043671P.
PR 11-APR-1997; 97US-0043672P.
PR 11-APR-1997; 97US-0043674P.
PR 23-MAY-1997; 97US-0047492P.
PR 23-MAY-1997; 97US-0047500P.
PR 23-MAY-1997; 97US-0047501P.
PR 23-MAY-1997; 97US-0047502P.
PR 23-MAY-1997; 97US-0047503P.
PR 23-MAY-1997; 97US-0047581P.
PR 23-MAY-1997; 97US-0047582P.
PR 23-MAY-1997; 97US-0047583P.
PR 23-MAY-1997; 97US-0047584P.
PR 23-MAY-1997; 97US-0047585P.
PR 23-MAY-1997; 97US-0047586P.
PR 23-MAY-1997; 97US-0047587P.
PR 23-MAY-1997; 97US-0047588P.
PR 23-MAY-1997; 97US-0047589P.
PR 23-MAY-1997; 97US-0047590P.
PR 23-MAY-1997; 97US-0047592P.
PR 23-MAY-1997; 97US-0047593P.
PR 23-MAY-1997; 97US-0047594P.
PR 23-MAY-1997; 97US-0047595P.
PR 23-MAY-1997; 97US-0047596P.
PR 23-MAY-1997; 97US-0047597P.
PR 23-MAY-1997; 97US-0047598P.
PR 23-MAY-1997; 97US-0047599P.
PR 23-MAY-1997; 97US-0047600P.
PR 23-MAY-1997; 97US-0047601P.
PR 23-MAY-1997; 97US-0047612P.
PR 23-MAY-1997; 97US-0047613P.
PR 23-MAY-1997; 97US-0047614P.
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PR 23-MAY-1997; 97US-0047617P.
PR 23-MAY-1997; 97US-0047618P.
PR 23-MAY-1997; 97US-0047632P.
PR 23-MAY-1997; 97US-0047633P.
PR 06-JUN-1997; 97US-0048964P.
PR 06-JUN-1997; 97US-0048974P.
PR 13-JUN-1997; 97US-0049610P.
PR 08-JUL-1997; 97US-0051526P.
PR 16-JUL-1997; 97US-0052874P.
PR 18-AUG-1997; 97US-0055724P.
PR 22-AUG-1997; 97US-0056631P.
PR 22-AUG-1997; 97US-0056632P.
PR 22-AUG-1997; 97US-0056636P.
PR 22-AUG-1997; 97US-0056637P.
PR 22-AUG-1997; 97US-0056662P.
PR 22-AUG-1997; 97US-0056664P.
PR 22-AUG-1997; 97US-0056845P.
PR 22-AUG-1997; 97US-0056862P.
PR 22-AUG-1997; 97US-0056864P.
PR 22-AUG-1997; 97US-0056872P.
PR 22-AUG-1997; 97US-0056874P.
PR 22-AUG-1997; 97US-0056875P.

PR 22-AUG-1997; 97US-0056876P.
PR 22-AUG-1997; 97US-0056877P.
PR 22-AUG-1997; 97US-0056878P.
PR 22-AUG-1997; 97US-0056879P.
PR 22-AUG-1997; 97US-0056880P.
PR 22-AUG-1997; 97US-0056881P.
PR 22-AUG-1997; 97US-0056882P.
PR 22-AUG-1997; 97US-0056884P.
PR 22-AUG-1997; 97US-0056886P.
PR 22-AUG-1997; 97US-0056887P.
PR 22-AUG-1997; 97US-0056888P.
PR 22-AUG-1997; 97US-0056889P.
PR 22-AUG-1997; 97US-0056892P.
PR 22-AUG-1997; 97US-0056893P.
PR 22-AUG-1997; 97US-0056894P.
PR 22-AUG-1997; 97US-0056903P.
PR 22-AUG-1997; 97US-0056908P.
PR 22-AUG-1997; 97US-0056909P.
PR 22-AUG-1997; 97US-0056910P.
PR 22-AUG-1997; 97US-0056911P.
PR 05-SEP-1997; 97US-0057650P.
PR 05-SEP-1997; 97US-0057669P.
PR 05-SEP-1997; 97US-0057761P.
PR 12-SEP-1997; 97US-0058785P.
PR 02-OCT-1997; 97US-0061060P.

(HUMA-) HUMAN GENOME SCI INC.

PA Ruben SM, Rosen CA, Fischer CL, Soppet DR, Carter KC;
PI Bednarik DP, Endress GA, Yu G, Ni J, Feng P, Young PR, Greene JM;
PI Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;
PI Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
XX WPI; 1998-506364/43.
DR N-PSDB; AAV59735.

XX New isolated human genes and the secreted polypeptide(s) they encode -
PT useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders.

XX Claim 1; Page 670; 721pp; English.

XX This sequence represents a secreted human protein encoded by the nucleic
CC acid molecule designated Gene 66 from the human cDNA clone HTCC052
CC (deposited as clone ATCC 97900 and ATCC 209046). The gene can be used to
CC generate fusion proteins by linking to the gene to a human immunoglobulin
CC Fc portion (e.g. AAV59502) for increasing the stability of the fused to
CC protein as compared to the human protein only. The invention relates to
CC 186 novel genes and their fragments (nucleic acid sequences: AAV59511-
CC V59812; amino acid sequences AAV74731-W75026) which are useful for
CC preventing, treating or ameliorating medical conditions e.g. by protein
CC or gene therapy. Also, pathological conditions can be diagnosed by
CC determining the amount of the new polypeptides in a sample or by
CC determining the presence of mutations in the new polynucleotides.
CC Specific uses are described for each of the 186 polynucleotides, based on
CC which tissues they are most highly expressed in (see AAV59511 for
CC described uses)

XX SQ Sequence 14 AA;

Query Match 36.4%; Score 28; DB 2; Length 14;
Best Local Similarity 36.4%; Pred. No. 8.5e+02;
Matches 4; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 FEVWTFKDVLL 12
|: :|:
Db 2 FDFLSYFKDLL 12

RESULT 12
ABG95408
ID ABG95408 standard; protein; 14 AA.
XX

AC ABG95408;
 XX 15-JAN-2003 (first entry)
 XX DE Human novel secreted protein #229.
 XX
 XX Human; secreted protein; autoimmune disease; chemotaxis;
 KW rheumatoid arthritis; hyperproliferative disorder; breast neoplasm;
 KW liver neoplasm cardiovascular disorder; cardiac arrest; skin aging;
 KW cerebrovascular disorder; cerebral ischaemia; angiogenesis; sunburn;
 KW nervous system disorders; Alzheimer's disease; infection;
 KW ocular disorder; corneal infection; wound healing; tissue regeneration;
 KW epithelial cell proliferation; organ transplantation; food additive;
 KW preservative; nutritional.
 XX
 XX Homo sapiens.
 XX US6420526-B1.
 XX
 XX 16-JUL-2002.
 XX
 XX 08-SEP-1998; 98US-00149476.
 XX
 XX 07-MAR-1997; 97US-0038621P.
 XX 07-MAR-1997; 97US-0040161P.
 XX 07-MAR-1997; 97US-0040162P.
 XX 07-MAR-1997; 97US-0040163P.
 XX 07-MAR-1997; 97US-0040333P.
 XX 07-MAR-1997; 97US-0040334P.
 XX 07-MAR-1997; 97US-0040336P.
 XX 07-MAR-1997; 97US-0040826P.
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 XX 11-APR-1997; 97US-0043312P.
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 XX 11-APR-1997; 97US-0043569P.
 XX 11-APR-1997; 97US-0043576P.
 XX 11-APR-1997; 97US-0043578P.
 XX 11-APR-1997; 97US-0043580P.
 XX 11-APR-1997; 97US-0043669P.
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 XX 11-APR-1997; 97US-0043674P.
 XX 23-MAY-1997; 97US-0047492P.
 XX 23-MAY-1997; 97US-0047500P.
 XX 23-MAY-1997; 97US-0047501P.
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 XX 23-MAY-1997; 97US-0047581P.
 XX 23-MAY-1997; 97US-0047582P.
 XX 23-MAY-1997; 97US-0047583P.
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 XX 23-MAY-1997; 97US-0047599P.
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 XX 23-MAY-1997; 97US-0047612P.
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 PR 23-MAY-1997; 97US-0047617P.
 PR 23-MAY-1997; 97US-0047618P.
 PR 23-MAY-1997; 97US-0047632P.
 PR 23-MAY-1997; 97US-0047633P.
 PR 06-JUN-1997; 97US-0048964P.
 PR 06-JUN-1997; 97US-0048974P.
 PR 13-JUN-1997; 97US-0049610P.
 PR 08-JUL-1997; 97US-0051926P.
 PR 16-JUL-1997; 97US-0052874P.
 PR 18-AUG-1997; 97US-0055724P.
 PR 22-AUG-1997; 97US-0056630P.
 PR 22-AUG-1997; 97US-0056631P.
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 PR 22-AUG-1997; 97US-0056637P.
 PR 22-AUG-1997; 97US-0056662P.
 PR 22-AUG-1997; 97US-0056664P.
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 PR 22-AUG-1997; 97US-0056882P.
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 PR 22-AUG-1997; 97US-0056889P.
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 PR 22-AUG-1997; 97US-0056893P.
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 PR 22-AUG-1997; 97US-0056908P.
 PR 22-AUG-1997; 97US-0056909P.
 PR 22-AUG-1997; 97US-0056910P.
 PR 22-AUG-1997; 97US-0056911P.
 PR 05-SEP-1997; 97US-0057650P.
 PR 05-SEP-1997; 97US-0057659P.
 PR 05-SEP-1997; 97US-0057761P.
 PR 12-SEP-1997; 97US-0058785P.
 PR 02-OCT-1997; 97US-0061060P.
 PR 06-MAR-1998; 98WO-US004493.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Ruben SM, Rosen CA, Fischer CL, Soppet DP, Carter KC;
 PI Bednarik DR, Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM;
 PI Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;
 PI Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
 XX
 XX WPI; 2002-634796/68.
 DR N-PSDB; ABS73726.
 XX
 XX New isolated human secreted protein for diagnosing, preventing, treating
 PT or ameliorating medical conditions and used as a food additive or
 PT preservative.
 XX
 XX Example 1; SEQ ID NO 548; 129pp; English.
 PS
 XX The invention relates to an isolated protein that is one of 186 human
 CC secreted proteins, given in the specification, encoded by one of 309 cDNA
 CC sequences also given in the specification. The protein is used in a
 CC pharmaceutical composition used to prevent, treat or ameliorate a medical
 CC condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs,


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PR 23-MAY-1997; 97US-0047586P.
PR 23-MAY-1997; 97US-0047587P.
PR 23-MAY-1997; 97US-0047588P.
PR 23-MAY-1997; 97US-0047589P.
PR 23-MAY-1997; 97US-0047590P.
PR 23-MAY-1997; 97US-0047592P.
PR 23-MAY-1997; 97US-0047593P.
PR 23-MAY-1997; 97US-0047594P.
PR 23-MAY-1997; 97US-0047595P.
PR 23-MAY-1997; 97US-0047596P.
PR 23-MAY-1997; 97US-0047597P.
PR 23-MAY-1997; 97US-0047598P.
PR 23-MAY-1997; 97US-0047599P.
PR 23-MAY-1997; 97US-0047600P.
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PR 23-MAY-1997; 97US-0047612P.
PR 23-MAY-1997; 97US-0047613P.
PR 23-MAY-1997; 97US-0047614P.
PR 23-MAY-1997; 97US-0047615P.
PR 23-MAY-1997; 97US-0047617P.
PR 23-MAY-1997; 97US-0047618P.
PR 23-MAY-1997; 97US-0047632P.
PR 23-MAY-1997; 97US-0047633P.
PR 06-JUN-1997; 97US-0048964P.
PR 06-JUN-1997; 97US-0048974P.
PR 13-JUN-1997; 97US-0049610P.
PR 08-JUL-1997; 97US-0051926P.
PR 16-JUL-1997; 97US-0052874P.
PR 18-AUG-1997; 97US-0055724P.
PR 22-AUG-1997; 97US-0056630P.
PR 22-AUG-1997; 97US-0056631P.
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PR 22-AUG-1997; 97US-0056864P.
PR 22-AUG-1997; 97US-0056872P.
PR 22-AUG-1997; 97US-0056874P.
PR 22-AUG-1997; 97US-0056875P.
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PR 22-AUG-1997; 97US-0056877P.
PR 22-AUG-1997; 97US-0056878P.
PR 22-AUG-1997; 97US-0056879P.
PR 22-AUG-1997; 97US-0056880P.
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PR 22-AUG-1997; 97US-0056889P.
PR 22-AUG-1997; 97US-0056892P.
PR 22-AUG-1997; 97US-0056893P.
PR 22-AUG-1997; 97US-0056894P.
PR 22-AUG-1997; 97US-0056899P.
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PR 22-AUG-1997; 97US-0056909P.
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PR 05-SEP-1997; 97US-0057650P.
PR 05-SEP-1997; 97US-0057669P.
PR 12-SEP-1997; 97US-0057761P.
PR 09-OCT-1997; 97US-0061660P.
PR 06-MAR-1998; 98WO-US004493.
PR 08-SEP-1998; 98US-00149476.
PR 17-MAR-2000; 2000US-0190068P.
PR 16-MAR-2001; 2001US-00809391.
XX PA
(RUBE/) RUBEN S M.

PA (ROSE/) ROSEN C A.
PA (SOPP/) SOPPET D R.
PA (CART/) CARTER K C.
PA (BEDN/) BEDNARIK D P.
PA (ENDR/) ENDRESS G A.
PA (YUGG/) YU G.
PA (NIJJ/) NI J.
PA (FENG/) FENG P.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (DUAN/) DUAN D R.
PA (HUJJ/) HU J.
PA (FLOR/) FLORENCE K A.
PA (OLSE/) OLSEN H S.
PA (FISC/) FISCHER C L.
PA (EBNE/) EBNER R.
PA (BREW/) BREWER L A.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (LAF/) LAFLEUR D W.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
XX
PI Ruben SM, Rosen CA, Soppet DR, Carter KC, Bednarik DP;
PI Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Ferrie AM;
PI Duan DR, Hu J, Florence KA, Olsen HS, Fischer CL, Ebner R;
PI Brewer LA, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
XX
WPI; 2003-898535/82.
DR N-PSDB; ADI22954.
XX
PI New nucleic acid molecule, useful for preparing a medicament for
PT diagnosing, preventing, treating or ameliorating a medical condition
PT e.g., cancer.
XX
Claim 11; SEQ ID NO 548; 256pp; English.
XX
The invention describes an isolated nucleic acid comprising a sequence
CC having 95 % identity with: a polynucleotide fragment of a sequence not
CC given in the specification, or its allelic variant; a polynucleotide
CC fragment of the cDNA sequence; a polynucleotide sequence encoding a
CC polypeptide, or its fragment, domain, epitope or species homologue; or a
CC polynucleotide that hybridises under stringent conditions to any one of
CC the sequences of (a)-(c). The nucleic acid is useful for preparing a
CC medicament for diagnosing, preventing, treating or ameliorating a medical
CC condition e.g., cancer. The is the amino acid sequence of a novel human
CC secreted protein of the invention.
XX
SQ Sequence 14 AA;

Query Match 36.4%; Score 28; DB 7; Length 14;
Best Local Similarity 36.4%; Pred. No. 8.5e+02;
Matches 4; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 FEVWTFLEKDV L 12
|:|:|:|:|:|
Db 2 FDFLSYFKDLL 12

RESULT 15
ADH74265
ID ADH74265 standard; protein; 14 AA.
XX
AC ADH74265;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human secreted protein #229.
XX
KW human; secreted protein; cancer; haematopoietic disorder;
endocrine disorder; immune system disease; inflammatory disorder.
```


XX OS Homo sapiens.
XX PN US2003225248-A1.
XX PD 04-DEC-2003.
XX PF 10-JUN-2002; 2002US-00164861.
XX PR 07-MAR-1997; 97US-0038621P.
XX PR 07-MAR-1997; 97US-0040161P.
XX PR 07-MAR-1997; 97US-0040162P.
XX PR 07-MAR-1997; 97US-0040163P.
XX PR 07-MAR-1997; 97US-0040333P.
XX PR 07-MAR-1997; 97US-0040334P.
XX PR 07-MAR-1997; 97US-0040336P.
XX PR 07-MAR-1997; 97US-0040626P.
XX PR 11-APR-1997; 97US-0043311P.
XX PR 11-APR-1997; 97US-0043312P.
XX PR 11-APR-1997; 97US-0043313P.
XX PR 11-APR-1997; 97US-0043314P.
XX PR 11-APR-1997; 97US-0043315P.
XX PR 11-APR-1997; 97US-0043568P.
XX PR 11-APR-1997; 97US-0043569P.
XX PR 11-APR-1997; 97US-0043576P.
XX PR 11-APR-1997; 97US-0043578P.
XX PR 11-APR-1997; 97US-0043580P.
XX PR 11-APR-1997; 97US-0043669P.
XX PR 11-APR-1997; 97US-0043670P.
XX PR 11-APR-1997; 97US-0043671P.
XX PR 11-APR-1997; 97US-0043672P.
XX PR 11-APR-1997; 97US-0043674P.
XX PR 23-MAY-1997; 97US-0047492P.
XX PR 23-MAY-1997; 97US-0047500P.
XX PR 23-MAY-1997; 97US-0047501P.
XX PR 23-MAY-1997; 97US-0047502P.
XX PR 23-MAY-1997; 97US-0047503P.
XX PR 23-MAY-1997; 97US-0047581P.
XX PR 23-MAY-1997; 97US-0047582P.
XX PR 23-MAY-1997; 97US-0047583P.
XX PR 23-MAY-1997; 97US-0047584P.
XX PR 23-MAY-1997; 97US-0047585P.
XX PR 23-MAY-1997; 97US-0047586P.
XX PR 23-MAY-1997; 97US-0047587P.
XX PR 23-MAY-1997; 97US-0047588P.
XX PR 23-MAY-1997; 97US-0047589P.
XX PR 23-MAY-1997; 97US-0047590P.
XX PR 23-MAY-1997; 97US-0047592P.
XX PR 23-MAY-1997; 97US-0047593P.
XX PR 23-MAY-1997; 97US-0047594P.
XX PR 23-MAY-1997; 97US-0047595P.
XX PR 23-MAY-1997; 97US-0047596P.
XX PR 23-MAY-1997; 97US-0047597P.
XX PR 23-MAY-1997; 97US-0047598P.
XX PR 23-MAY-1997; 97US-0047599P.
XX PR 23-MAY-1997; 97US-0047600P.
XX PR 23-MAY-1997; 97US-0047601P.
XX PR 23-MAY-1997; 97US-0047612P.
XX PR 23-MAY-1997; 97US-0047613P.
XX PR 23-MAY-1997; 97US-0047614P.
XX PR 23-MAY-1997; 97US-0047615P.
XX PR 23-MAY-1997; 97US-0047617P.
XX PR 23-MAY-1997; 97US-0047618P.
XX PR 23-MAY-1997; 97US-0047632P.
XX PR 23-MAY-1997; 97US-0047633P.
XX PR 06-JUN-1997; 97US-0048964P.
XX PR 06-JUN-1997; 97US-0048974P.
XX PR 13-JUN-1997; 97US-0049610P.
XX PR 08-JUL-1997; 97US-0051926P.
XX PR 16-JUL-1997; 97US-0052874P.
XX PR 18-AUG-1997; 97US-0055724P.
XX PR 22-AUG-1997; 97US-0056630P.
XX PR 22-AUG-1997; 97US-0056631P.
XX PR 22-AUG-1997; 97US-0056632P.
XX PR 22-AUG-1997; 97US-0056636P.
XX PR 22-AUG-1997; 97US-0056637P.
XX PR 22-AUG-1997; 97US-0056662P.
XX PR 22-AUG-1997; 97US-0056664P.
XX PR 22-AUG-1997; 97US-0056845P.
XX PR 22-AUG-1997; 97US-0056862P.
XX PR 22-AUG-1997; 97US-0056864P.
XX PR 22-AUG-1997; 97US-0056872P.
XX PR 22-AUG-1997; 97US-0056874P.
XX PR 22-AUG-1997; 97US-0056875P.
XX PR 22-AUG-1997; 97US-0056876P.
XX PR 22-AUG-1997; 97US-0056877P.
XX PR 22-AUG-1997; 97US-0056878P.
XX PR 22-AUG-1997; 97US-0056879P.
XX PR 22-AUG-1997; 97US-0056880P.
XX PR 22-AUG-1997; 97US-0056881P.
XX PR 22-AUG-1997; 97US-0056882P.
XX PR 22-AUG-1997; 97US-0056884P.
XX PR 22-AUG-1997; 97US-0056886P.
XX PR 22-AUG-1997; 97US-0056887P.
XX PR 22-AUG-1997; 97US-0056888P.
XX PR 22-AUG-1997; 97US-0056889P.
XX PR 22-AUG-1997; 97US-0056892P.
XX PR 22-AUG-1997; 97US-0056893P.
XX PR 22-AUG-1997; 97US-0056894P.
XX PR 22-AUG-1997; 97US-0056903P.
XX PR 22-AUG-1997; 97US-0056908P.
XX PR 22-AUG-1997; 97US-0056909P.
XX PR 22-AUG-1997; 97US-0056910P.
XX PR 22-AUG-1997; 97US-0056911P.
XX PR 05-SEP-1997; 97US-0057650P.
XX PR 05-SEP-1997; 97US-0057669P.
XX PR 05-SEP-1997; 97US-0057761P.
XX PR 12-SEP-1997; 97US-0058785P.
XX PR 02-OCT-1997; 97US-0061060P.
XX PR 06-MAR-1998; 98WO-US004493.
XX PR 08-SEP-1998; 98US-00149476.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Ruben SM, Rosen CA, Soppet DR, Carter KC, Bednarik DP;
PI Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Ferrie AM;
PI Duan R, Hu J, Florence KA, Olsen HS, Fischer CL, Ebner R;
PI Brewer LA, Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
XX WPI: 2004-131264/13.
XX N-PSDB; ADH73956.
XX Isolated nucleic acid molecules encoding human secreted proteins, useful
PT for preventing, diagnosing and treating disorders associated with
PT aberrant expression and activity.
XX Claim 11; SEQ ID NO 548; 142pp; English.
XX The invention relates to isolated nucleic acid molecules and the human
CC secreted proteins (SPs) they encode. The proteins and nucleic acids may
CC be used in the prevention, diagnosis and treatment of diseases associated
CC with inappropriate SP expression e.g. cancer, haematopoietic disorders,
CC endocrine disorders, diseases of the immune system, inflammatory
CC disorders and many others. Full details of disorders that may be
CC prevented, diagnosed and/or treated by the above methods are given in the
CC specification. The nucleic acid molecules may be used to produce their
CC proteins. The nucleic acid and it's complementary sequences may also be
CC used as DNA probes in diagnostic assays to detect and quantitate the
CC presence of similar nucleic acids in samples, and therefore which
CC patients may be in need of restorative therapy. The SPs may also be used
CC as antigens in the production of antibodies against the proteins and in
CC assays to identify modulators of SP expression and activity. The anti-SP
CC antibodies and antagonists may also be used to down regulate expression
CC and activity. The anti-SP antibodies may also be used as diagnostic
CC agents for detecting the presence of the proteins in samples (e.g. by
CC enzyme linked immunosorbant assay (ELISA)). The present sequence

CC represents the amino acid sequence of a human secreted protein.
XX
SQ Sequence 14 AA;

Query Match 36.4%; Score 28; DB 8; Length 14;
Best Local Similarity 36.4%; Pred. No. 8.5e+02;
Matches 4; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 FEWTFELKDVL 12
| : : : | : |
Db 2 FDFLSYFKDLL 12

Search completed: February 22, 2005, 09:24:46
Job time : 67.6667 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 22, 2005, 09:08:09 ; Search time 11.1333 Seconds
(without alignments)
129,633 Million cell updates/sec

Title: US-08-991-628-10

Perfect score: 72

Sequence: 1 DRLMLFAKDVVSRN 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 2523

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23	31.9	13	2 PNO168	phosphopyruvate hy
2	23	31.9	14	2 A61308	hemocyanin chain 2
3	23	31.9	14	2 D61308	hemocyanin chain 5
4	22	30.6	13	2 S29488	GRP-binding protei
5	22	30.6	15	2 PA0093	emniatin synthetas
6	21	29.2	11	2 S42449	anti protein - pha
7	20	27.8	11	2 E61308	hemocyanin chain 3
8	20	27.8	14	2 PH1356	Ig heavy chain DJ
9	20	27.8	14	2 G61308	hemocyanin chain 3
10	19	26.4	12	2 S01222	translation elonga
11	19	26.4	11	2 PH1590	Ig H chain V-D-J r
12	18	25.0	15	2 B49164	chromogranin-B - r
13	18	25.0	11	2 PC2372	S8K heat shock pro
14	18	25.0	14	2 PS0371	hypothetical prote
15	18	25.0	14	2 S23789	hypothetical prote
16	18	25.0	14	2 F83754	hypothetical prote
17	18	25.0	15	2 PA0052	protein QF200015 -
18	18	25.0	15	2 D28587	T-cell receptor be
19	18	25.0	15	2 PA0075	fructose-bisphosph
20	17	23.6	11	2 PT0229	Ig heavy chain CDR
21	17	23.6	12	4 PC2121	aminotransferase c
22	17	23.6	14	1 QMVHP2	mastoparan C - Eur
23	17	23.6	14	2 S19803	ubiquitin - potato
24	17	23.6	15	2 S61438	hypothetical prote
25	17	23.6	15	2 PA0102	fructose-bisphosph
26	17	23.6	15	2 PA0063	ubiquitin - fungus
27	17	23.6	15	2 I46909	voltage-dependent
28	16	22.2	6	2 I59142	platelet-derived g
29	16	22.2	8	2 E60588	sperm-activating p

30 16 22.2 11 2 S33782 acetolactate synth
31 16 22.2 12 2 S47360 T-cell antigen rec
32 16 22.2 12 2 PH1587 Ig H chain V-D-J r
33 16 22.2 12 2 B61497 seed protein ws-17
34 16 22.2 12 2 A34858 proteinase E - bla
35 16 22.2 13 2 PNO122 Oil protein - vacc
36 16 22.2 13 2 A61288 spore proteinase g
37 16 22.2 13 2 S36887 ribosomal protein
38 16 22.2 13 2 S01043 glutamate-ammonia
39 16 22.2 14 2 E33098 214K exoantigen (v
40 16 22.2 14 2 PH1327 Ig heavy chain DJ
41 16 22.2 14 2 JS0272 hypothetical 1.5K
42 16 22.2 14 2 PH1617 Ig H chain V-D-J r
43 16 22.2 14 2 S14336 mastoparan B - hor
44 16 22.2 15 2 A60834 angiotensin I prec
45 16 22.2 15 2 S55312 TSH protein beta c

ALIGNMENTS

RESULT 1

PNO168

phosphopyruvate hydratase (EC 4.2.1.11) - fungus (Fusarium sporotrichioides) (fragment)
C:Species: Fusarium sporotrichioides
C:Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 09-Jul-2004
C:Accession: PNO168
R:Fukaya, N.; Chow, L.P.; Sugiura, Y.; Tsugita, A.; Ueno, Y.; Tabuchi, K.
submitted to JPIID, May 1994

A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichi

A:Reference number: PNO168

A:Accession: PNO168

A:Molecule type: protein

A:Residues: 1-13 <PUK>

A:Cross-references: UNIPROT:Q7M4Y6

C:Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 31.9%; Score 23; DB 2; Length 13;
Best Local Similarity 25.0%; Pred. No. 6e+02;
Matches 3; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 3 LMLMLFAKDVVSR 14

DB 2 IVLVFAKDVVSR 13

RESULT 2

A61308

hemocyanin chain 2 - Sahara scorpion (fragment)
C:Species: Androctonus australis (Sahara scorpion)
C:Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 09-Jul-2004
C:Accession: A61308
R:Jolles, J.; Jolles, P.; Lamy, J.; Lamy, J.

FEBS Lett. 106, 289-291, 1979

A:Title: Structural characterization of seven different subunits in Androctonus australis

A:Reference number: A61308; MUID:80047238; PMID:499512

A:Accession: A61308

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-14 <JOL>

A:Cross-references: UNIPROT:Q7M488

Query Match 31.9%; Score 23; DB 2; Length 14;
Best Local Similarity 57.1%; Pred. No. 6.5e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DRLMLF 7

DB 7 DRIPLF 13

RESULT 3

D61308

hemocyanin chain 5A - Sahara scorpion (fragment)
 C/Species: Androctonus australis (Sahara scorpion)
 C/Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 09-Jul-2004
 C/Accession: D61308
 R/Jolles, J.; Jolles, P.; Lamy, J.; Lamy, J.
 FEBS Lett. 106, 289-291, 1979
 A/Title: Structural characterization of seven different subunits in Androctonus australis
 A/Reference number: A61308; MUID:80047238; PMID:499512
 A/Accession: D61308
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-14 <VOL>
 A/Cross-references: UNIPROT:Q7M486

Query Match 31.9%; Score 23; DB 2; Length 14;
 Best Local Similarity 71.4%; Pred. No. 6.5e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DRLMLF 7
 :||| |
 Db 7 ERLPLF 13

RESULT 4
 S29488
 GTP-binding protein o-rab3 - marbled electric ray (fragment)
 C/Species: Torpedo marmorata (marbled electric ray)
 C/Date: 22-Nov-1993 #sequence_revision 27-Feb-1997 #text_change 13-Mar-1997
 C/Accession: S29488
 R/Volkandt, W.; Pevsner, J.; Elferink, L.A.; Scheller, R.H.
 FEBS Lett. 317, 53-56, 1993
 A/Title: Association of three small GTP-binding proteins with cholinergic synaptic vesicle
 A/Reference number: S29485; MUID:93154521; PMID:8428634
 A/Accession: S29488
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-13 <VOL>

Query Match 30.6%; Score 22; DB 2; Length 13;
 Best Local Similarity 57.1%; Pred. No. 9.3e+02;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 KDVVSRN 15
 ||| |
 Db 1 KDVDQN 7

RESULT 5
 PA0093
 enniatin synthetase - fungus (Fusarium sporotrichioides) (fragment)
 C/Species: Fusarium sporotrichioides
 C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
 C/Accession: PA0093
 R/Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
 submitted to JIPID, October 1994
 A/Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichi
 A/Reference number: PA0051
 A/Accession: PA0093
 A/Molecule type: protein
 A/Residues: 1-15 <CHO>
 A/Cross-references: UNIPROT:Q7M426

Query Match 30.6%; Score 22; DB 2; Length 15;
 Best Local Similarity 80.0%; Pred. No. 1.1e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 LFAKD 10
 :||| |
 Db 8 LYAKD 12

RESULT 6
 S42449

ant1 protein - phase P7
 C/Species: phase P7
 C/Date: 07-Sep-1994 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
 C/Accession: S42449
 R/Citron, M.; Schuster, H.
 Cell 62, 591-598, 1990
 A/Title: The c4 repressors of bacteriophages P1 and P7 are antisense RNAs.
 A/Reference number: S42448; MUID:90335968; PMID:1696181
 A/Accession: S42449
 A/Status: preliminary; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-11 <CIT>
 A/Cross-references: UNIPROT:Q38415; EMBL:W35139; NID:g215705; PIDN:AAA32437.1; PID:g2157

Query Match 29.2%; Score 21; DB 2; Length 11;
 Best Local Similarity 57.1%; Pred. No. 1.2e+03;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 9 KDVVSRN 15
 | : |||
 Db 3 KPLVTRN 9

RESULT 7
 E61308
 hemocyanin chain 3B - Sahara scorpion (fragment)
 C/Species: Androctonus australis (Sahara scorpion)
 C/Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 07-May-1999
 C/Accession: E61308
 R/Jolles, J.; Jolles, P.; Lamy, J.; Lamy, J.
 FEBS Lett. 106, 289-291, 1979
 A/Title: Structural characterization of seven different subunits in Androctonus australis
 A/Reference number: A61308; MUID:80047238; PMID:499512
 A/Accession: E61308
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-14 <JOL>

Query Match 27.8%; Score 20; DB 2; Length 14;
 Best Local Similarity 66.7%; Pred. No. 2.4e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RLLMLF 7
 | : |||
 Db 8 RILKLF 13

RESULT 8
 PH1356
 Ig heavy chain DJ region (clone C178-97) - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C/Accession: PH1356
 R/Wasserman, R.; Gallili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
 J. Exp. Med. 176, 1577-1581, 1992
 A/Title: Predominance of fetal type DJH joining in young children with B precursor lymph
 A/Reference number: PH1302; MUID:93094761; PMID:1460419
 A/Accession: PH1356
 A/Molecule type: DNA
 A/Residues: 1-14 <WAS>
 C/Keywords: heterotetramer; immunoglobulin

Query Match 27.8%; Score 20; DB 2; Length 14;
 Best Local Similarity 33.3%; Pred. No. 2.4e+03;
 Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 LLMLEAKDV 11
 | : |||
 Db 1 ITMIIGMDV 9

RESULT 9
 G61308

hemocyanin chain 3C - Sahara scorpion (fragment)
C:Species: Androctonus australis (Sahara scorpion)
C:Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 09-Jul-2004
C:Accession: G61308
R:Jolles, J.; Jolles, P.; Lamy, J.; Lamy, J.
PDBS Lett. 106, 289-291, 1979
A:Title: Structural characterization of seven different subunits in Androctonus australis
A:Reference number: A61308; MUID:80047238; PMID:499512
A:Accession: G61308
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-14 <JOL>
A:Cross-references: UNIPROT:Q7M487

Query Match 27.8%; Score 20; DB 2; Length 14;
Best Local Similarity 66.7%; Pred. No. 2.4e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RLMLF 7
|:|:|
Db 8 RLSLF 13

RESULT 10
S01222
Translation elongation factor EF-Tu - Pseudomonas aeruginosa (fragment)
C:Species: Pseudomonas aeruginosa
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
C:Accession: S01222
R:Hughes, M.A.; Jones, D.S.
Nucleic Acids Res. 16, 7193, 1988
A:Title: A fragment of the Pseudomonas aeruginosa genome contains five tRNA genes, four
A:Reference number: S01222; MUID:88303352; PMID:3136442
A:Accession: S01222
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-12 <HUG>
A:Cross-references: UNIPROT:P09591; EMBL:X07950; NID:g45426; PIDN:CAA30775.1; PID:g45427
C:Genetics:
A:Gene: tuftB
C:Superfamily: translation elongation factor Tu; translation elongation factor Tu homolog
C:Keywords: GTP binding; protein biosynthesis

Query Match 26.4%; Score 19; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 3.1e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 8 AKDVSRN 15
|:|:|
Db 2 AKEKERN 9

RESULT 11
PH1590
Ig H chain V-D-J region (wild-type clone 141) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C:Accession: PH1590
R:Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
A:Reference number: PH1580; MUID:93301609; PMID:8315387
A:Accession: PH1590
A:Molecule type: DNA
A:Residues: 1-15 <LEV>
A:Experimental source: bone marrow pre-B lymphocyte
C:Keywords: immunoglobulin

Query Match 26.4%; Score 19; DB 2; Length 15;
Best Local Similarity 42.9%; Pred. No. 3.9e+03;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 8 AKDVVSR 14

Db 2 ARDMILR 8
|:|:|
|:|:|

RESULT 12
B49164
Chromogranin-B - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 31-Oct-1997
C:Accession: B49164
R:Nielsen, E.; Welinder, B.S.; Madsen, O.D.
Endocrinology 129, 3147-3156, 1991
A:Title: Chromogranin-B, a putative precursor of eight novel rat glucagonoma peptides th
A:Reference number: A49164; MUID:92063871; PMID:1954895
A:Accession: B49164
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-11 <NIE>
A>Note: sequence extracted from NCBI backbone (NCBI:66370)
C:Superfamily: chromogranin B precursor

Query Match 25.0%; Score 18; DB 2; Length 11;
Best Local Similarity 60.0%; Pred. No. 4.4e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 FAKDV 11
|:|:|
Db 2 FSEDV 6

RESULT 13
PC2372
58K heat shock protein groEL [similarity] - Bacillus cereus (strain ts-4) (fragment)
C:Species: Bacillus cereus
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: PC2372
R:Matsumoto, K.; Miyamoto, T.; Yamaguchi, K.; Sayed, M.A.; Kajiwara, T.; Hatano, S.
Biosci. Biotechnol. Biochem. 59, 231-235, 1995
A:Title: Identification of DNA-binding proteins changed after induction of sporulation
A:Reference number: PC2369; MUID:95218265; PMID:7766022
A:Accession: PC2372
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-11 <MAS>
C:Keywords: heat shock; molecular chaperone; stress-induced protein

Query Match 25.0%; Score 18; DB 2; Length 11;
Best Local Similarity 75.0%; Pred. No. 4.4e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 AKDV 11
|:|:|
Db 1 AKDI 4

RESULT 14
PS0371
Hypothetical protein (psaC region) - Synechococcus sp. (fragment)
C:Species: Synechococcus sp.
C:Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 08-Oct-1999
C:Accession: PS0371
R:Rhiel, E.; Stirewalt, V.L.; Gasparich, G.E.; Bryant, D.A.
Gene 112, 123-128, 1992
A:Title: The psaC genes of Synechococcus sp. PCCT002 and Cyanophora paradoxa: cloning a
A:Reference number: JS0694; MUID:92201692; PMID:1551590
A:Accession: PS0371
A:Molecule type: DNA
A:Residues: 1-14 <RHI>
A:Cross-references: GB:M66238; NID:g154574; PIDN:AAA27351.1; PID:g552030

Query Match 25.0%; Score 18; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 5.7e+03;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 FAKQVSR 14
| | | |
Db 4 FKLDVTGR 11

RESULT 15
S29789
hypochemical protein - Thermoplasma acidophilum (fragment)
C:Species: Thermoplasma acidophilum
C:Date: 25-Feb-1994 #sequence_revision 26-May-1995 #text_change 26-May-1995
C:Accession: S29789
R:Bright, J.R.; Byrom, D.; Danson, M.J.; Hough, D.W.; Townner, P.
Eur. J. Biochem. 211, 549-554, 1993
A:Title: Cloning, sequencing and expression of the gene encoding glucose dehydrogenase f
A:Reference number: S29788; MUID:93170285; PMID:8436115
A:Accession: S29789
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-14 <BRI>
A:Cross-references: EMBL:X59788

Query Match 25.0%; Score 18; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 9 KQVSR 14
| | | |
Db 2 KDLKLR 7

Search completed: February 22, 2005, 09:46:28
Job time : 12.1333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 22, 2005, 08:53:13 ; Search time 52.6 seconds
(without alignments)
146.030 Million cell updates/sec

Title: US-08-991-628-10

Perfect score: 72

Sequence: 1 DRLLMLFAKVVVSRN 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 6622

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	36.1	12	1 UN39_CLOPA	P81359 clostridium
2	25	34.7	15	2 Q9S8D3	Q9S8D3 cynara card
3	23	31.9	13	2 Q7M4Y6	Q7M4Y6 fusarium sp
4	23	31.9	14	2 Q7M486	Q7M486 androctonus
5	23	31.9	14	2 Q7M488	Q7M488 androctonus
6	23	31.9	15	1 GTE2_PSEUO	P83000 pseudomonas
7	22	30.6	12	2 Q9UR28	Q9UR28 cryptococcus
8	22	30.6	14	2 Q15998	Q15998 homo sapien
9	22	30.6	15	2 Q7M426	Q7M426 fusarium sp
10	21	29.2	11	2 Q38415	Q38415 bacterioph
11	21	29.2	11	2 Q9R7U8	Q9R7U8 pseudomonas
12	21	29.2	13	2 Q6TU17	Q6TU17 ascaris suu
13	21	29.2	15	2 Q950P6	Q950P6 rhizophyidiu
14	20	27.8	10	1 GS09_BACSU	P80243 bacillus su
15	20	27.8	14	2 Q7M487	Q7M487 androctonus
16	20	27.8	14	2 Q7R889	Q7R889 plasmodium
17	20	27.8	14	2 Q661E1	Q661E1 borrelia ga
18	20	27.8	15	2 Q9UWH4	Q9UWH4 pyrococcus.
19	20	27.8	15	2 Q9UWH6	Q9UWH6 thermococcus
20	19	26.4	9	2 Q7S182	Q7S182 neurospora
21	19	26.4	11	2 Q7RBB2	Q7RBB2 plasmodium
22	19	26.4	12	2 Q6JDK3	Q6JDK3 canis famil
23	19	26.4	12	2 Q9QZD0	Q9QZD0 mus musculu
24	19	26.4	13	1 CH60_CANFA	P49818 canis famil
25	19	26.4	13	2 Q81ZRO	Q81ZRO homo sapien
26	19	26.4	13	2 Q6LCB1	Q6LCB1 rattus norv
27	19	26.4	14	2 Q8J1G3	Q8J1G3 aebhya goss
28	19	26.4	14	2 Q8WVR7	Q8WVR7 homo sapien
29	19	26.4	14	2 Q9UHM5	Q9UHM5 homo sapien
30	19	26.4	15	2 Q8K1P5	Q8K1P5 sciurus vul
31	19	26.4	15	2 Q8K1W5	Q8K1W5 castor cana

32 19 26.4 15 2 Q9QXZ5 Q9QXZ5 mus musculu
33 18.5 25.7 14 1 UN46_CLOPA P81362 clostridium
34 18.5 25.7 15 2 Q9TNF0 Q9TNF0 mus sp. m
35 18 25.0 10 1 MALE_KLRPN Q05564 klebsiella
36 18 25.0 10 1 RCA_FINPS P81084 pinus pinas
37 18 25.0 10 2 Q6LEW6 Q6LEW6 homo sapien
38 18 25.0 10 2 Q90344 Q90344 gb virus c/
39 18 25.0 11 2 Q9QVH3 Q9QVH3 rattus sp.
40 18 25.0 11 2 Q66200 Q66200 transmissib
41 18 25.0 12 2 Q6EGT2 Q6EGT2 stemphylium
42 18 25.0 12 2 Q6EGV5 Q6EGV5 pleospora g
43 18 25.0 12 2 Q7QYL7 Q7QYL7 homo sapien
44 18 25.0 12 2 Q90QD1 Q90QD1 human immun
45 18 25.0 13 1 BP37_LEUMA P81754 leucophaea

ALIGNMENTS

RESULT 1

UN39_CLOPA STANDARD; PRT; 12 AA.
AC P81359;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Unknown protein CP 39 from 2D-PAGE (Fragment).
OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=W5;
RX MEDLINE=98291870; PubMed=9629918;
RA Flengstrand R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
sequence analysis of proteins from Clostridium pasteurianum W5.";
RL Electrophoresis 19:802-806(1998).
CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 5.4, its MW is: 29.5 kDa.
KW Direct protein sequencing.
FT NON TER 12
SQ SEQUENCE 12 AA; 1432 MW; 940561B66BD2CB01 CRC64;

Query Match 36.1%; Score 26; DB 1; Length 12;

Best Local Similarity 36.4%; Pred. No. 1.3e+03;

Matches 4; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 5 MLFAKVVVSRN 15

DB 1 MIYSTEVVNNN 11

RESULT 2

Q9S8D3 PRELIMINARY; PRT; 15 AA.
ID Q9S8D3;
AC Q9S8D3;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE CARDOSIN B (Fragment).
OS Cynara cardunculus (Cardoon).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC campanulids; Asterales; Asteraceae; Carduoideae; Cynara.
OX NCBI_TaxID=4265;
RN [1]
RP SEQUENCE.
RX MEDLINE=96073661; PubMed=8540346;
RA Faro C., Verissimo P., Lin Y., Tang J., Pires E.;
RT "Cardosin A and B, aspartic proteases from the flowers of cardoon.";
RL Adv. Exp. Med. Biol. 362:373-377(1995).

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SQ SEQUENCE 15 AA; 1571 MW; 1DD25E8CB119379B CRC64;

Query Match 34.7%; Score 25; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 2.5e+03;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 8 AKDVVSRN 15
Db :|:|:|:|
-2 AEDIVNNN 9

RESULT 3
Q7M4Y6 PRELIMINARY; PRT; 13 AA.
AC Q7M4Y6;
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Phosphopyruvate hydratase (EC 4.2.1.11) (Fragment).
OS Fusarium sporotrichoides.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreaomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
OX NCBI_TaxID=5514;
RN [1]
RP SEQUENCE.
RA Fukaya N., Chow L.P., Sugiura Y., Tsugita A., Ueno Y., Tabuchi K.;
RL Submitted (MAY-1994) to the PIR data bank.
DR PIR; PNO168; PNO168.
DR GO; GO:0004634; P:phosphopyruvate hydratase activity; IEA.
FT NON_TER 1
FT NON_TER 13
FT NON_TER 13
SQ SEQUENCE 13 AA; 1481 MW; CFEA8596A8A10DD9 CRC64;

Query Match 31.9%; Score 23; DB 2; Length 13;
Best Local Similarity 25.0%; Pred. No. 5.2e+03;
Matches 3; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 3 LLMLFAKDVVSR 14
Db :|:|:|:|
2 IVLVARSVDK 13

RESULT 4
Q7M486 PRELIMINARY; PRT; 14 AA.
AC Q7M486;
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Hemocyanin chain 5A (Fragment).
OS Androctonus australis (Sahara scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Buthida; Buthoidea;
OX NCBI_TaxID=6858;
RN [1]
RP SEQUENCE.
RA Jolles J., Jolles P., Lamy J., Lamy J.;
RT "Structural characterization of seven different subunits in
RT Androctonus australis haemocyanin.";
RL FEBS Lett. 106:289-291(1979).
DR PIR; D61308; D61308.
FT NON_TER 1
FT NON_TER 14
FT NON_TER 14
SQ SEQUENCE 14 AA; 1658 MW; 6FA4342770FEAF0B CRC64;

Query Match 31.9%; Score 23; DB 2; Length 14;
Best Local Similarity 71.4%; Pred. No. 5.6e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DRLLMLF 7
Db :|:|:|:|
7 ERLLPLF 13

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RESULT 5
Q7M488 PRELIMINARY; PRT; 14 AA.
AC Q7M488;
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Hemocyanin chain 2 (Fragment).
OS Androctonus australis (Sahara scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Buthida; Buthoidea;
OX NCBI_TaxID=6858;
RN [1]
RP SEQUENCE.
RA Jolles J., Jolles P., Lamy J., Lamy J.;
RT "Structural characterization of seven different subunits in
RT Androctonus australis haemocyanin.";
RL FEBS Lett. 106:289-291(1979).
DR PIR; A61308; A61308.
FT NON_TER 1
FT NON_TER 14
FT NON_TER 14
SQ SEQUENCE 14 AA; 1716 MW; 9B14357E859E400A CRC64;

Query Match 31.9%; Score 23; DB 2; Length 14;
Best Local Similarity 57.1%; Pred. No. 5.6e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DRLLMLF 7
Db :|:|:|:|
7 DRILPLF 13

RESULT 6
GTE2_PSEU STANDARD; PRT; 15 AA.
AC P83000;
DT 05-JUN-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Glutathione S-transferase (EC 2.5.1.18) (Fragment).
OS Pseudomonas sp. (strain M1).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=95619;
RN [1]
RP SEQUENCE, FUNCTION, CATALYTIC ACTIVITY, SUBUNIT, AND SUBCELLULAR
RP LOCATION.
RX MEDLINE=21896940; PubMed=11900268; DOI=10.1016/S0923-2508(01)01293-1;
RA Santos P.M., Mignogna G., Heipieper H.J., Zennaro E.;
RT "Occurrence and properties of glutathione S-transferases in phenol-
RT degrading Pseudomonas strains.";
RL Res. Microbiol. 153:89-98(2002).
CC -1- FUNCTION: Conjugation of reduced glutathione to a wide number of
CC exogenous and endogenous hydrophobic electrophiles.
CC -1- CATALYTIC ACTIVITY: RX + glutathione = HX + R-S-glutathione.
CC -1- SUBUNIT: Monomer and homodimer.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the GST superfamily.
DR GO; GO:0005737; C:cytoplasm; NAS.
DR GO; GO:0004364; P:glutathione transferase activity; NAS.
DR GO; GO:0008152; P:metabolism; IC.
KW Direct protein sequencing; Transferase.
FT NON_TER 15
FT NON_TER 15
SQ SEQUENCE 15 AA; 1608 MW; 571C90DA7595077A CRC64;

Query Match 31.9%; Score 23; DB 1; Length 15;
Best Local Similarity 38.5%; Pred. No. 6e+03;
Matches 5; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 3 LLMLFAKDVVSRN 15
Db :|:|:|:|
2 LLVIGSKNLSSTN 14

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RESULT 7
Q9UR28      PRELIMINARY;      PRT;      12 AA.
AC Q9UR28;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE STE12 alpha (Fragment).
GN Name=STE12alpha;
OS Cryptococcus bacillisporus (Filobasidiella neoformans var.
bacillispora).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
OC Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
OX NCBI_TaxID=37769;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99380307; PubMed=10449476;
RA Halliday C.L., Bui T., Krockenberger M., Malik R., Ellis D.H.,
RA Carter D.A.;
RT "Presence of alpha and a mating types in environmental and clinical
RT collections of Cryptococcus neoformans var. gattii strains from
RT Australia.";
RL J. Clin. Microbiol. 37:2920-2926(1999).
DR EMBL; AF155346; AAF20371.1; -
DR EMBL; AF155343; AAF20368.1; -
DR EMBL; AF155344; AAF20369.1; -
DR EMBL; AF155345; AAF20370.1; -
DR EMBL; AF155342; AAF20367.1; -
FT NON_TER 1
FT NON_TER 12
SQ SEQUENCE 12 AA; 1477 MW; 460BA17AB8A729C7 CRC64;

Query Match      30.6%; Score 22; DB 2; Length 12;
Best Local Similarity 57.1%; Pred. No. 7.5e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DRLLMLF 7
DB 3 DRLFLTF 9

RESULT 8
Q15998      PRELIMINARY;      PRT;      14 AA.
AC Q15998;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Neurofibromatosis type 1 gene protein (Fragment).
GN Name=neurofibromatosis type 1 gene;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93216281; PubMed=8395067;
RA Ainsworth P.J., Rodenhiser D.I., Costa M.T.;
RT "Identification and characterization of sporadic and inherited
RT mutations in exon 31 of the neurofibromatosis (NF1) gene.";
RL Hum. Genet. 91:151-156(1993).
DR EMBL; S57966; AAD13890.1; -
FT NON_TER 14
FT NON_TER 14
SQ SEQUENCE 14 AA; 1660 MW; DC7FB5EB30767332 CRC64;

Query Match      30.6%; Score 22; DB 2; Length 14;
Best Local Similarity 66.7%; Pred. No. 8.6e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 RLMLLF 7
DB 1 : : : :

RESULT 9
Q7M4Z6      PRELIMINARY;      PRT;      15 AA.
ID Q7M4Z6;
AC Q7M4Z6;
DT 01-MAR-2004 (TRENBLrel. 26, Created)
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Emiatiin synthetase (Fragment).
OS Fusarium sporotrichoides.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
OX NCBI_TaxID=5514;
RN [1]
RP SEQUENCE.
RA Chow L.P., Fukaya N., Sugiura Y., Ueno Y., Tabuchi K., Teugita A.;
RL Submitted (OCT-1994) to the PIR data bank.
PIR; PA0093; PA0093.
FT NON_TER 1
FT NON_TER 15
SQ SEQUENCE 15 AA; 1828 MW; 5C31D6723D77F4D9 CRC64;

Query Match      30.6%; Score 22; DB 2; Length 15;
Best Local Similarity 80.0%; Pred. No. 9.2e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 LPAKD 10
DB 8 LYAKD 12

RESULT 10
Q38415      PRELIMINARY;      PRT;      11 AA.
ID Q38415;
AC Q38415;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Anti protein (Fragment).
OS Bacteriophage P7.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC P1-like viruses.
OX NCBI_TaxID=10682;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90335968; PubMed=1696181; DOI=10.1016/0092-8674(90)90023-8;
RA Citron M., Schuster H.;
RT "The c4 repressors of bacteriophages P1 and P7 are antisense RNAs.";
RL Cell 62:591-598(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93319637; PubMed=1620606;
RA Citron M., Schuster H.;
RT "The c4 repressor of bacteriophage P1 is a processed 77 base antisense
RT RNA.";
RL Nucleic Acids Res. 20:3085-3090(1992).
DR EMBL; M35139; AAA32437.1; -
DR PIR; S42449; S42449.
FT NON_TER 11
FT NON_TER 11
SQ SEQUENCE 11 AA; 1315 MW; 38A55C6D11B2C737 CRC64;

Query Match      29.2%; Score 21; DB 2; Length 11;
Best Local Similarity 57.1%; Pred. No. 1.1e+04;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 9 KDVWSRN 15
DB 3 KPLVTRN 9

RESULT 11
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Q9R7U8
ID Q9R7U8 PRELIMINARY; PRT; 11 AA.
AC Q9R7U8
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE DNR protein (a regulatory protein for the expression of the nir and
DE nor genes), complete cds. (Fragment).
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PA01;
RX MEDLINE=95226457; PubMed=7711073; DOI=10.1016/0167-4781(95)00018-C;
RA Arai H., Igarashi Y., Kodama T.;
RT "The structural genes for nitric oxide reductase from Pseudomonas
RT aeruginosa.";
RL Biochim. Biophys. Acta 1261:279-284(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=PA01;
RX MEDLINE=95394152; PubMed=7664887; DOI=10.1016/0014-5793(95)00885-D;
RA Arai H., Igarashi Y., Kodama T.;
RT "Expression of the nir and nor genes for denitrification of
RT Pseudomonas aeruginosa requires a novel CRP/FNR-related
RT transcriptional regulator, DNR, in addition to ANR.";
RL FEBS Lett. 371:73-76(1995).
DR EMBL; D50019; BAA08746.1; -.
FT NON TER 1
SQ SEQUENCE 11 AA; 1543 MW; DF363CAE141B5736 CRC64;

Query Match 29.2%; Score 21; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. NO. 1.1e+04;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RLLMLPAK 9
Db 1 RLLQLYRR 8

RESULT 12
Q6TU17 PRELIMINARY; PRT; 13 AA.
ID Q6TU17
AC Q6TU17
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE AF17 D (Fragment).
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_TaxID=6253;
RN [1]
RP SEQUENCE FROM N.A.
RA Nanda J.C., Stretton A.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY386839; AAQ0312.1; -.
FT NON TER 1
SQ SEQUENCE 13 AA; 1531 MW; 18DA23119D6C79C4 CRC64;

Query Match 29.2%; Score 21; DB 2; Length 13;
Best Local Similarity 55.6%; Pred. NO. 1.2e+04;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DRLLMLPAK 9
Db 1 DRNFNMFCK 9

RESULT 13
Q950P6

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ID Q950P6 PRELIMINARY; PRT; 15 AA.
AC Q950P6
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Orf15 (Fragment).
GN Name=orf15;
OS Rhizophydium sp. 136.
OC Mitochondrion.
OC Eukaryota; Fungi; Chytridiomycota; Chytridiales; Chytridiaceae;
OC Rhizophydium.
OX NCBI_TaxID=60187;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=136;
RX MEDLINE=21851207; PubMed=11861890;
RA Forget L., Ustinova J., Wang Z., Hues V.A.R., Lang B.F.;
RT "Hyaloraphidium curvatum: a linear mitochondrial genome, tRNA editing,
RT and an evolutionary link to lower fungi.";
RL Mol. Biol. Evol. 19:310-319(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=136;
RL Lang F.B.P.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF040306; AAK84262.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 1
SQ SEQUENCE 15 AA; 1721 MW; 99ABBEFDA9D6BCAE CRC64;

Query Match 29.2%; Score 21; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. NO. 1.4e+04;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LLMMLPA 8
Db 9 LMLLPA 14

RESULT 14
GS09 BACSU STANDARD; PRT; 10 AA.
ID GS09 BACSU
AC P80243, 1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE General stress protein 9 (GSP9) (Fragment).
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE.
RC STRAIN=168 / ISS58;
RX MEDLINE=94282319; PubMed=8012595;
RA Voelker U., Engelmann S., Maul B., Riethdorf S., Voelker A.,
RA Schmid R., Mach H., Hecker M.;
RT "Analysis of the induction of general stress proteins of Bacillus
RT subtilis.";
RL Microbiology 140:741-752(1994).
CC -I- INDUCTION: By heat shock, salt stress, oxidative stress, glucose
CC limitation and oxygen limitation.
CC -I- CAUTION: Could not be found in the genome of B.subtilis 168.
KW Direct protein sequencing; Heat shock.
FT NON TER 10
SQ SEQUENCE 10 AA; 1168 MW; 99766442D5A2C05A CRC64;

Query Match 27.8%; Score 20; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. NO. 1.5e+04;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 8 AKDVVS 13
:::|:|

```

Db 1 SRDIVS 6

RESULT 15

Q7M487
 ID Q7M487 PRELIMINARY; PRT; 14 AA.
 AC Q7M487;
 DT 01-MAR-2004 (TREMELrel. 26, Created)
 DT 01-MAR-2004 (TREMELrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
 DE Hemocyanin chain 3C (Fragment)
 OS Androctonus australis (Sahara scorpion).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
 OC Buthida; Buthoidea; Buthidae; Androctonus.
 OX NCBI_TaxID=6858;
 RN [1]
 RP SEQUENCE.
 RA Jolles J., Jolles P., Lamy J., Lamy J.;
 RT "Structural characterization of seven different subunits in
 RT Androctonus australis haemocyanin."
 RL FEBS Lett. 106:289-291(1979).
 DR PIR; G61308; G61308.
 FT NON_TER 1 1
 FT NON_TER 14 14
 SQ SEQUENCE 14 AA; 1670 MW; 7516B699DF604114 CRC64;

Query Match 27.8%; Score 20; DB 2; Length 14;
 Best Local Similarity 66.7%; Pred. No. 2e+04;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RLIMLF 7

Db 8 RILSLF 13

Search completed: February 22, 2005, 09:37:59
 Job time : 53.6667 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 22, 2005, 08:52:23 ; Search time 65.6667 Seconds
(without alignments)
88.346 Million cell updates/sec

Title: US-08-991-628-10

Perfect score: 72

Sequence: 1 DRLMLFAKQVVSRN 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 632537

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	72	100.0	15	2	Aaw04850 Internal
2	31	43.1	15	7	Adk82698 Beta-amy1
3	30	41.7	15	3	Aab19295 Immunogen
4	29	40.3	10	8	Adk08674 Human pap
5	29	40.3	15	2	Aaw97806 PTEN pept
6	28	38.9	15	6	Abu79062 Aggregati
7	28	38.9	15	7	Abw00196 Peptide #
8	27	37.5	10	4	Aab46229 Human APP
9	27	37.5	10	4	Aac96422 Human com
10	27	37.5	11	4	Aam52586 Peptide #
11	27	37.5	12	2	Aar60372 Beta-amy1
12	27	37.5	12	3	Aab10957 Bovine AD
13	27	37.5	12	8	Adr16408 Human Abe
14	27	37.5	13	5	ABP46621 Human Bly
15	27	37.5	13	6	Aas35465 Abeta pep
16	27	37.5	13	7	Aas35467 Abeta pep
17	27	37.5	13	7	Adg97448 scfV VHCD
18	27	37.5	13	8	ADQ37408 Amyloid-b
19	27	37.5	13	8	ADQ37290 Vaccine a
20	27	37.5	14	2	Aay02792 Fragment
21	27	37.5	14	4	Aas03423 Peptide c
22	27	37.5	14	5	ABP46357 Human Bly
23	27	37.5	14	5	ABP46557 Human Bly
24	27	37.5	14	7	ADa07483 Human sec
25	27	37.5	14	7	ADG97184 scfV VHCD

ALIGNMENTS

RESULT 1

AAW04850

ID AAW04850 standard; peptide; 15 AA.

AC AAW04850;

DT 18-FEB-1997 (first entry)

DE Internal fragment of Pseudomonas aeruginosa phosphomannomutase.

KW Tolerisation; self-epitope; antigen; autoimmune disease; autoantigen;
HLA; human leukocyte antigen; T-cell; thymocyte; pemphigus vulgaris;
desmoglein; multiple sclerosis; herpes simplex virus; adenovirus;
phosphomannomutase; human papillomavirus; Epstein-Barr virus;
DNA polymerase; influenza; haemagglutinin; reovirus; sigma protein.

OS Pseudomonas aeruginosa.

PN WO9627387-A1.

PD 12-SEP-1996.

PF 07-MAR-1996; 96WO-US003182.

PR 07-MAR-1995; 95US-00400796.

PA (HARD) HARVARD COLLEGE.

PI Strominger JL, Wucherpfennig KW;

DR WPI; 1996-425218/42.

PT Pemphigus vulgaris auto-antigens and multiple sclerosis non-self antigens
- useful in disease treatment, and method for identification of other
self and non-self antigens implicated in auto-immune disease.

PS Claim 2; Page 44; 58pp; English.

CC Pharmaceutical preparations for tolerisation to antigens comprise either
an isolated human non-collagen or non-mysin basic protein (MBP)
polypeptide which is capable of tolerising an individual to an
autoantigen; or an isolated human pathogen polypeptide capable of
tolerising an individual to that polypeptide. In both cases, the
polypeptide (whether self or non-self) includes an amino acid sequence
corresponding to a sequence motif for a MHC class II protein, such as HLA
-DR, which is associated with a human autoimmune disease and which binds
to the polypeptide to activate autoreactive T-cells in individuals with
the autoimmune disease. This peptide is an internal peptide of

26	27	37.5	14	7	ADG97384	Adg97384 scfV VHCD
27	27	37.5	14	8	ADN41360	Adn41360 Novel hum
28	27	37.5	14	8	ADN36955	Adn36955 Peptide f
29	27	37.5	15	2	AAW02334	Aaw02334 Beta-amy1
30	27	37.5	15	2	AAW89354	Aaw89354 Beta-amy1
31	27	37.5	15	3	AAW65509	Aay65509 Oestrogen
32	27	37.5	15	5	ABG71014	Abg71014 Long form
33	27	37.5	15	5	ABB05162	Abb05162 Beta amy1
34	27	37.5	15	5	AAU86246	Aau86246 Oestrogen
35	27	37.5	15	5	AAE26271	Aae26271 Human bet
36	27	37.5	15	5	ABU79057	Abu79057 Aggregati
37	27	37.5	15	6	ABU79064	Abu79064 Aggregati
38	27	37.5	15	6	ABU79058	Abu79058 Aggregati
39	27	37.5	15	6	ABU79055	Abu79055 Aggregati
40	27	37.5	15	6	ABU79056	Abu79056 Aggregati
41	27	37.5	15	7	ABW00192	Abw00192 Peptide #
42	27	37.5	15	7	ABW00190	Abw00190 Peptide #
43	27	37.5	15	7	ABW00198	Abw00198 Peptide #
44	27	37.5	15	7	ABW00189	Abw00189 Peptide #
45	27	37.5	15	7	ABW00191	Abw00191 Peptide #

CC Pseudomonas aeruginosa phosphomannomutase protein and is implicated as a
 CC foreign epitope involved in the aetiology or in remissions of multiple
 CC sclerosis. It has been shown capable of inducing the proliferation of
 CC autoreactive T-cell clones isolated from multiple sclerosis patients
 XX
 SQ Sequence 15 AA;

Query Match 100.0%; Score 72; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.5e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRLLMLFAKDVVSRN 15
 Db 1 DRLLMLFAKDVVSRN 15

RESULT 2
 ADK82698
 ID ADK82698 standard; peptide; 15 AA.
 XX
 AC ADK82698;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Beta-amyloid peptide #4 recognised by antibody to treat senile dementia.
 XX
 KW fusion antibody; senile dementia; beta-amyloid peptide; fibre;
 immunocell.
 XX
 OS Homo sapiens.
 XX
 PN CN1396183-A.
 XX
 PD 12-FEB-2003.
 XX
 PF 13-JUL-2001; 2001CN-00120278.
 XX
 PR 13-JUL-2001; 2001CN-00120278.
 XX
 PA (ZHAN/) ZHANG X.
 XX
 PI Zhang X, Zhang J;
 XX
 DR WPI; 2003-442233/42.
 XX
 PT Human fusion antibody for reducing cerebral amyloid fibers associated
 with senile dementia.
 XX
 PS Claim 1; Page 2; 26pp; Chinese.
 XX

The invention relates to a human fusion antibody for preventing and
 treating senile dementia. The antibody recognises and binds the beta-
 amyloid peptide and the fibres generated by it. The human antibody FC
 segment recognized by human immunocells are sequentially contained by its
 C terminals from N to C. The fusion gene coding for the antibody is also
 disclosed. This sequence represents a beta-amyloid peptide recognised by
 the antibody.
 XX
 SQ Sequence 15 AA;

Query Match 43.1%; Score 31; DB 7; Length 15;
 Best Local Similarity 70.0%; Pred. No. 81;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 LMLFAKDVVS 13
 Db 2 LVFFAKDVGS 11

RESULT 3
 AAB19295
 ID AAB19295 standard; peptide; 15 AA.
 XX

AC AAB19295;
 XX
 DT 19-FEB-2001 (first entry)
 XX
 DE Immunogenic peptide useful for generating antigen specific T cells.
 XX
 KW Immunogenic peptide; antigen specific T cell; cell proliferation; cancer;
 inflammation; autoimmune disease; dermatological disorder;
 neurodegenerative disorder; atherosclerosis; rheumatoid arthritis;
 osteoporosis; chronic ulcer; psoriasis; cardiovascular disease;
 infectious disease.
 XX
 OS Physeter catodon.
 XX
 PN WO200057920-A2.
 XX
 PD 05-OCT-2000.
 XX
 PF 30-MAR-2000; 2000WO-GB001225.
 XX
 PR 30-MAR-1999; 99GB-00007366.
 XX
 PA (MEDI-) MEDICAL RES COUNCIL.
 XX
 PI Fisher A;
 XX
 DR WPI; 2000-647208/62.
 XX

Regulating expression of transgenes encoding enzymes or hormones in
 mammals, by transforming expandable population of cells with desired
 transgene and regulating cell proliferation by administration of an
 agent.
 XX
 PS Disclosure; Page 22; 37pp; English.
 XX

The present sequence represents an immunogenic peptide, derived from
 myoglobin, which is useful for generating antigen specific T cells. It
 may be used in the course of the invention. The specification describes
 the use of an agent which regulates cell proliferation for modulating the
 levels of production of a gene product of interest in a host organism.
 The method comprises transforming an expandable population of cells with
 a transgene encoding the gene product, expressing the gene in the host
 and regulating proliferation of the population of cells by administration
 of the agent. The method is useful for regulating cell proliferation. The
 method is also useful for delivering one or more transgenes useful in the
 treatment of cancer, inflammation, autoimmune disease, dermatological
 disorder, neurodegenerative disorder, atherosclerosis, rheumatoid
 arthritis, osteoporosis, chronic ulcers, psoriasis, cardiovascular
 diseases and infectious diseases
 XX
 SQ Sequence 15 AA;

Query Match 41.7%; Score 30; DB 3; Length 15;
 Best Local Similarity 35.7%; Pred. No. 1.3e+02;
 Matches 5; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DRLLMLFAKDVVSR 14
 :: ||| ||| ::
 Db 1 NKALELFRKDIAAK 14

RESULT 4
 ADK08674
 ID ADK08674 standard; peptide; 10 AA.
 XX
 AC ADK08674;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Human papillomavirus peptide #729.
 XX
 KW pathogenic virus; alternative reading frame; antigenic determinant;
 virucide; vaccine; therapeutic agent; infection; HPV.

XX OS Human papillomavirus.
 XX PN WO2004011650-A2.
 XX PD 05-FEB-2004.
 XX PF 24-JUL-2003; 2003WO-EP008112.
 XX PR 24-JUL-2002; 2002AT-00001124.
 XX PR 11-JUL-2003; 2003EP-00450171.
 XX PA (INTE-) INTERCELL AG.
 XX PI Mattner F, Schmidt W, Habel A;
 XX DR WPI; 2004-169243/16.
 XX This new polypeptide encoded by an alternative reading frame of a pathogenic PT virus comprising an antigenic determinant, useful for treating or preventing an infection with the pathogenic virus.
 XX PS Claim 18; Page 181; 220pp; English.
 XX CC This invention relates to a novel polypeptide encoded by an alternative reading frame of a pathogenic virus, where the polypeptide starts with a methionine amino acid residue, which comprises an antigenic determinant and more than 7 amino acid residues. The invention may be useful for the production of compounds with a virucide activity or the development of a vaccine. The polypeptide or its fragments may be useful as a therapeutic agent. It is also useful for the manufacture of a medicament for treating or preventing an infection with the pathogenic virus. The present sequence is that of a human papillomavirus (HPV) epitope peptide of the invention.

XX SQ Sequence 10 AA;
 Query Match 40.3%; Score 29; DB 8; Length 10;
 Best Local Similarity 75.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 5 MLPAKDVV 12
 :|||
 Db 1 ILFLKDVV 8

RESULT 5
 AAW97806
 ID AAW97806 standard; peptide; 15 AA.
 XX AC AAW97806;
 XX DT 21-MAY-1999 (first entry)
 XX DE PTEN peptide (aa6-19) used for antibody generation.
 XX KW PTEN; MMAC1; protein tyrosine phosphatase; human; prostate cancer;
 KW brain cancer; prostate cancer; tumour suppressor; Cowden's disease;
 KW neurodegenerative disease; Parkinson's disease; diagnosis; therapy;
 KW antibody.
 XX OS Synthetic.
 OS Homo sapiens.
 XX PN WO9902704-A2.
 XX PD 21-JAN-1999.
 XX PF 08-JUL-1998; 98WO-US014205.
 XX PR 08-JUL-1997; 97US-0051908P.
 XX PR 29-JUN-1998; 98US-0090984P.

PA (COLD-) COLD SPRING HARBOR LAB.
 XX Tonks NK, Myers MP;
 XX DR WPI; 1999-120905/10.
 XX New use of PTEN phosphatase - for developing products for the diagnosis and treatment of hyperproliferative disorders, e.g. cancers or neurodegenerative disorders such as Parkinson's disease.
 XX PS Example 2; Page 35; 60pp; English.
 XX CC This peptide corresponds to amino acids Lys6-Asp19 of PTEN (see AAW97802), a novel human dual specificity phosphatase that has tumour suppressor activity. It also includes a C-terminal Cys residue, not found in the wild-type PTEN, which was added to aid in the conjugation of the peptide to keyhole limpet haemocyanin. PTEN peptides (see AAW97805-08) were used to immunise rabbits. A rabbit injected with PTEN Glu388-Val403 produced antibodies that recognised endogenous PTEN on immunoblots and in immunoprecipitations; this antibody was termed PTEN486. All other rabbits failed to produce antibodies that could recognise PTEN. PTEN polypeptides and polynucleotides (see AAX07339) can be used to develop products for the diagnosis and treatment of hyperproliferative disorders such as cancers, or neurodegenerative disorders such as Parkinson's disease

XX SQ Sequence 15 AA;
 Query Match 40.3%; Score 29; DB 2; Length 15;
 Best Local Similarity 71.4%; Pred. No. 1.9e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 9 KDVVSRN 15
 :|||
 Db 1 KEIVSRN 7

RESULT 6
 ABU79062
 ID ABU79062 standard; peptide; 15 AA.
 XX AC ABU79062;
 XX DT 17-JUN-2003 (first entry)
 XX DE Aggregation blocking peptide #14.
 XX KW Amyloid formation; amyloid-like deposit; Alzheimer's disease;
 KW pathological beta-sheet-rich conformation; Down's syndrome;
 KW amyloidosis disorder; human prion disease; kuru; CJD;
 KW Creutzfeldt-Jakob disease; Gerstmann-Strausler-Scheinker syndrome; GSS;
 KW prion associated human neurodegenerative disease; animal prion disease;
 KW scrapie; spongiform encephalopathy; transmissible mink encephalopathy;
 KW chronic wasting disease.
 XX OS Unidentified.
 OS US6462171-B1.
 XX PN 08-OCT-2002.
 XX PF 12-DEC-1996; 96US-00766596.
 XX PR 07-JUN-1995; 95US-00478326.
 XX PR 10-APR-1996; 96US-00630645.
 XX PA (UJNY) UNIV NEW YORK STATE.
 XX PI Soto-Jara C, Baumann MH, Frangione B;
 XX DR WPI; 2003-379012/36.
 XX Novel inhibitory peptides which inhibit and structurally block abnormal folding of protein into amyloid or amyloid-like deposit and into

PT pathological beta-sheet rich conformation, useful for treating
 PT Alzheimer's disease.
 XX
 PS Disclosure; Col 51-52; 51pp; English.
 XX
 CC The invention describes an isolated inhibitory peptide (I) which
 CC interacts with a hydrophobic beta-sheet forming cluster of amino acid
 CC residues on a protein or peptide for amyloid or amyloid-like deposit
 CC formation, and inhibits or structurally blocks the abnormal folding of
 CC proteins and peptides into amyloid or amyloid-like deposits and into
 CC pathological beta-sheet rich conformation. (I) is useful for disorders or
 CC diseases associated with abnormal protein folding into amyloid or amyloid
 CC -like deposits or into pathological beta-sheet-rich precursors of such
 CC disorders, human prion diseases, such as kuru, Creutzfeldt-Jakob disease
 CC (CJD), Gerstmann-Strausler-Scheinker syndrome (GSS), prion associated
 CC human neurodegenerative diseases as well as animal prion diseases such as
 CC scrapie, spongiform encephalopathy, transmissible mink encephalopathy and
 CC chronic wasting disease of mule deer and elk. (I) is also useful for
 CC detecting and diagnosing the presence or absence of amyloid or amyloid-
 CC like deposits in vivo and its precursors. This is the amino acid sequence
 CC of peptide associated with the inhibition of amyloid or amyloid like
 XX deposits
 XX
 SQ Sequence 15 AA;

Query Match 38.9%; Score 28; DB 6; Length 15;
 Best Local Similarity 60.0%; Pred. No. 3e+02; Indels 0; Gaps 0;
 Matches 6; Conservative 2; Mismatches 2;

Qy 4 LMLFAKDQVVS 13
 | : ||: ||
 Db 6 LVFPADQVPS 15

RESULT 7
 ABW00196
 ID ABW00196 standard; peptide; 15 AA.

AC ABW00196;

DT 15-JAN-2004 (first entry)

DE Peptide #14 used in the invention.

XX Amyloid-like fibril deposit; prion related encephalopathy; gene therapy;
 KW Alzheimer's disease.

OS Unidentified.

PN US2003087407-A1.

PD 08-MAY-2003.

PF 06-SEP-2002; 2002US-00235483.

PR 07-JUN-1995; 95US-00478326.

PR 10-APR-1996; 96US-00630645.

XX 12-DEC-1996; 96US-00766596.

PA (UUNY) UNIV NEW YORK STATE.

PI Soto-Jara C, Baumann MH, Frangione B;

DR WPI; 2003-616149/58.

XX New inhibitory peptide, useful for preparing a composition for
 PT diagnosing, preventing or treating disorders associated with amyloid-like
 PT fibril deposits, e.g. Alzheimer's disease, or prion related
 PT encephalopathies.

PS Claim 1; Page 27; 52pp; English.

XX

CC The invention relates to inhibitory peptide comprising a portion of at
 CC least three amino acid residues and a sequence predicted not to adopt a
 CC beta-sheet structure that associates with a hydrophobic beta-sheet
 CC cluster on a protein or peptide involved in the abnormal folding into a
 CC beta-sheet structure, to structurally block the abnormal folding of the
 CC protein or peptide. The inhibitory peptide is useful for preparing a
 CC composition for preventing, treating or detecting disorders or diseases
 CC associated with amyloid-like fibril deposits e.g. Alzheimer's disease and
 CC prion related encephalopathies. The invention is also useful in gene
 CC therapy. The present sequence is a peptide used in the invention
 XX

SQ Sequence 15 AA;

Query Match 38.9%; Score 28; DB 7; Length 15;

Best Local Similarity 60.0%; Pred. No. 3e+02; Indels 0; Gaps 0;
 Matches 6; Conservative 2; Mismatches 2;

Qy 4 LMLFAKDQVVS 13
 | : ||: ||
 Db 6 LVFPADQVPS 15

RESULT 8

AAB46229
 ID AAB46229 standard; peptide; 10 AA.

XX AAB46229;

DT 04-APR-2001 (first entry)

DB Human APP derived immunogenic peptide #25.

XX Amyloid deposit; APP; Abeta; brain; human; clearing response; nootropic;
 KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;
 KW amyloid precursor protein; Alzheimer's disease.

OS Homo sapiens.

PN WO2000072880-A2.

PD 07-DEC-2000.

PF 26-MAY-2000; 2000WO-US014810.

PR 28-MAY-1999; 99US-00322289.

XX (NEUR-) NEURALAB LTD.

PI Schenk DB, Bard F, Vasquez NJ, Yednock T;

XX WPI; 2001-032104/04.

XX Preventing or treating a disease associated with amyloid deposits,
 PT especially Alzheimer's disease, comprises administering amyloid specific
 PT antibody.

PS Disclosure; Fig 19; 143pp; English.

XX This invention describes a novel method of preventing or treating a
 CC disease associated with amyloid deposits of amyloid precursor protein
 CC (APP) Abeta fragments in the brain of a patient, which comprises
 CC administering to the patient: (a) an antibody that binds to Abeta, the
 CC antibody binds to an amyloid deposit and induces a clearing response (Fc
 CC receptor mediated phagocytosis) against it (b) a polypeptide containing
 CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
 CC that induces an immunogenic response against residues 1-3 to 7-11 of
 CC Abeta. The products of the invention have nootropic and neuroprotective
 CC activity. The method is also useful for monitoring a course of treatment
 CC being administered to a patient e.g. active and passive immunization. The
 CC methods are useful for prophylactic and therapeutic treatment of
 CC Alzheimer's disease

XX Sequence 10 AA;

XX

Query Match 37.5%; Score 27; DB 4; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.9e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 LMLFAKDVS 13
: : : : :
DB 1 LVFFAEDVGS 10

RESULT 9
AAG96422
ID AAG96422 standard; peptide; 10 AA.
XX
AC AAG96422;
XX
DT 18-SEP-2001 (first entry)
XX
DE Human complementary peptide, SEQ ID NO: 2616.
XX
KW Human; complementary peptide; ligand; drug discovery; drug design.
XX
OS Homo sapiens.
XX
PN WO200142277-A2.
XX
PD 14-JUN-2001.
XX
PF 13-DEC-2000; 2000WO-GB004776.
XX
PR 13-DEC-1999; 99GB-00029464.
XX
PA (PROT-) PROTEOM LTD.
XX
PI Roberts GW, Heal JR;
XX
DR WPI; 2001-408419/43.
XX
PT A set of peptide ligands consisting of specific complementary peptides to
PT proteins encoded by genes of the human genome, useful in an assay for
PT screening and identifying of one or more novel peptides which are drug
PT candidates or pro-drugs.
XX
PS Example 4; Page 416; 646pp; English.
XX
CC The invention relates to a set of complementary peptide ligands generated
CC from the human genome. The complementary peptides interact with their
CC relevant target proteins encoded in the human genome. They can be used as
CC reagents in drug discovery and as lead ligands to facilitate drug design
CC and development. The present sequence is a complementary peptide provided
CC in the specification
XX
SQ Sequence 10 AA;

Query Match 37.5%; Score 27; DB 4; Length 10;
Best Local Similarity 44.4%; Pred. No. 2.9e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 7 FAKDVSRN 15
: : : : :
DB 2 YSKDTLGRN 10

RESULT 10
AAM52586
ID AAM52586 standard; peptide; 11 AA.
XX
AC AAM52586;
XX
DT 07-FEB-2002 (first entry)
XX
DE Peptide #16 for illustrating method of anticipating protein interaction.
XX

KW Protein interaction; biochemistry; molecular biology; drug development;
KW agrochemical; bioengineering.
XX
OS Unidentified.
XX
PN WO200167299-A1.
XX
PD 13-SEP-2001.
XX
PF 09-MAR-2001; 2001WO-JP001846.
XX
PR 10-MAR-2000; 2000JP-00072485.
XX
PA (DAUC) DAIICHI PHARM CO LTD.
XX
PI (FUIT) FUJITSU LTD.
XX
PI Doi H, Suzuki A;
XX
DR WPI; 2001-570799/64.
XX
PT Method for assaying a specific protein for assaying anticipated
PT information.
XX
PS Example 14; Page 34; 64pp; Japanese.
XX
CC The present invention relates to a method for anticipating interaction
CC between proteins. The method comprises (1) digesting protein A into
CC oligopeptides; (2) searching a protein sequence database for polypeptides
CC (polypeptide C) containing these oligopeptide sequences or D their
CC homologues; (3) performing a local alignment of A and detected C or D;
CC and (4) using a value calculated from the amino acid or oligonucleotide
CC frequencies, anticipating that C or D is polypeptide B that interacts
CC with A. The method is useful for assaying anticipated information about
CC proteins in biochemical, molecular biology, drug development,
CC agrochemical and bioengineering areas. The present sequence was used to
CC illustrate the method
XX
SQ Sequence 11 AA;

Query Match 37.5%; Score 27; DB 4; Length 11;
Best Local Similarity 60.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 LMLFAKDVS 13
: : : : :
DB 2 LVFFAEDVGS 11

RESULT 11
AAR60372
ID AAR60372 standard; peptide; 12 AA.
XX
AC AAR60372;
XX
DT 25-MAR-2003 (revised)
XX
DT 15-MAR-1995 (first entry)
XX
DE Beta-amyloid (17-28).
XX
KW Amyloid precursor protein; APP; Alzheimer's disease; beta-amyloid;
KW anti-beta-amyloid antibody; diagnosis.
XX
OS Homo sapiens.
XX
PN WO9417197-A1.
XX
PD 04-AUG-1994.
XX
PF 24-JAN-1994; 94WO-JP000089.
XX
PR 25-JAN-1993; 93JP-00010132.
XX
PR 05-FEB-1993; 93JP-00019035.
XX
PR 16-NOV-1993; 93JP-00286985.

PR 28-DEC-1993; 93JP-00334773.
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX Suzuki N, Odaka A, Kitada C;
 FI WPI; 1994-264110/32.
 XX Antibodies recognising specific parts of beta-amyloid - can be used for
 PT diagnosis of diseases implicating beta-amyloid, such as Alzheimer's
 PT disease.
 XX Disclosure; Page 85; 116pp; Japanese.
 XX Antibodies which recognise specific subfragments of the beta-amyloid
 CC protein are claimed. Specifically, the antibodies (which are pref.
 CC monoclonal) recognise residues 1-16 and/or 1-28 from the N-terminal
 CC portion of beta-amyloid or they recognise residues 25-35 or 35-43 from
 CC the C-terminal portion. The antibodies are useful for assaying beta-
 CC amyloid and its derivatives for diagnosis of Alzheimer's disease.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX Sequence 12 AA;
 SQ Query Match 37.5%; Score 27; DB 2; Length 12;
 Best Local Similarity 60.0%; Pred. No. 3.6e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 4 LMLFAKDVS 13
 | : ||| |
 Db 1 LVFFAEDVGS 10
 | : ||| |
 RESULT 12
 AAB10957
 ID AAB10957 standard; protein; 12 AA.
 XX AAB10957;
 XX 07-FEB-2001 (first entry)
 DT DT
 DE Bovine ADAM 10 peptide substrate #2.
 XX APP; amyloid precursor protein; human; alpha-secretase; ADAM 10;
 KW disintegrin-metalloprotease; protease; neuroprotective;
 KW gene therapy; Alzheimer's disease.
 XX Bos taurus.
 OS DE19910108-A1.
 PN 21-SEP-2000.
 PD 08-MAR-1999; 99DE-01010108.
 XX 08-MAR-1999; 99DE-01010108.
 PR (FAHR/) FAHRENHOLZ F.
 PA Fahrenheit F, Postina R;
 XX WPI; 2000-588391/56.
 XX Recombinant cells, for identifying alpha-secretase active agents and
 PT identifying risk factors associated with Alzheimer's disease, comprise
 PT amyloid precursor protein and alpha-secretase.
 XX Disclosure; Page 6; 24pp; German.
 XX This invention describes a novel recombinant cell comprising recombinant
 CC nucleic acids encoding a region of human amyloid precursor protein
 CC containing an alpha-secretase cleavage site and a protease or a
 CC heterologous RNA coding for a substrate protein and a protease. The

CC invention also describes a recombinant cell, characterized in that it
 CC contains recombinant nucleic acids comprising either: (a) a gene for a
 CC substrate protein (SP), which comprises a sequence region of 18 amino
 CC acids of the human amyloid precursor protein (APP) or a homologous
 CC protein, where the sequence region contains the alpha-secretase cleavage
 CC site at a reference of 6 residues at the N-terminal and 12 residues at
 CC the C-terminal; and (b) a gene for a protease protein (PP), that either
 CC comprises a proteolytically active necessary sequence region or a
 CC sequence region of the disintegrin metalloprotease ADAM 10 from a cow
 CC (Bos taurus), from a human or other mammal or a mutant of this, which
 CC shows the same enzymatic properties, where the genes are under the
 CC control of heterologous promoters; or a heterologous RNA coding for a SP
 CC and a PP. The products of the invention have neurotropic and
 CC neuroprotective activity and can be used for gene therapy. The protease
 CC proteins of the invention are useful for proteolytic cleavage of
 CC substrate proteins, especially human amyloid precursor protein. Dominant
 CC negative forms of bovine, human or other mammalian disintegrin-
 CC metalloprotease ADAM 10 proteins and their coding sequences are useful
 CC for suppressing the alpha-secretase activity of a cell. Nucleic acid
 CC sequences encoding the proteases are useful for constructing vectors for
 CC gene therapy. The proteins and recombinant cells are useful for
 CC identifying secretases and pharmaceutical agents and to identify risk
 CC factors associated with Alzheimer's disease
 XX Sequence 12 AA;
 SQ Query Match 37.5%; Score 27; DB 3; Length 12;
 Best Local Similarity 60.0%; Pred. No. 3.6e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 4 LMLFAKDVS 13
 | : ||| |
 Db 1 LVFFAEDVGS 10
 | : ||| |
 RESULT 13
 ADR16408
 ID ADR16408 standard; peptide; 12 AA.
 XX ADR16408;
 AC ADR16408;
 XX 21-OCT-2004 (first entry)
 DT DT
 DE Human Abeta (amyloid-beta) tryptic peptide.
 XX Alzheimer's Disease; AD; ocular tissue; lens; amyloidogenic disorder;
 KW Creutzfeld-Jakob disease; spongiform encephalopathy; Prion disease;
 KW scrapie; bovine spongiform encephalopathy; veterinary prionopathy;
 KW Parkinson's disease; Huntington's disease; trinucleotide repeat disease;
 KW amyotrophic lateral sclerosis; Down's Syndrome; Pick's Disease;
 KW Frontotemporal Dementia; Lewy Body Disease; Hallervorden-Spatz Disease;
 KW synucleinopathy; multiple system atrophy;
 KW neuronal intranuclear inclusion disease; tauopathy;
 KW progressive supranuclear palsy; corticobasal degeneration; human;
 KW amyloid-beta; Abeta.
 XX Homo sapiens.
 OS US2004152068-A1.
 XX 05-AUG-2004.
 PD 18-NOV-2003; 2003US-00715776.
 PF 21-AUG-2000; 2000US-0226590P.
 XX 27-APR-2001; 2001US-0287124P.
 PR 21-AUG-2001; 2001US-00935126.
 PR 25-APR-2002; 2002US-00132779.
 PR 18-NOV-2002; 2002US-0427153P.
 PR 05-MAR-2003; 2003US-0452336P.
 XX (GOLD/) GOLDSTEIN L E.
 PA (CHYL/) CHYLACK L T.

XX Goldstein LE, Chylack LT;
XX WPI; 2004-580178/56.
XX Method for diagnosing Alzheimer's disease in a mammal involves contacting
PT an ocular tissue with a detectably-labeled compound that binds to an
PT amyloid protein or use of magnetic resonance imaging.
XX
XX Example 3; SEQ ID NO 1; 23pp; English.
XX
XX The invention relates to a method for diagnosing or providing a prognosis
CC regarding the state of Alzheimer's Disease (AD) in a mammal. The method
CC involves contacting an ocular tissue with a detectably-labeled compound
CC that binds to an amyloid protein where an increase in binding of the
CC compound to the ocular tissue compared to the normal control level of
CC binding indicates that the mammal is suffering from or is at risk of
CC developing AD. The method is also used for the diagnosis of amyloidogenic
CC disorder e.g. Familial AD, Sporadic AD, Creutzfeld-Jakob disease, variant
CC Creutzfeld-Jakob disease, spongiform encephalopathies, Prion diseases
CC (including scrapie, bovine spongiform encephalopathy and other veterinary
CC prionopathies), Parkinson's disease, Huntington's disease (and
CC trinucleotide repeat diseases), amyotrophic lateral sclerosis, Down's
CC Syndrome (trisomy 21), Pick's disease (Frontotemporal Dementia), Lewy
CC Body Disease, neurodegeneration with brain iron accumulation
CC (Hallervorden-Spatz Disease), synucleinopathies (including Parkinson's
CC disease, multiple system atrophy, dementia with Lewy Bodies, and others),
CC neuronal intranuclear inclusion disease, tauopathies (including
CC progressive supranuclear palsy, Pick's disease, corticobasal
CC degeneration, hereditary frontotemporal dementia (with or without
CC Parkinsonism) and Guam amyotrophic lateral sclerosis/parkinsonism
CC dementia complex). The present sequence is human amyloid-beta (Abeta)
CC peptide. This sequence is used to illustrate the method of the invention.
XX
XX Sequence 12 AA;
SQ

Query Match 37.5%; Score 27; DB 8; Length 12;
Best Local Similarity 60.0%; Pred. No. 3.6e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 4 LMLFAKDVVS 13
|: ||: ||: |
DB 1 LVFFAEDVGS 10

RESULT 14
ABP46621
ID ABP46621 standard; peptide; 13 AA.
XX
XX ABP46621;
XX
XX 19-AUG-2002 (first entry)
XX
XX Human Blys binding scFv VH CDR3 SEQ ID 2632.
XX
XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
KW tumour necrosis factor; B cell proliferation; B cell differentiation;
KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
KW common variable immunodeficiency; acquired immunodeficiency syndrome.
XX
XX Homo sapiens.
XX
XX WO200202641-A1.
XX
XX 10-JAN-2002.
XX
XX 15-JUN-2001; 2001WO-US019110.
XX
XX 16-JUN-2000; 2000US-0212210P.
XX
XX 17-OCT-2000; 2000US-0240816P.
XX
XX 16-MAR-2001; 2001US-0276248P.

PR 21-MAR-2001; 2001US-0277379P.
PR 25-MAY-2001; 2001US-0293499P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX WPI; 2002-114799/15.
XX
XX Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
PT diagnosis and treatment of cancers and immune disorders.
XX
XX Claim 2; Page 3023; 3148pp; English.
XX
XX This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX
XX Sequence 13 AA;
SQ

Query Match 37.5%; Score 27; DB 5; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.9e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 2 RLMLFAKDVVS 13
|: ||: ||: |
DB 2 RDLLEFPNDALS 13

RESULT 15
AAE35465
ID AAE35465 standard; peptide; 13 AA.
XX
XX AAE35465;
XX
XX 17-JUN-2003 (first entry)
XX
XX Abeta peptide #36.
XX
XX All-D-amyloid-beta peptide; Alzheimer's disease; rheumatoid arthritis;
KW cerebral amyloid angiopathy; amyloid disease; ankylosing spondylitis;
KW psoriasis; Reiter's syndrome; Adult Still's disease; Bechet's syndrome;
KW Crohn's disease; infection; leprosy; tuberculosis; carcinoma; neurotropic;
KW chronic pyelonephritis; osteomyelitis; Whipple's disease; vasotropic;
KW Hodgkin's lymphoma; neuroprotective; bronchiectasis; ophthalmological;
KW ulcer; antiinflammatory; cytostatic; uropathic; therapy.
XX
XX Unidentified.
XX
XX OS
XX Key Location/Qualifiers
FH Misc-difference 1. .6
FT /note= "D-form residues"
XX
XX WO200296937-A2.
XX
XX 05-DEC-2002.
XX
XX 29-MAY-2002; 2002WO-CA000763.

XX 29-MAY-2001; 2001US-00867847.
PR (NEUR-) NEUROCHEM INC.
XX Gervais F, Hebert L, Chalifour RJ, Kong X;
XX WPI; 2003-201269/19.
DR Prevention and/or treatment of an amyloid-related disease e.g.
XX Alzheimer's disease, comprises use of all-D-amyloid-beta peptides.
PT Claim 1; Page 61; 44pp; English.
XX
XX The invention relates to a method for prevention and/or treatment of an
CC amyloid-related disease which comprises administration of an all-D -
CC amyloid-beta peptide. The method is used for preventing and/or treating
CC Alzheimer's and other amyloid related disease e.g. cerebral amyloid
CC angiopathy; for altering serum levels of amyloid-beta in a mammal and
CC favours the clearance of soluble amyloid-beta or fibril amyloid-beta from
CC the mammal; and reducing or inhibiting the formation of plaques. It is
CC also used for treating AA (reactive) amyloid diseases including
CC inflammatory diseases e.g. rheumatoid arthritis, juvenile chronic
CC arthritis, ankylosing spondylitis, psoriasis, psoriatic arthropathy,
CC Reiter's syndrome, Adult Still's disease, Bechet's syndrome and Crohn's
CC disease. AA deposits are also produced as a result of chronic microbial
CC infections (preferably leprosy, tuberculosis, bronchiectasis, decubitus
CC ulcers, chronic pyelonephritis, osteomyelitis and Whipple's disease).
CC Certain malignant neoplasms can also result in AA fibril amyloid deposits
CC including Hodgkin's lymphoma, renal carcinoma, carcinomas of gut, lung
CC and urogenital tract, basal cell carcinoma and hairy cell leukaemia. The
CC present sequence is an Abeta peptide used to illustrate the method of the
CC invention
XX
SQ Sequence 13 AA;

Query Match 37.5%; Score 27; DB 6; Length 13;
Best Local Similarity 60.0%; Pred. NO. 3.9e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 LMLFAKDVVS 13
| : | : | : |
Db 2 LVFFAEDVGS 11

Search completed: February 22, 2005, 09:24:48
Job time : 67.6667 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 22, 2005, 09:08:09 ; Search time 11.1333 Seconds
(without alignments)
129.633 Million cell updates/sec

Title: US-08-991-628-11

Perfect score: 79

Sequence: 1 IGRVHFVKDISPIA 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 2523

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	32.9	15	2 PH0775	T-cell receptor al
2	26	32.9	15	2 PH0779	T-cell receptor al
3	26	32.9	15	2 PH1455	T-cell receptor al
4	24	30.4	12	2 S26557	T-cell receptor be
5	23	29.1	14	2 S29632	xylan 1,4-beta-xy
6	22	27.8	10	2 A58365	neuropeptide FRFa
7	22	27.8	11	2 S60354	retinal oxidase -
8	21	26.6	10	2 A60476	S-layer protein -
9	21	26.6	11	2 PC2330	cycloinulooligosac
10	21	26.6	12	2 S01749	collagen alpha 1(I
11	21	26.6	14	2 PN0151	omega-gliadin 2,
12	20	25.3	9	2 PT0670	T-cell receptor be
13	20	25.3	13	2 S15755	actin 7 - soybean
14	20	25.3	14	2 PH0804	T-cell receptor al
15	20	25.3	14	2 FC4376	telomeric and tet
16	20	25.3	15	2 S24159	leukocyte elastase
17	20	25.3	15	2 PA0054	protein QF200017 -
18	20	25.3	15	2 PA0061	protein QF200039 -
19	19	24.1	7	2 PN0150	omega-gliadin 1,
20	19	24.1	11	2 A34243	H-hyosphorin - Ja
21	19	24.1	12	2 A09985	gamma-crystallin -
22	19	24.1	12	2 PT0228	lg heavy chain CDR
23	19	24.1	13	2 D61491	seed protein ws-4
24	19	24.1	14	2 F33160	H+-transporting tw
25	19	24.1	14	2 PN0147	omega-gliadin 1 a
26	19	24.1	15	2 PT0205	insulin-like growt
27	19	24.1	15	2 PD0444	coupling factor 6
28	18	22.8	11	2 FC2173	triacylglycerol 11
29	18	22.8	11	2 S57575	T cell receptor V-

30 18 22.8 12 2 P00730 unidentified 5.4/3
31 18 22.8 13 2 S47380 T-cell antigen rec
32 18 22.8 13 2 H56046 urinary tract ston
33 18 22.8 14 2 PH0762 T-cell receptor be
34 18 22.8 15 2 PS0185 27K protein A 3.4/
35 18 22.8 15 2 S29485 GTP-binding protei
36 18 22.8 15 2 S47387 T-cell antigen rec
37 18 22.8 15 2 A61247 urogenital tumor m
38 18 22.8 15 2 G49732 NADH2 dehydrogenas
39 17 21.5 4 2 J01273 neuropeptide Antho
40 17 21.5 7 2 I48086 DNA topoisomerase
41 17 21.5 7 2 PT0667 T-cell receptor be
42 17 21.5 9 2 D24180 fibrinogen beta ch
43 17 21.5 9 2 F28854 fibrinopeptide B -
44 17 21.5 9 2 PT0634 T-cell receptor be
45 17 21.5 9 2 A42266 peptidylglycine mo

ALIGNMENTS

RESULT 1

PH0775

T-cell receptor alpha chain (B28) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PH0775

R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.

J. Exp. Med. 174, 1371-1383, 1991
A>Title: T cell receptor genes in a series of class I major histocompatibility complex-
allelic exclusion and antigen-specific repertoire.

A:Reference number: PH0746; MUID:92078846; PMID:1836010

A:Accession: PH0775

A:Molecule type: mRNA

A:Residues: 1-15 <CAS>

A:Cross-references: EMBL:X60871

A:Experimental source: T lymphocyte

C:Keywords: T-cell receptor

Query Match 32.9%; Score 26; DB 2; Length 15;

Best Local Similarity 80.0%; Pred. No. 2.9e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GRVHF 7

|||

10 GRLHF 14

RESULT 2

PH0779

T-cell receptor alpha chain (B83) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PH0779

R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.

J. Exp. Med. 174, 1371-1383, 1991
A>Title: T cell receptor genes in a series of class I major histocompatibility complex-
allelic exclusion and antigen-specific repertoire.

A:Reference number: PH0746; MUID:92078846; PMID:1836010

A:Accession: PH0779

A:Molecule type: mRNA

A:Residues: 1-15 <CAS>

A:Cross-references: EMBL:X60877

A:Experimental source: T lymphocyte

C:Keywords: T-cell receptor

Query Match 32.9%; Score 26; DB 2; Length 15;

Best Local Similarity 80.0%; Pred. No. 2.9e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GRVHF 7

|||

10 GRLHF 14

RESULT 3
PH1455
T-cell receptor alpha chain (clone A24/PEF4) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 15-Mar-2004
C:Accession: PH1455
R;Caanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; Kojima, Y.; Exp. Med. 177, 811-820, 1993
A:Title: T cell receptor selection by and recognition of two class I major histocompatibility complex peptides
A:Reference number: PH1430; MUID:93171821; PMID:8436911
A:Accession: PH1455
A:Molecule type: mRNA
A:Residues: 1-15 <CAS>
A:Experimental source: cytolytic T-lymphocyte
C:Keywords: receptor; T-cell

Query Match 32.9%; Score 26; DB 2; Length 15;
Best Local Similarity 80.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GRVHF 7
Db 10 GRLHF 14

RESULT 4
S26557
T-cell receptor beta chain (clone Cw3/HLA2A3) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 17-Apr-1998 #text_change 17-Mar-1999
C:Accession: S26557
R;Caanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Widmer, J.; Exp. Med. 176, 439-447, 1992
A:Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor peptides
A:Reference number: S26512; MUID:92364546; PMID:1380061
A:Accession: S26557
A:Molecule type: mRNA
A:Residues: 1-12 <CAS>
A:Experimental source: EMBL:X68007
A:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor

Query Match 30.4%; Score 24; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 5.3e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GRVHFP 8
Db 6 GRVEYF 11

RESULT 5
S29632
Xylan 1,4-beta-xylosidase (EC 3.2.1.37) - Thermotoga sp. (strain FjSS3-B.1) (fragment)
N:Alternate names: beta-xylosidase
C:Species: Thermotoga sp.
A:Variety: FjSS3-B.1
C:Date: 19-Mar-1997 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C:Accession: S29632
R;Ruttersmith, L.D.; Daniel, R.M.; Biochim. Biophys. Acta 1156, 167-172, 1993
A:Title: Thermostable beta-glucosidase and beta-xylosidase from Thermotoga sp. strain FjSS3-B.1
A:Reference number: S29631; MUID:93152594; PMID:8427876
A:Accession: S29632
A:Molecule type: protein
A:Residues: 1-14 <RUT>
A:Experimental source: UNIPROT:Q7MQ06
C:Comment: Although the beta-xylosidase enzyme activity was apparently confirmed for this strain, the xylanase activity was not confirmed.
C:Function:

A:Description: hydrolyzes short chain oligosaccharides and xylobiose to produce D-xylose
A:Note: Plays an important role in the relief of end-product inhibition of endoxylanase
C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 29.1%; Score 23; DB 2; Length 14;
Best Local Similarity 66.7%; Pred. No. 9.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 VHPFKD 10
Db 5 VYFPAD 10

RESULT 6
A58365
neuropeptide FPRFamide - blue mussel
N:Alternate names: FPRFamide-related decapeptide; Mytilus FPRFamide
C:Species: Mytilus edulis (blue mussel)
C:Date: 20-Nov-1996 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004
C:Accession: A58365
R;Fujisawa, Y.; Ikeda, T.; Nomoto, K.; Yasuda-Kamatani, Y.; Minakata, H.; Kenny, P.T.M.; Comp. Biochem. Physiol. C 102, 91-95, 1992
A:Title: The FPRFamide-related decapeptide of Mytilus contains a D-amino acid residue.
A:Reference number: A58365; MUID:93047882; PMID:1358533
A:Accession: A58365
A:Molecule type: protein
A:Residues: 1-10 <FOU>
A:Cross-references: UNIPROT:P42560
A:Experimental source: anterior byssus retractor muscle
C:Keywords: amidated carboxyl end; D-amino acid; neuropeptide
F;2/Modified site: D-leucine (Ileu) #status experimental
F;10/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 27.8%; Score 22; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 9.9e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 HPEK 9
Db 6 HPEK 9

RESULT 7
S60354
retinal oxidase - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C:Accession: S60354
R;Huang, D.Y.; Ichikawa, Y.; Biochim. Biophys. Acta 1243, 431-436, 1995
A:Title: Identification of essential lysyl and cysteinyl residues, and the amino acid sequence of retinal oxidase from rabbit
A:Reference number: S60354; MUID:95244596; PMID:7727518
A:Accession: S60354
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-11 <HUA>

Query Match 27.8%; Score 22; DB 2; Length 11;
Best Local Similarity 80.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGRVH 6
Db 1 GGDVH 5

RESULT 8
A60476
S-layer protein - Bacillus thuringiensis (fragment)
C:Species: Bacillus thuringiensis
C:Date: 20-Feb-1993 #sequence_revision 20-Feb-1993 #text_change 09-Jul-2004
C:Accession: A60476
R;Luckevich, M.D.; Beveridge, T.J.

J. Bacteriol. 171, 6656-6667, 1989
A>Title: Characterization of a dynamic S layer on *Bacillus thuringiensis*.
A:Reference number: A60476; MUID:90078111; PMID:2592346
A:Accession: A60476
A:Molecule type: protein
A:Residues: 1-10 <LUC>
A:Cross-references: UNIPROT:P49325
C:Comment: The S-layer, or surface array, is the outermost component of several archaea

Query Match 26.6%; Score 21; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 FPKDISP 13
| | | |
DB 5 FPDVXP 10

RESULT 9
PC2330
cyclooligooligosaccharide fructanotransferase (EC 2.4.-.-) - *Bacillus circulans* (MCI-255)
C:Species: *Bacillus circulans*
C:Date: 21-Mar-1995 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C:Accession: PC2330
R:Kushibe, S.; Mitsu, K.; Yamagishi, M.; Yamada, K.; Morimoto, Y.
Biosci. Biotechnol. Biochem. 59, 31-34, 1995
A>Title: Purification and characterization of cyclooligooligosaccharide fructanotransferase
A:Reference number: PC2330; MUID:95201377; PMID:7765973
A:Accession: PC2330
A:Molecule type: protein
A:Residues: 1-11 <KUS>
A:Cross-references: UNIPROT:Q7MOL3
C:Comment: This enzyme hydrolyzes beta-(2-1) glycosidic linkages and acts in intermolecular
C:Keywords: glycosyltransferase; hexosyltransferase

Query Match 26.6%; Score 21; DB 2; Length 11;
Best Local Similarity 37.5%; Pred. No. 1.7e+03;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 HFFKDISP 13
| | | |
DB 2 HLFYQWNP 9

RESULT 10
S01749
collagen alpha 1(I) chain - mouse (fragment)
C:Species: *Mus musculus* (house mouse)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C:Accession: S01749; S21415
R:Mooslehner, K.; Harbers, K.
Nucleic Acids Res. 16, 773, 1988
A>Title: Two mRNAs of mouse pro alpha-1(I) collagen gene differ in the size of the 3'-untranslated region
A:Reference number: S01749; MUID:88124276; PMID:3340560
A:Accession: S01749
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-12 <MOO>
A:Cross-references: UNIPROT:Q925V7; EMBL:X06753; NID:G50499; PIDN:CAA29927.1; PID:G50500
R:Mooslehner, K.; Harbers, K.
submitted to the EMBL Data Library, July 1989
A:Reference number: S21415
A:Accession: S21415
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-12 <MO2>
A:Cross-references: EMBL:X15896; NID:G50497; PIDN:CAA33904.1; PID:G50498
C:Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology;

Query Match 26.6%; Score 21; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 1.8e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 FPKDISP 14
| | | |
DB 2 FGLDIGPV 9

RESULT 11
PN0151
omega-gliadine 2' - *Aegilops longissima* (fragment)
C:Species: *Aegilops longissima*
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: PN0151
R:Odintsova, T.I.; Egorov, T.A.
Biochimia 55, 509-516, 1990
A>Title: N-Terminal sequences of omega-gliadins of *Aegilops longissima*: On the origin of
A:Reference number: PN0146; MUID:90283493; PMID:2354218
A:Accession: PN0151
A:Molecule type: protein
A:Residues: 1-14 <ODI>
A:Experimental source: strain K-907

Query Match 26.6%; Score 21; DB 2; Length 14;
Best Local Similarity 66.7%; Pred. No. 2.2e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 KDISP 14
| | | |
DB 2 RQISP 7

RESULT 12
PT0670
T-cell receptor beta chain V-D-J region (121-1BN) - mouse (fragment)
C:Species: *Mus musculus* (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0670
R:Peeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A>Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0670
A>Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-9 <PEE>
A:Experimental source: day 4 postnatal thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 25.3%; Score 20; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 IGGRV 5
| | | |
DB 5 LGGRM 9

RESULT 13
S15755
actin 7 - soybean (fragment)
C:Species: *Glycine max* (soybean)
C:Date: 20-Feb-1995 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C:Accession: S15755
R:Pearson, L.; Meagher, R.B.
Plant Mol. Biol. 14, 513-526, 1990
A>Title: Diverse soybean actin transcripts contain a large intron in the 5' untranslated
A:Reference number: S15754; MUID:91346640; PMID:2102831
A:Accession: S15755
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-13 <PEA>
A:Cross-references: UNIPROT:P15987; EMBL:X17120; NID:G18527; PIDN:CAA34980.1; PID:G18528
C:Superfamily: actin
C:Keywords: cytoskeleton; structural protein

Query Match 25.3%; Score 20; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 3e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 9 KDISPI 14
:|:|:
Db 5 EDIQPL 10

RESULT 14

PH0804
T-cell receptor alpha chain (L4) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PH0804
R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A;Title: T cell receptor genes in a series of class I major histocompatibility complex-
allelic exclusion and antigen-specific repertoire.
A;Reference number: PH0746; MUID:92078846; PMID:1836010
A;Accession: PH0804
A;Molecule type: mRNA
A;Residues: 1-14 <CAS>
A;Cross-references: EMBL:X60913
A;Experimental source: T lymphocyte
C;Keywords: T-cell receptor

Query Match 25.3%; Score 20; DB 2; Length 14;
Best Local Similarity 57.1%; Pred. No. 3.2e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGRVHF 8
|||:
Db 7 GGRALIF 13

RESULT 15

PC4376
telomeric and tetraplex DNA binding protein qTBP42 VII - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Oct-1997 #sequence_revision 28-Oct-1997 #text_change 09-Jul-2004
C;Accession: PC4376
R;Sarif, G.; Weisman-Shomer, P.; Fry, M.
Biochem. Biophys. Res. Commun. 237, 617-623, 1997
A;Title: Telomeric and tetraplex DNA binding properties of qTBP42: A homologue of the CA
A;Reference number: PC4371; MUID:97445086; PMID:9299414
A;Accession: PC4376
A;Molecule type: protein
A;Residues: 1-14 <SAR>
A;Cross-references: UNIPROT:Q9QX80; UNIPROT:Q920U8; UNIPROT:O88311; UNIPROT:Q9QX81
C;Comment: This protein binds either strand of the telomeric DNA as well as unimolecular

Query Match 25.3%; Score 20; DB 2; Length 14;
Best Local Similarity 42.9%; Pred. No. 3.2e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 8 FKDISPI 14
||:|:
Db 7 FKEDPV 13

Search completed: February 22, 2005, 09:46:28

Job time : 11.133 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 22, 2005, 08:53:13 ; Search time 52.6 Seconds
(without alignments)
146.030 Million cell updates/sec

Title: US-08-991-628-11

Perfect score: 79

Sequence: 1 IGRVHFFKDISPIA 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 6622

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	30.4	11	2 Q70Y70	Q70Y70 thornicrofti
2	24	30.4	11	2 Q6YBF2	Q6YBF2 streptococc
3	23.5	29.7	14	2 Q71H50	Q71H50 andrena acc
4	23	29.1	10	1 ARHX LOEMI	P81626 locusta mig
5	23	29.1	14	2 Q71GY0	Q71GY0 andrena ofe
6	23	29.1	14	2 Q71H20	Q71H20 andrena dis
7	23	29.1	14	2 Q7M0Q6	Q7M0Q6 thermotoga
8	23	29.1	15	2 Q9TWF3	Q9TWF3 dictyosteli
9	22	27.8	10	1 FARP MYTED	P42560 mytilus edu
10	22	27.8	12	2 Q88575	Q88575 theiler's e
11	22	27.8	12	2 Q88576	Q88576 theiler's e
12	22	27.8	12	2 Q88577	Q88577 theiler's e
13	22	27.8	12	2 Q88578	Q88578 theiler's e
14	22	27.8	12	2 Q88579	Q88579 theiler's e
15	22	27.8	12	2 Q88580	Q88580 theiler's e
16	22	27.8	12	2 Q88581	Q88581 theiler's e
17	22	27.8	12	2 Q88582	Q88582 theiler's e
18	22	27.8	14	2 Q71GL0	Q71GL0 andrena ili
19	22	27.8	14	2 Q71GS8	Q71GS8 andrena aff
20	22	27.8	14	2 Q71GZ6	Q71GZ6 andrena kri
21	22	27.8	14	2 Q71H10	Q71H10 andrena hel
22	22	27.8	14	2 Q71H46	Q71H46 andrena ali
23	22	27.8	15	2 Q9MYT7	Q9MYT7 sus scrofa
24	21	26.6	8	2 Q70Y68	Q70Y68 prostather
25	21	26.6	10	1 SLAP BACTG	P49325 bacillus th
26	21	26.6	10	2 Q9UCU6	Q9UCU6 homo sapien
27	21	26.6	10	2 Q8UVW2	Q8UVW2 oreochromis
28	21	26.6	10	2 Q6R7V4	Q6R7V4 carlia zuma
29	21	26.6	11	2 Q7M0L3	Q7M0L3 bacillus ci
30	21	26.6	11	2 Q68LE0	Q68LE0 pyriglena l
31	21	26.6	11	2 Q68LE9	Q68LE9 myrmotherul

32 21 26.6 12 2 Q925V7 mus musculus
33 21 26.6 12 2 Q8UVV8 squalus aca
34 21 26.6 12 2 Q8UVW0 rana catesb
35 21 26.6 14 2 Q6R7V0 carlia viva
36 21 26.6 15 2 Q9OV01 mus sp. 1
37 20 25.3 10 2 Q9TR33 sus scrofa
38 20 25.3 13 1 ACT7 SOYBN P15987 glycine max
39 20 25.3 13 1 IDHC_PIG P20304 sus scrofa
40 20 25.3 13 2 Q9L8K1 Q9L8K1 enterococc
41 20 25.3 13 2 Q8JJ32 Q8JJ32 ficedula al
42 20 25.3 13 2 Q00789 Q00789 human t-lym
43 20 25.3 13 2 Q76R60 Q76R60 human t-lym
44 20 25.3 14 1 NEJ2_FASHE P80526 fasciola he
45 20 25.3 14 2 Q9JHK8 Q9JHK8 mus musculus

ALIGNMENTS

RESULT 1

ID Q70Y70 PRELIMINARY; PRT; 11 AA.
AC Q70Y70;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Ribosomal protein (Fragment).
GN Name=rpel6;
OS Thornicroftia longiflora.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Thornecroftia.
OX NCBI_taxID=204202;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15019625; DOI=10.1016/j.ympev.2003.08.002;
RA Paton A., Springate D.A., Sudde S., Otieno D., Grayer R., Harley M.M.,
RA Willis F., Simmonds M.S.J., Powell M.P., Savolainen V.;
RT "Phylogeny and evolution of basils and allies (Ocimeae, Labiatae)
based on three plastid DNA regions";
RL Mol. Phylogenet. Evol. 31:277-299(2004).
DR EMBL; AJ505401; CAD45521.1; -.
KW Ribosomal protein.
FT NON_TER 1
FT NON_TER 11
SQ SEQUENCE 11 AA; 1201 MW; 396BE78821F2C058 CRC64;

Query Match 30.4%; Score 24; DB 2; Length 11;
Best Local Similarity 57.1%; Pred. No. 3.5e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 2 GGRVHFF 8
Db 3 GGIVHLY 9

RESULT 2

ID Q6YBF2 PRELIMINARY; PRT; 11 AA.
AC Q6YBF2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Wzx (Fragment).
GN Name=wzx;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_taxID=1313;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=NZSPN00/353, and 018319;
RX MEDLINE=22979121; PubMed=14614062; DOI=10.1099/jmm.0.05277-0;
RA Kong F., Gilbert G.L.;
RT "Using cpnA-cpsB sequence polymorphisms and serotype-/group-specific
RL PCR to predict 51 Streptococcus pneumoniae capsular serotypes.";
RJ J. Med. Microbiol. 52:1047-1058(2003).
DR EMBL; AY163225; AAO60516.1; -.
DR EMBL; AY163224; AAO60514.1; -.
FT NON_TER 1
SQ SEQUENCE 11 AA; 1475 MW; 6C6B29B7C721F1B4 CRC64;

Query Match 30.4%; Score 24; DB 2; Length 11;
Best Local Similarity 66.7%; Pred. No. 3.5e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 RVHFFK 9
Db 4 RTHLPK 9

RESULT 3
Q71H50
ID Q71H50 PRELIMINARY; PRT; 14 AA.
AC Q71H50;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome oxidase subunit I (fragment).
OS Andrena accepta.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Andrenidae; Andreninae; Andrena.
OX NCBI_TaxID=205209;
RN [1]
RP SEQUENCE FROM N.A.
RA Larkin L.L., Neff J.L., Simpson B.B.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF504314; AAQ07599.1; -.
DR EMBL; AF504313; AAQ07597.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1707 MW; 6852BA42A4FF1D5B CRC64;

Query Match 29.7%; Score 23.5; DB 2; Length 14;
Best Local Similarity 66.7%; Pred. No. 5.5e+03;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 6 HFFKDISPI 14
Db 3 HSPKEI-PI 10

RESULT 4
AKHX_LOCM1
ID AKHX_LOCM1 STANDARD; PRT; 10 AA.
AC P81626;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Peptide hormone.
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RC TISSUE=Corpora cardiaca;
RA Siegfert K.J.;
RL Submitted (DEC-1998) to Swiss-Prot.
CC -!- FUNCTION: Probably involved in the regulation of locust

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CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the AKH / HPTH / RPCH family.
DR InterPro; IPR002047; AKH.
DR PROSITE; PS00256; AKH; 1.
KW Amidation; Direct protein sequencing; Neuropeptide;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1
FT MOD_RES 10 10 Pyrrolidone carboxylic acid.
FT MOD_RES 10 10 Proline amide.
SQ SEQUENCE 10 AA; 1222 MW; 81BFF67AB415B9D1 CRC64;

Query Match 29.1%; Score 23; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 4.8e+03;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 4 RVHFFKDISP 13
Db 1 QVTFSRDWS 10

RESULT 5
Q71GY0
ID Q71GY0 PRELIMINARY; PRT; 14 AA.
AC Q71GY0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome oxidase subunit I.
OS Andrena ofella.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Andrenidae; Andreninae; Andrena.
OX NCBI_TaxID=205244;
RN [1]
RP SEQUENCE FROM N.A.
RA Larkin L.L., Neff J.L., Simpson B.B.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF504349; AAQ07669.1; -.
DR EMBL; AF504348; AAQ07667.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
SQ SEQUENCE 14 AA; 1679 MW; 7463A554622E595B CRC64;

Query Match 29.1%; Score 23; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 6.8e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 6 HFFKDISPIA 15
Db 3 HSFNEIPMIA 12

RESULT 6
Q71H20
ID Q71H20 PRELIMINARY; PRT; 14 AA.
AC Q71H20;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome oxidase subunit I (fragment).
OS Andrena discreta.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Andrenidae; Andreninae; Andrena.
OX NCBI_TaxID=205225;
RN [1]
RP SEQUENCE FROM N.A.
RA Larkin L.L., Neff J.L., Simpson B.B.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF504329; AAQ07629.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.

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KW Mitochondrion.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1622 MW; 747525547677BESB CRC64;

Query Match 29.1%; Score 23; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 6.8e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 6 HFFKDISPIA 15
| : | |
| : | |
Db 3 HSFNEIPVIA 12

RESULT 7
Q7MOQ6 PRELIMINARY; PRT; 14 AA.
AC Q7MOQ6;
DT 01-MAR-2004 (TRENBLrel. 26, Created)
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
DE Xylan 1,4-beta-xylosidase (BC 3.2.1.37) (Fragment).
OS Thermotoga sp.
OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
OX NCBI_TaxID=28240;
RN [1]
RP SEQUENCE.
RX MEDLINE=93152594; PubMed=8427876; DOI=10.1016/0304-4165(93)90132-R;
RA Rutter-Smith L.D., Daniel R.M.;
RT "Thermotable beta-glucosidase and beta-xylosidase from Thermotoga sp.
strain Pj83-B.1.";
RL Biochim. Biophys. Acta 1156:167-172(1993).
DR PIR; S29632; S29632.
DR GO; GO:0009044; F:xylian 1,4-beta-xylosidase activity; IEA.
FT NON_TER 1
FT NON_TER 14
SQ SEQUENCE 14 AA; 1709 MW; CB22131BE55ADCC9 CRC64;

Query Match 29.1%; Score 23; DB 2; Length 14;
Best Local Similarity 66.7%; Pred. No. 6.8e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 VHFPPD 10
| : | |
| : | |
Db 5 VYFPAD 10

RESULT 8
Q9TWF3 PRELIMINARY; PRT; 15 AA.
AC Q9TWF3;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TRENBLrel. 14, Last annotation update)
DE V-ATPase D-subunit (Fragment).
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE.
RX MEDLINE=96019266; PubMed=7593293;
RA Adessi C., Chapel A., Vincon M., Rabilloud T., Klein G., Satre M.,
Garin J.;
RT "Identification of major proteins associated with Dictyostelium
discoideum endocytic vesicles.";
RL J. Cell Sci. 108:3331-3337(1995).
SQ SEQUENCE 15 AA; 1608 MW; EA91C650A853EA CRC64;

Query Match 29.1%; Score 23; DB 2; Length 15;
Best Local Similarity 80.0%; Pred. No. 7.2e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGRVH 6
| | | |

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Db 4 GGRKH 8

RESULT 9
FARP MYTD
ID FARP MYTD STANDARD; PRT; 10 AA.
AC F42560;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE FMRamide-like neuropeptide ALAGDHFFRF-amide.
OS Mytilus edulis (Blue mussel).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
OC Mytiloidea; Mytilidae; Mytilus.
OX NCBI_TaxID=6550;
RN [1]
RP SEQUENCE.
RX MEDLINE=93047883; PubMed=1358534; DOI=10.1016/0742-8413(92)90104-F;
RA Walker R.J.;
RT "Neuroactive peptides with an RFamide or Famide carboxyl terminal.";
RL Comp. Biochem. Physiol. 102C:213-222(1992).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the FARP (FMRamide related peptide)
family.
DR PIR; A58365; A58365.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD_RES 10
| : | |
| : | |
SQ SEQUENCE 10 AA; 1180 MW; C2F80CC9C1EAA87D CRC64;

Query Match 27.8%; Score 22; DB 1; Length 10;
Best Local Similarity 75.0%; Pred. No. 7.2e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 HFFK 9
| | | |
| | | |
Db 6 HFFR 9

RESULT 10
Q88575 PRELIMINARY; PRT; 12 AA.
AC Q88575;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Theiler's murine encephalomyelitis virus 5' flank and 5' end cda.
DE (Fragment).
OS Theiler's encephalomyelitis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Cardiovirus.
OX NCBI_TaxID=12124;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FA;
RX MEDLINE=92194426; PubMed=1548749;
RA Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipton H.L.;
RT "A single base deletion in the 5' noncoding region of Theiler's virus
attenuates neurovirulence.";
RL J. Virol. 66:1951-1958(1992).
DR EMBL; M80883; AAA73154.1; -.
FT NON_TER 12
| : | |
| : | |
SQ SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;

Query Match 27.8%; Score 22; DB 2; Length 12;
Best Local Similarity 37.5%; Pred. No. 8.7e+03;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 HFFKDISP 13
| : | |
| : | |
Db 5 HGYPDVCP 12

RESULT 11

```

```

Q88576
ID Q88576 PRELIMINARY; PRT; 12 AA.
AC Q88576;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Theiler's murine encephalomyelitis virus 5' flank and 5' end cds.
DE (Fragment).
OS Theiler's encephalomyelitis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Cardiovirus.
OX NCBI_TaxID=12124;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MHG;
RX MEDLINE=92194426; PubMed=1548749;
RA Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipton H.L.;
RT "A single base deletion in the 5' noncoding region of Theiler's virus
RT attenuates neurovirulence.";
RL J. Virol. 66:1951-1958(1992).
DR EMBL; M80884; AAA73155.1; -.
FT NON TER 12 12
SQ SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;

Query Match 27.8%; Score 22; DB 2; Length 12;
Best Local Similarity 37.5%; Pred. No. 8.7e+03;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 6 HFFKDISP 13
Db 5 HGYPDVCP 12

RESULT 12
Q88577
ID Q88577 PRELIMINARY; PRT; 12 AA.
AC Q88577;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Theiler's murine encephalomyelitis virus 5' flank and 5' end cds.
DE (Fragment).
OS Theiler's encephalomyelitis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Cardiovirus.
OX NCBI_TaxID=12124;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TO;
RX MEDLINE=92194426; PubMed=1548749;
RA Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipton H.L.;
RT "A single base deletion in the 5' noncoding region of Theiler's virus
RT attenuates neurovirulence.";
RL J. Virol. 66:1951-1958(1992).
DR EMBL; M80885; AAA73156.1; -.
FT NON TER 12 12
SQ SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;

Query Match 27.8%; Score 22; DB 2; Length 12;
Best Local Similarity 37.5%; Pred. No. 8.7e+03;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 6 HFFKDISP 13
Db 5 HGYPDVCP 12

RESULT 13
Q88578
ID Q88578 PRELIMINARY; PRT; 12 AA.
AC Q88578;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)

```

```

DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Theiler's murine encephalomyelitis virus 5' flank and 5' end cds.
DE (Fragment).
OS Theiler's encephalomyelitis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Cardiovirus.
OX NCBI_TaxID=12124;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TO;
RX MEDLINE=92194426; PubMed=1548749;
RA Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipton H.L.;
RT "A single base deletion in the 5' noncoding region of Theiler's virus
RT attenuates neurovirulence.";
RL J. Virol. 66:1951-1958(1992).
DR EMBL; M80886; AAA73157.1; -.
FT NON TER 12 12
SQ SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;

Query Match 27.8%; Score 22; DB 2; Length 12;
Best Local Similarity 37.5%; Pred. No. 8.7e+03;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 6 HFFKDISP 13
Db 5 HGYPDVCP 12

RESULT 14
Q88579
ID Q88579 PRELIMINARY; PRT; 12 AA.
AC Q88579;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Theiler's murine encephalomyelitis virus 5' flank and 5' end cds.
DE (Fragment).
OS Theiler's encephalomyelitis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Cardiovirus.
OX NCBI_TaxID=12124;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VL;
RX MEDLINE=92194426; PubMed=1548749;
RA Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipton H.L.;
RT "A single base deletion in the 5' noncoding region of Theiler's virus
RT attenuates neurovirulence.";
RL J. Virol. 66:1951-1958(1992).
DR EMBL; M80887; AAA73158.1; -.
FT NON TER 12 12
SQ SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;

Query Match 27.8%; Score 22; DB 2; Length 12;
Best Local Similarity 37.5%; Pred. No. 8.7e+03;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 6 HFFKDISP 13
Db 5 HGYPDVCP 12

RESULT 15
Q88580
ID Q88580 PRELIMINARY; PRT; 12 AA.
AC Q88580;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Theiler's murine encephalomyelitis virus 5' flank and 5' end cds.
DE (Fragment).
OS Theiler's encephalomyelitis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;

```

OC Cardiovirus.
OX NCBI_TaxID=12124;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Vilyuisk;
RX MEDLINE=92194426; PubMed=1548749;
RA Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipton H.L.;
RT "A single base deletion in the 5' noncoding region of Theiler's virus
attenuates neurovirulence.";
RL J. Virol. 66:1951-1958(1992).
DR EMBL: M80888; AAA73159.1; -.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;

Query Match 27.8%; Score 22; DB 2; Length 12;
Best Local Similarity 37.5%; Pred. No. 8.7e+03;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 6 HFFKDISP 13
| : | : |
Db 5 HGYPDVCP 12

Search completed: February 22, 2005, 09:38:01
Job time : 54.6667 secs

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OM protein - protein search, using sw model

Run on: February 22, 2005, 08:52:23 ; Search time 65.6667 Seconds
(without alignments)
88.346 Million cell updates/sec

Title: US-08-991-628-11

Perfect score: 79

Sequence: 1 IGRVHFVKDISPIA 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 632537

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	79	100.0	15	2 AAW04851	Internal
2	39	49.4	13	7 ADC51728	Human MBP
3	39	49.4	13	7 ADC51729	Human MBP
4	37	46.8	11	4 AAB70569	Human MBP
5	37	46.8	11	5 AAO21025	Isomerase
6	37	46.8	12	3 AAB26883	Human mye
7	35	44.3	13	2 AAR74902	Myelin Ba
8	35	44.3	13	5 ABB84347	MBP epit
9	35	44.3	15	3 AAY85541	Human MBP
10	35	44.3	15	3 AAB12643	Modified
11	35	44.3	15	4 AAM99034	Vaccine r
12	35	44.3	15	4 AAM99033	Vaccine r
13	34	43.0	7	2 AAW72354	Human mye
14	34	43.0	8	2 AAR61755	MBP pepti
15	34	43.0	8	8 ADR48840	Inhibitor
16	34	43.0	8	8 ADR48797	Inhibitor
17	34	43.0	9	2 AAR61856	MBP pepti
18	34	43.0	9	2 AAR61871	MBP pepti
19	34	43.0	9	2 AAR91918	Generic p
20	34	43.0	9	8 ADM12852	MHC class
21	34	43.0	9	8 ADO39090	Human mye
22	34	43.0	10	2 AAR61949	MBP pepti
23	34	43.0	10	2 AAR61952	MBP pepti
24	34	43.0	10	2 AAR91921	Peptide c
25	34	43.0	10	2 AAR91919	Peptide c

26	34	43.0	10	2 AAR91920	Aar91920 Peptide c
27	34	43.0	10	2 AAR91922	Aar91922 Peptide c
28	34	43.0	10	2 AAW72358	Human mye
29	34	43.0	10	2 AAW72355	Human mye
30	34	43.0	10	2 AAW72357	Human mye
31	34	43.0	10	2 AAW72356	Human mye
32	34	43.0	10	7 ADB89021	Human mye
33	34	43.0	10	7 ADC06706	Myelin ba
34	34	43.0	10	7 ADE38270	Immunomod
35	34	43.0	11	2 AAW54673	Peptide f
36	34	43.0	12	8 ADN65365	HLA bindi
37	34	43.0	13	2 AAR29955	TCR pepti
38	34	43.0	13	2 AAR74910	Myelin Ba
39	34	43.0	13	2 AAR74911	Myelin Ba
40	34	43.0	13	2 AAR74909	Myelin Ba
41	34	43.0	13	2 AAR74904	Myelin Ba
42	34	43.0	13	2 AAR74903	Myelin Ba
43	34	43.0	13	2 AAR85133	Human MBP
44	34	43.0	13	2 AAY04452	Myelin ba
45	34	43.0	13	2 AAR95363	Residues

ALIGNMENTS

RESULT 1

AAW04851
ID AAW04851 standard; peptide; 15 AA.

AC AAW04851;

DT 27-AUG-2003 (revised)
DT 18-FEB-1997 (first entry)

XX Internal fragment of human papilloma virus type 7 L2 protein.

XX Tolerisation; self-epitope; antigen; autoimmune disease; autoantigen;
KW HLA; human leukocyte antigen; T-cell; thymocyte; pemphigus vulgaris;
KW desmoglein; multiple sclerosis; herpes simplex virus; adenovirus;
KW phosphomannomutase; human papillomavirus; Epstein-Barr virus;
KW DNA polymerase; influenza; haemagglutinin; reovirus; sigma protein.

OS Human papillomavirus type 7.

XX WO9627387-A1.

XX 12-SEP-1996.

XX 07-MAR-1996; 96WO-US003182.

XX 07-MAR-1995; 95US-00400796.

XX (HARD) HARVARD COLLEGE.

XX Strominger JL, Wuchterfennig KW;

XX WPI; 1996-425218/42.

XX Pemphigus vulgaris auto-antigens and multiple sclerosis non-self antigens
PT - useful in disease treatment, and method for identification of other
self and non-self antigens implicated in auto-immune disease.

XX Claim 2; Page 44; 58pp; English.

XX Pharmaceutical preparations for tolerisation to antigens comprise either
CC an isolated human non-collagen or non-myelin basic protein (MBP)
CC polypeptide which is capable of tolerising an individual to an
CC autoantigen; or an isolated human pathogen polypeptide capable of
CC tolerising an individual to that polypeptide. In both cases, the
CC polypeptide (whether self or non-self) includes an amino acid sequence
CC corresponding to a sequence motif for a MHC class II protein, such as HLA
CC -DR, which is associated with a human autoimmune disease and which binds
CC to the polypeptide to activate autoreactive T-cells in individuals with

CC the autoimmune disease. This peptide is an internal peptide of human
 CC papilloma virus type 7 L2 protein and is implicated as a foreign epitope
 CC involved in the aetiology of in remissions of multiple sclerosis. It has
 CC been shown capable of inducing the proliferation of autoreactive T-cell
 CC clones isolated from multiple sclerosis patients. (Updated on 27-AUG-2003
 CC to correct OS field.)
 XX
 SQ Sequence 15 AA;

Query Match 100.0%; Score 79; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IGGVHFFKDISPTA 15
 Db 1 IGGVHFFKDISPTA 15

RESULT 2

ADC51728
 ID ADC51728 standard; peptide; 13 AA.

AC
 AC ADC51728;

DT 18-DEC-2003 (first entry)

DE Human MBP87-99 peptide #2.

XX human; PCMT1; IAMT; L-Isoaspartyl (D-aspartyl)O-methyltransferase; IAMT;
 KW autoimmune; celiac disease; Crohn's disease;
 KW insulin dependent diabetes mellitus; Grave's disease; multiple sclerosis;
 KW myasthenia gravis; psoriasis; rheumatoid arthritis; Sjogren's syndrome;
 KW systemic lupus erythematosus; ulcerative colitis; MBP87-99.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 6 /label= Diso

FT WO2003057204-A2.

PN 17-JUL-2003.

PD 07-JAN-2003; 2003WO-EP000079.

PF 08-JAN-2002; 2002DK-00000026.

PR 08-JAN-2002; 2002US-0346709P.

XX (NORD-) NORDIC BIOSCIENCE AS.

XX Cloos PAC;

PI WPI; 2003-645976/61.

DR Example 1; Fig 3; 34pp; English.

XX The invention relates to the novel use of a regulator of L-Isoaspartyl (D
 CC -aspartyl)O-methyltransferase (IAMT) activity (A) or IAMT or IAMT
 CC encoding nucleic acid sequence or their functional derivatives in the
 CC preparation of a composition for the prevention, treatment or alleviation
 CC of an autoimmune response and/or disease. The composition of the
 CC invention is used for the prevention, treatment or alleviation of an
 CC autoimmune response and/or disease in a mammal e.g. celiac disease,
 CC Crohn's disease, insulin dependent diabetes mellitus, Grave's disease,
 CC multiple sclerosis, myasthenia gravis, psoriasis, rheumatoid arthritis,
 CC Sjogren's syndrome, systemic lupus erythematosus or ulcerative colitis.
 CC The present sequence is used in the exemplification of the invention.

XX Sequence 13 AA;

Query Match 49.4%; Score 39; DB 7; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.3;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 VHPFKDI 11
 Db 1 VHPFKDI 7

RESULT 3

ADC51729
 ID ADC51729 standard; peptide; 13 AA.

AC
 AC ADC51729;

DT 18-DEC-2003 (first entry)

DE Human MBP87-99 peptide #3.

XX human; PCMT1; IAMT; L-Isoaspartyl (D-aspartyl)O-methyltransferase; IAMT;
 KW autoimmune; celiac disease; Crohn's disease;
 KW insulin dependent diabetes mellitus; Grave's disease; multiple sclerosis;
 KW myasthenia gravis; psoriasis; rheumatoid arthritis; Sjogren's syndrome;
 KW systemic lupus erythematosus; ulcerative colitis; MBP87-99.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 6 /note= "D-form residue"

FT WO2003057204-A2.

PN 17-JUL-2003.

PD 07-JAN-2003; 2003WO-EP000079.

PF 08-JAN-2002; 2002DK-00000026.

PR 08-JAN-2002; 2002US-0346709P.

XX (NORD-) NORDIC BIOSCIENCE AS.

XX Cloos PAC;

PI WPI; 2003-645976/61.

XX Use of L-Isoaspartyl (D-aspartyl)O-methyltransferase (IAMT) activity
 CC regulator, IAMT, IAMT encoding nucleic acid sequence or their functional
 CC derivatives for preparing composition for the treatment of an autoimmune
 CC response and/or disease.

XX Example 1; Fig 3; 34pp; English.

XX The invention relates to the novel use of a regulator of L-Isoaspartyl (D
 CC -aspartyl)O-methyltransferase (IAMT) activity (A) or IAMT or IAMT
 CC encoding nucleic acid sequence or their functional derivatives in the
 CC preparation of a composition for the prevention, treatment or alleviation
 CC of an autoimmune response and/or disease. The composition of the
 CC invention is used for the prevention, treatment or alleviation of an
 CC autoimmune response and/or disease in a mammal e.g. celiac disease,
 CC Crohn's disease, insulin dependent diabetes mellitus, Grave's disease,
 CC multiple sclerosis, myasthenia gravis, psoriasis, rheumatoid arthritis,
 CC Sjogren's syndrome, systemic lupus erythematosus or ulcerative colitis.
 CC The present sequence is used in the exemplification of the invention.

XX Sequence 13 AA;

Query Match 49.4%; Score 39; DB 7; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.3;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


```

QY 5 VHFFKDI 11
Db 1 VHFFKDI 7

RESULT 4
AAB70569
ID AAB70569 standard; peptide; 11 AA.
XX
AC AAB70569;
XX
DT 10-MAY-2001 (first entry)
XX
DE Human immunoglobulin G (IgG) epitope #10.
XX
KW Immunoglobulin G; IgG; myelin basic protein; MBP; MOG; Crohn's disease;
KW myelin oligodendrocyte glycoprotein; alphaB-crystallin; MS; psoriasis;
KW multiple sclerosis; rheumatoid arthritis; autoimmune disease; IDDM;
KW immune system; insulin dependent diabetes mellitus; myasthenia gravis;
KW coeliac disease; Chaga's disease; diagnosis.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 7
FT /note= "Asx can be alpha-D Asn or Asp, or is beta-D or
FT beta-L Asp"
XX
PN WO200113110-A2.
XX
PD 22-FEB-2001.
XX
PP 16-AUG-2000; 2000WO-EP007973.
XX
PR 17-AUG-1999; 99GB-00019452.
XX
PA (OSTE-) OSTEOMETER BIOTECH AS.
XX
PI Cloos PAC, Christgau S;
XX
PS WPI; 2001-234923/24.
XX
PT Diagnostic assay useful for quantitative/qualitative determination of
PT autoimmune reactivity comprising determining an immune system component
PT recognizing epitope containing isomerized peptide linkage and/or
PT optically inverted amino acid.
XX
PS Claim 7; Page 64; 74pp; English.
XX
CC The present invention describes a diagnostic assay (M1) comprising
CC quantitative or qualitative determination of an auto-reactive immune
CC system component specifically recognising an epitope (E) containing an
CC isomerised peptide linkage and/or optically inverted amino acid, an auto-
CC antigen or its fragment containing (E) and/or a non-self antigen or its
CC fragment which contains (E) and is capable of inducing an autoimmune
CC response. The diagnostic assay is useful for quantitative and qualitative
CC determination of autoimmune reactivity of an isomerised protein sequence,
CC which is an indicative of an autoimmune disease such as rheumatoid
CC arthritis, multiple sclerosis, insulin dependent diabetes mellitus,
CC myasthenia gravis, coeliac disease, Chaga's disease, psoriasis or Crohn's
CC disease. The present sequence represents a specifically claimed example
CC of (E) for use in the diagnostic assay
XX
SQ Sequence 11 AA;
Query Match 46.8%; Score 37; DB 4; Length 11;
Best Local Similarity 85.7%; Pred. No. 6.7;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 VHFFKDI 11
Db 2 VHFFKBI 8

RESULT 6
AAB26883
ID AAB26883 standard; peptide; 12 AA.
XX
AC AAB26883;
XX
DT 01-FEB-2001 (first entry)
XX

```

```

RESULT 5
AAO21025
ID AAO21025 standard; peptide; 11 AA.
XX
AC AAO21025;
XX
DT 19-JUL-2002 (first entry)
XX
DE Isomerised/optically inverted epitope #8 for recognition by antibody.
XX
KW Immunosuppressive; antirheumatic; antiarthritic; antidiabetic; epitope;
KW antithyroid; neuroprotective; antiinflammatory; autoimmune disease;
KW antipsoriatic; selective suppression; auto-antigen; immunological;
KW isomerised peptide linkage; optionally inverted; rheumatoid arthritis;
KW vaccine; multiple sclerosis; insulin dependent diabetes mellitus;
KW myasthenia gravis; coeliac disease; Chagas' disease; psoriasis;
KW Crohn's disease.
XX
OS Unidentified.
XX
PN WO200213844-A2.
XX
PD 21-FEB-2002.
XX
PP 09-AUG-2001; 2001WO-EP009205.
XX
PR 16-AUG-2000; 2000GB-00020238.
XX
PA (OSTE-) OSTEOMETER BIOTECH AS.
XX
PI Cloos PAC, Christgau S;
XX
PS WPI; 2002-339411/37.
XX
PT Use of protein, peptide or their analogs containing an epitope recognized
PT by an auto-reactive immune system for the treatment of autoimmune
PT disease.
XX
PS Claim 5; Page 92; 111pp; English.
XX
CC The invention relates to methods and compositions for the treatment of an
CC autoimmune disease involving the selective suppression of autoimmune
CC activity against an auto-antigen. The activity involves immunological
CC reactivity with an epitope containing an isomerised peptide linkage and/
CC or an optionally inverted amino acid. The epitopes of the invention can
CC be used for therapeutic or prophylactic treatment of the autoimmune
CC diseases for the vaccination against autoimmune diseases e.g. rheumatoid
CC arthritis, multiple sclerosis, insulin dependent diabetes mellitus,
CC myasthenia gravis, coeliac disease, Chagas' disease, psoriasis and
CC Crohn's disease. This sequence represents an isomerised/optically
CC inverted epitope of the invention
XX
SQ Sequence 11 AA;
Query Match 46.8%; Score 37; DB 5; Length 11;
Best Local Similarity 85.7%; Pred. No. 6.7;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 VHFFKDI 11
Db 2 VHFFKBI 8

RESULT 6
AAB26883
ID AAB26883 standard; peptide; 12 AA.
XX
AC AAB26883;
XX
DT 01-FEB-2001 (first entry)
XX

```

DE Human myelin basic protein fragment.
 KW Immunosuppressant; neuroprotective; multiple sclerosis; treatment.
 XX Homo sapiens.
 OS WO200058354-A1.
 FN 05-OCT-2000.
 XX 29-MAR-1999; 99WO-EP002268.
 XX 29-MAR-1999; 99WO-EP002268.
 PR (TECN-) TECNOCEN SCPA.
 PA Martino M, Ippolito A, Fassina G;
 FI WPI; 2000-628344/60.
 XX New glycine-rich peptides, useful for treatment of multiple sclerosis by
 PT induction of energy in autoreactive T cells.
 XX Disclosure; Page 2-3; 23pp; English.
 XX Peptides AAB26878-B26881 represent four glycine rich peptide which may be
 CC N-acetylated and/or C-amidated and contain amino acids with L or D
 CC configuration. Included in the invention is a pharmaceutical composition
 CC containing at least one of the peptides and an inert ingredient. The
 CC peptides have immunosuppressant and neuroprotective activity and induce
 CC energy of autoreactive T lymphocytes without inducing an autoreactive
 CC response. The peptides are used to treat multiple sclerosis. The present
 CC sequence represents a fragment of the human myelin basic protein which is
 CC used in the invention in the design of the peptides of the invention
 XX
 SQ Sequence 12 AA;
 Query Match 46.8%; Score 37; DB 3; Length 12;
 Best Local Similarity 66.7%; Pred. No. 7.3;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 OY 5 VHFFKDISP 13
 DB 1 VHFFKIVTP 9
 ||||| : :
 ||||| : :
 RESULT 7
 AAR74902
 ID AAR74902 standard; peptide; 13 AA.
 AC AAR74902;
 XX 25-MAR-2003 (revised)
 DT 29-NOV-1995 (first entry)
 DE Myelin Basic protein epitope alanine substituted peptide ala8.
 XX T-cell Receptor; TcR; variable region; multiple sclerosis;
 KW autoimmune disease; neurodegeneration; myelin basic protein; MBP;
 KW oligopeptide immunogen; competitor peptide; antagonist.
 XX Synthetic.
 OS WO9508572-A1.
 FN 30-MAR-1995.
 PD 22-SEP-1994; 94WO-US010728.
 PF 22-SEP-1993; 93US-00125407.
 XX (STRD) UNIV LELAND STANFORD JUNIOR.
 XX

PI Steinman L, Oksenberg J, Bernard C, Zamvil S, Mitchell DJ;
 PI Karin N;
 XX WPI; 1995-139558/18.
 DR Determining relation between auto-immune degenerative diseases and
 XX specific variable regions of T-cell receptors - as associated with the
 PT host HLA or T-cells associated with combating neoproliferative diseases.
 XX Claim 6; Page 116; 122pp; English.
 XX A set of substituted peptides based on the sequence corresp. to the I-E
 CC restricted epitope MBP 89-99 in the rat was synthesised and tested for
 CC MHC binding. Six of the peptides (see AAR74899-R74904) have substantially
 CC reduced MHC binding affinity, a reduced ability to stimulate T-cells in
 CC vitro and a reduced ability to induce autoimmune disease. They are useful
 CC as competitor peptides to antagonise the T-cell receptor, e.g. to block
 CC the CDR3 region involved in multiple sclerosis. Oligopeptide immunogens
 CC comprising one of the 6 amino acid sequences are also claimed. (Updated
 CC on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 13 AA;
 Query Match 44.3%; Score 35; DB 2; Length 13;
 Best Local Similarity 75.0%; Pred. No. 19;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 OY 5 VHFFKDIS 12
 DB 1 VHFFKNIA 8
 ||||| :
 ||||| :
 RESULT 8
 ABB84347
 ID ABB84347 standard; peptide; 13 AA.
 AC ABB84347;
 XX 17-OCT-2002 (first entry)
 DT MBP epitope analogue SEQ ID 47.
 DE MBP; myelin basic protein; tolerance; immune system; multiple sclerosis;
 KW autoimmune response; autoimmune disease; immunosuppressive;
 KW neuroprotective.
 XX Synthetic.
 OS US2002076412-A1.
 FN 20-JUN-2002.
 PD 07-JUN-1995; 95US-00484409.
 XX 17-AUG-1987; 87US-00086694.
 PR 12-JUL-1989; 89US-00379500.
 PR 01-MAY-1990; 90US-00517245.
 PR 01-MAY-1991; 91WO-US002991.
 PR 30-APR-1992; 92US-00877444.
 PR 21-MAY-1993; 93US-00066325.
 PR 22-SEP-1993; 93US-00125407.
 XX (STEI/) STEINMAN L.
 FA (ZAWV/) ZAMVIL S.
 XX Steinman L, Zamvil S;
 PI WPI; 2002-598709/64.
 DR Modulating or tolerizing the immune system, useful for treating multiple
 XX sclerosis, by administering a peptide derived from human myelin binding
 PT protein.
 XX

PS Example II; Page 17; 2lpp; English.

CC This invention describes a novel method for modulating or tolerizing the
 CC immune system, and for treating multiple sclerosis comprising
 CC administering a peptide derived from MBP (human myelin basic protein).
 CC The peptide induces an autoimmune response (T cell) to a self-antigen (or
 CC part of it), and binds to an MHC (major histocompatibility complex)
 CC antigen of a host susceptible to autoimmune diseases, i.e. competes with
 CC binding to MBP and inhibit proliferation of MBP-reactive cells. The
 CC peptide has immunosuppressive and neuroprotective activity. This sequence
 CC represents a synthetic analogue of the human MBP protein I-E restricted
 CC epitope

XX Sequence 13 AA;

Query Match 44.3%; Score 35; DB 5; Length 13;
 Best Local Similarity 75.0%; Pred. No. 19;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 VHFFKDIS 12
 |||||:
 Db 1 VHFFKNIA 8

RESULT 9

AA85541
 ID AA85541 standard; peptide; 15 AA.

XX AC AA85541;

XX DT 23-JUN-2000 (first entry)

XX DE Human MBP peptide variant 96A.

XX KW MBP; CD4+ T cell; myelin basic protein; multiple sclerosis; HLA;
 XX KW human leukocyte antigen; epitope; cytokine; interleukin-4; variant;
 XX KW transforming growth factorbeta.

XX OS Homo sapiens.

XX PN US6036957-A.

XX PD 14-MAR-2000.

XX PF 06-JUN-1995; 95US-00469640.

XX PR 30-MAR-1990; 90US-00502559.

XX PR 28-FEB-1992; 92US-00843752.

XX PR 09-APR-1992; 92US-00865318.

XX PR 09-APR-1993; 93US-00046354.

XX PA (AUTO-) AUTOIMMUNE INC.

XX PI Hafner DA, Miller A, Al-Sabbagh A, Weiner HL;

XX DR WPI; 2000-246181/21.

XX PT Suppressing T cell response to myelin basic protein, useful for treating

XX PT multiple sclerosis, by administering a peptide containing immunodominant

XX PT epitope of the protein.

XX PS Disclosure; Fig 11; 40pp; English.

XX CC The invention relates to a method of suppressing the immune function of
 CC CD4+ T cells, reactive with myelin basic protein (MBP) in patients with
 CC multiple sclerosis. The method comprises administering a peptide (I) that
 CC stimulates (in a proliferation assay) the subgroup of HLA (human
 CC leukocyte antigen)-DR2b-restricted T clones, from remitting-relapsing
 CC patients, that is reactive with another peptide. (I) contains
 CC immunodominant epitopes of MBP (residues 84-102) and when administered
 CC orally actively suppress T cells reactive with this epitope (by inducing
 CC CD8+ suppressor cells that express cytokines such as transforming growth
 CC factorbeta and interleukin-4), or when administered intravenously they

CC induce clonal anergy. The method is used for treatment of multiple
 CC sclerosis. Sequences AA85530-545 represent variants of human MBP,
 CC derived from residues 85-99

XX Sequence 15 AA;

Query Match 44.3%; Score 35; DB 3; Length 15;
 Best Local Similarity 75.0%; Pred. No. 23;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 VHFFKDIS 12
 |||||:
 Db 5 VHFFKNIA 12

RESULT 10

AA812643

ID AA812643 standard; peptide; 15 AA.

XX AC AA812643;

XX DT 10-NOV-2000 (first entry)

XX DE Modified human myelin basic protein peptide #12.

XX KW Human; myelin basic protein; MBP; multiple sclerosis; MS; CNS;
 XX KW immunodominant; chronic inflammatory disease; central nervous system;
 XX KW autoimmune disease; neuroprotective; immunosuppressive; CD8+; CD4+.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN US6077509-A.

XX PD 20-JUN-2000.

XX PF 06-JUN-1995; 95US-00469648.

XX PR 30-MAR-1990; 90US-00502559.

XX PR 28-FEB-1992; 92US-00843752.

XX PR 09-APR-1992; 92US-00865318.

XX PR 09-APR-1993; 93US-00046354.

XX PA (AUTO-) AUTOIMMUNE INC.

XX PI Hafner DA, Weiner HL;

XX DR WPI; 2000-450923/39.

XX PT New pharmaceutical composition comprising peptide fragments of myelin
 XX PT basic protein, useful in suppressing the symptoms of multiple sclerosis.

XX PS Example 4; Fig 11; 26pp; English.

XX CC The present invention describes a pharmaceutical formulation comprising a
 CC peptide having a 30-amino acid sequence (AA812612) (I) or a segment of
 CC (I), provided that the segment comprises at least the 19-amino acid
 CC sequence given in AA812613. The pharmaceutical formulation has
 CC neuroprotective and immunosuppressive activities. The compositions and
 CC peptides from the present invention are useful in suppressing multiple
 CC sclerosis, which is due to the induction of CD8+ suppressor T-cells. The
 CC peptides are also useful in identifying CD4+ T-cells reactive with myelin
 CC basic protein (MBP). The peptides are also useful in identifying
 CC individuals with T-cells reactive to MBP. Oral administration of MBP
 CC suppressed central nervous system (CNS) inflammation in actively induced
 CC experimental allergic encephalomyelitis (EAE). There was a decreased
 CC inflammation in both the parenchyma and meninges when cells from MBP-fed
 CC animals were transferred. This suppression was observed when CD4+
 CC depleted, but not CD8+. The present sequence represents a modified human
 CC MBP peptide fragment, which is used in an example from the present
 CC invention

XX Sequence 15 AA;

```

Query Match      44.3%; Score 35; DB 3; Length 15;
Best Local Similarity 75.0%; Pred. No. 23;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 VHFPEKDIS 12
   |||||.:
Db 5 VHFPEKNIA 12

RESULT 11
AAM99034
ID AAM99034 standard; peptide; 15 AA.
XX
AC AAM99034;
XX
DT 07-DEC-2001 (first entry)
XX
DE Vaccine related MHC ligand peptide SEQ ID NO:137.
XX
KW Glutamic acid; glutamine; vaccine; major histocompatibility complex; MHC;
KW immunomodulator; antiallergic; endocrine; neuroprotectant; virucidal;
KW bactericidal; antiparasitic; fungicidal; cytostatic; medicine;
KW pharmaceutical; immune disorder; immune deficiency; autoimmune;
KW hypersensitivity; allergy; graft rejection; infection; hormonal disorder;
KW central nervous system disease; cancer; melanoma; anti-melanoma vaccine;
KW human immunodeficiency virus.
XX
OS Homo sapiens.
XX
PN WO200170772-A2.
XX
PD 27-SEP-2001.
XX
PF 22-MAR-2001; 2001WO-FR000872.
XX
PR 23-MAR-2000; 2000FR-00003711.
XX
PA (FABR ) FABRE MEDICAMENT SA PIERRE.
XX
PI Klinguer-Hamour C, Corvaia N, Beck A, Goetsch L;
DR WPI; 2001-611470/70.
XX
PT Stabilized pharmaceutical containing N-terminal glutamic acid or
PT glutamine, useful e.g. in anti-melanoma vaccines, is an addition salt
XX with strong acid.
XX
PS Claim 9; Page 54; 149pp; French.
XX
CC The present invention describes a pharmaceutical compound (I) that
CC contains an N-terminal glutamic acid (Glu) or glutamine (Gln) residue in
CC the form of an addition salt with a strong, physiologically acceptable
CC acid (II). Also described are: (a) a pharmaceutical composition
CC containing at least one (I); (b) a vaccine containing at least one (I)
CC where this is a major histocompatibility complex (MHC) ligand (Ia); (c) a
CC method for in vitro diagnosis of diseases associated with the presence of
CC (Ia); (d) a kit for method (c) that includes a (Ia); and (e) a process
CC for preparing (I). (I) has immunomodulator, endocrine, antiallergic,
CC neuroprotectant, virucidal, bactericidal, antiparasitic, fungicidal and
CC cytostatic activities. (I) are useful, in human or veterinary medicine,
CC in pharmaceutical compositions (for treating immune disorders, e.g.
CC immune deficiency, autoimmune states, hypersensitivity, allergy, graft
CC rejection, infection, hormonal disorders and central nervous system
CC diseases), also, where (I) is a MHC ligand (Ia), in vaccines for
CC treatment or prevention of: (i) viral, bacterial, parasitic or fungal
CC infections; or (ii) of cancers. A particular application is in anti-
CC melanoma vaccines. (I) are also useful for in vitro diagnosis of diseases
CC associated with interactions between MHC and (I) e.g. melanoma and human
CC immunodeficiency virus infection. AAM98898 to AAM99592 represent peptides
CC which can be used in pharmaceutical compounds from the present invention
XX
SQ Sequence 15 AA;

```

Sequence 15 AA;

Query Match 44.3%; Score 35; DB 4; Length 15;
 Best Local Similarity 75.0%; Pred. No. 23;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 VHFFKDI 12
 DB 5 VHFFKNI 12

RESULT 13

AAW72354
 ID AAW72354 standard; peptide; 7 AA.

AC AAW72354;
 XX

DT 16-DEC-1998 (first entry)
 XX

DE Human myelin basic protein peptide formula.
 XX

KW Human; myelin basic protein; MBP; multiple sclerosis; anti-MBP; MS.
 XX

OS Homo sapiens.
 XX

PH Key Location/Qualifiers
 FT Modified-site 1

FT /note= "Val can be attached to: hydrogen; hydroxy; an
 amino acid residue; and a polypeptide residue"

FT Modified-site 7
 FT /note= "Ile can be attached to: hydrogen; hydroxy; an
 amino acid residue; and a polypeptide residue"

XX WO9845327-A1.
 PN

XX 15-OCT-1998.
 PD

PF 03-APR-1998; 98WO-CA000290.
 XX

PR 04-APR-1997; 97CA-02201841.
 XX

PA (UYAL-) UNIV ALBERTA.
 XX

PI Warren KG, Catz I;
 XX

DR WPI; 1998-568336/48.
 XX

PT Peptide and its derivatives for treatment of multiple sclerosis - is
 capable of neutralising or modulating production of anti-myelin basic
 protein.

PS Claim 4; Page 46; 75pp; English.
 XX

CC The present sequence represents a myelin basic protein (MBP) peptide
 formula. MBP peptides are capable of neutralising or modulating the
 production of anti-myelin basic protein. The present invention also
 describes a method for treating multiple sclerosis (MS). The method
 comprises administering to the patient an MBP peptide of the formula: R1-
 CC Val-His-Phe-Phe-Lys-Asn-Ile-R2 where R1, R2 = H, OH, or an amino acid
 CC residue and a polypeptide residue, provided that R1 and R2 are not both H
 CC or OH at the same time

XX Sequence 7 AA;
 SQ

Query Match 43.0%; Score 34; DB 2; Length 7;
 Best Local Similarity 85.7%; Pred. No. 1.8e+06;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 VHFFKDI 11
 DB 1 VHFFKNI 7

RESULT 14

AAAR61755

ID AAR61755 standard; peptide; 8 AA.

XX
 AC AAR61755;

DT 25-MAR-2003 (revised)
 DT 12-MAY-1995 (first entry)

DE MBP peptide 86, potential binder of HLA-A2.1.
 XX

KW antigen; epitope; immunogenic target protein; PSA; HBVc; HBVs; EBV; HIV1;
 KW plasma specific antigen; hepatitis B virus; Epstein Barr;
 KW human immunodeficiency virus; human papilloma virus; p53; c-ERB2; MAGE-1;
 KW melanoma antigen-1; core antigen; surface antigen;
 KW pharmaceutical composition; in vivo; ex vivo; therapeutic; diagnostic;
 KW MHC class I molecule; major histocompatibility complex; HLA-A2.1; 9mer;
 KW 10mer; anchor; human leukocyte antigen; PLP; 8mer; algorithm prediction;
 KW MBP.

XX Homo sapiens.
 OS

XX WO9420127-A1.
 PN

XX 15-SEP-1994.
 PD

XX 04-MAR-1994; 94WO-US002353.
 PF

XX 05-MAR-1993; 93US-00027146.
 PR

XX 04-JUN-1993; 93US-00073205.
 PR

XX 29-NOV-1993; 93US-00159184.
 PR

XX (CYTE-) CYTEL CORP.
 PA

XX Grey HM, Sette A, Sidney J, Kast W;
 PI

XX WPI; 1994-302678/37.
 DR

XX Immunogenic peptide(s) having an HLA-A2.1 binding motif - used for
 treatment or prophylaxis of cancer, virus infection or autoimmune
 diseases.

XX Disclosure; Page 117; 138pp; English.
 PS

XX AAR61714-837 are potential peptide binders of HLA-A2.1 motif. These
 peptides are thus potentially immunogenic. They were predicted by using
 an algorithm, which assigns a score for each amino acid, at each position
 CC along a peptide. A peptide is scored in the 'Grouped Ratio' algorithm as
 CC a product of the scores of each of its residues. This value can then be
 CC used to predict a population of peptides with the highest occurrence of
 CC good binders. The peptides of the invention can induce cytotoxic T
 CC lymphocytes which can react with target cells. They can be used for the
 CC treatment or prophylaxis of cancer, eg. prostate cancer or lymphoma, etc.
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 8 AA;
 SQ

Query Match 43.0%; Score 34; DB 2; Length 8;
 Best Local Similarity 85.7%; Pred. No. 1.8e+06;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 VHFFKDI 11
 DB 2 VHFFKNI 8

RESULT 15

ADR48840

ID ADR48840 standard; peptide; 8 AA.

XX
 AC ADR48840;

XX 04-NOV-2004 (first entry)
 DT

XX

Job time : 67.6667 secs

DE Inhibitory compound #52.
XX Major histocompatibility complex; MHC class II molecule;
KW T cell proliferation inhibition; leukocyte antigen-DR2;
KW autoimmune disease; multiple sclerosis; Behcet's disease;
KW Crohn's disease; glomerulonephritis; Grave's disease;
KW Guillain-Barre syndrome; Hashimoto's thyroiditis;
KW idiopathic thrombocytopenic purpura; lichen planus; lupus erythematosus;
KW Meniere's disease; type 1 diabetes; psoriasis; Reiter's syndrome;
KW rheumatoid arthritis; scleroderma; Sjogren's syndrome;
KW Wegener's granulomatosis; myasthenia gravis; ulcerative colitis; uveitis;
KW stiff-man syndrome; vasculitis.
XX
OS Unidentified.
XX
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "Acetylated residue"
XX
XX US2004162242-A1.
XX
PD 19-AUG-2004.
XX
XX 13-FEB-2004; 2004US-00778756.
XX
XX 14-FEB-2003; 2003US-0447949P.
XX
XX (OLSON/) OLSON G L.
XX (COOK/) COOK C M.
XX (SELF/) SELF C R.
XX
XX Olson GL, Cook CM, Self CR;
XX
XX WPI; 2004-634115/61.
XX
XX New amino acid derivatives, used as modulators of antigen presentation by
PT human leukocyte antigen-DR class II major histocompatibility complex
PT molecules, for treating autoimmune diseases.
XX
XX Claim 10; Page 33; 35pp; English.
XX
XX The invention relates to amino acid derivatives/compounds or their salts.
XX The invention also relates to a pharmaceutical composition comprising a
XX compound of the invention and a carrier. The compound or its salt is
XX useful for treating or preventing a disease responsive to the inhibition
XX of antigen binding to an MHC class II molecule, a disease responsive to
XX the inhibition of antigen presentation by an MHC class II molecule or a
XX disease responsive to the inhibition of T cell proliferation, which
XX involves administering a compound or its salt to a patient in need of
XX treatment, where the MHC class II molecule is human leukocyte antigen-
XX DR2. The compound or its salt is useful for treating or preventing
XX autoimmune diseases, such as multiple sclerosis, Behcet's disease,
XX Crohn's disease, glomerulonephritis, Grave's disease, Guillain-Barre
XX syndrome, Hashimoto's thyroiditis, idiopathic thrombocytopenic purpura,
XX lichen planus, lupus erythematosus, Meniere's disease, type 1 diabetes,
XX psoriasis, Reiter's syndrome, rheumatoid arthritis, scleroderma,
XX Sjogren's syndrome, Wegener's granulomatosis, myasthenia gravis,
XX ulcerative colitis, uveitis, stiff-man syndrome and vasculitis. This
XX sequence represents an MHC class II antigen binding inhibitory compound
XX of the invention.
XX
SQ Sequence 8 AA;

Query Match 43.0%; Score 34; DB 8; Length 8;
Best Local Similarity 85.7%; Pred. No. 1.8e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 VHEFKDI 11
| | | | | |
Db 2 VHEFKNI 8

Search completed: February 22, 2005, 09:24:50

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 22, 2005, 09:08:09 ; Search time 11.1333 Seconds
(without alignments)
129.633 Million cell updates/sec

Title: US-08-991-628-12

Perfect score: 85

Sequence: 1 TGVVYHFVKKHVES 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 2523

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 79:*

2: PIR1:*

3: PIR2:*

4: PIR3:*

5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	28.2	13	PT0304	Ig heavy chain CRD
2	24	28.2	14	PC7079	unidentified 27.2K
3	23	27.1	14	S74128	superoxide dismuta
4	21	24.7	8	PL0184	capsid protein vp-
5	21	24.7	15	PN0662	dystrophin-associa
6	21	24.7	15	PQ0780	NADH2 dehydrogenas
7	20.5	24.1	14	PL0142	carbon-monoxide de
8	20	23.5	7	NYPG7	hypothalamic hepta
9	20	23.5	11	PQ0733	unidentified 6.0/1
10	20	23.5	14	S03530	Ig heavy chain J r
11	20	23.5	14	S57569	T cell receptor V-
12	20	23.5	14	S57638	T cell receptor V-
13	20	23.5	15	A61145	dihydrofolate redu
14	19.5	22.9	15	PA0093	emniatin synthetas
15	19	22.4	10	C61440	polygalacturonase
16	19	22.4	12	A33099	163K exoantigen -
17	19	22.4	12	PT0257	Ig heavy chain CRD
18	19	22.4	12	A34858	proteinase E - bla
19	19	22.4	14	PT0294	Ig heavy chain CRD
20	19	22.4	14	PH1601	Ig H chain V-D-J r
21	19	22.4	14	A47421	leukotriene B-4 12
22	19	22.4	15	S57201	basic proteinase I
23	19	22.4	15	PC1317	large granule L4 c
24	19	22.4	15	PH1613	Ig H chain V-D-J r
25	18	21.2	9	E28854	fibrinopeptide B -
26	18	21.2	10	S77980	cytochrome-c oxida
27	18	21.2	12	G64003	hypothetical prote
28	18	21.2	12	PH1464	T-cell receptor be
29	18	21.2	13	PT0263	Ig heavy chain CRD

30 18 21.2 13 2 S47380 T-cell antigen rec
31 18 21.2 13 2 AB0764 his operon leader
32 18 21.2 13 2 S60046 early nodulin 40 -
33 18 21.2 13 2 JQ2309 hypothetical 1.6K
34 18 21.2 13 2 JQ2319 hypothetical 1.6K
35 18 21.2 14 2 PT0254 Ig heavy chain CRD
36 18 21.2 14 2 PH0915 T-cell receptor be
37 18 21.2 14 2 S29632 xylan 1,4-beta-xyl
38 18 21.2 14 2 I54945 gene C protein - E
39 17 20.0 5 2 C53284 T-cell receptor be
40 17 20.0 6 2 JN0861 peptidyl-dipeptida
41 17 20.0 6 2 PT0723 T-cell receptor be
42 17 20.0 7 2 PT0719 T-cell receptor be
43 17 20.0 7 2 PT0702 T-cell receptor be
44 17 20.0 8 2 PT0595 T-cell receptor be
45 17 20.0 8 2 PT0530 T-cell receptor be

ALIGNMENTS

RESULT 1

PT0304

Ig heavy chain CRD3 region (clone 5-115B) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PT0304

R:Yanada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A>Title: Preferential utilization of specific immunoglobulin heavy chain diversity and

A:Reference number: PT0222; MUID:91108337; PMID:1899102

A:Accession: PT0304

A:Molecule type: DNA

A:Residues: 1-13 <YAM>

A:Experimental source: B lymphocyte

C:Keywords: heterotetramer; immunoglobulin

Query Match 28.2%; Score 24; DB 2; Length 13;

Best Local Similarity 36.4%; Pred. No. 6.8e+02;

Matches 4; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 3 GYVHFVKKHVH 13

DB 3 GYDFWSREAH 13

RESULT 2

PC7079

unidentified 27.2K protein - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004

C:Accession: PC7079

R:Tsugita, A.; Kawakami, T.; Uchida, T.; Sakai, T.; Kano, M.; Matsui, T.; Watanabe, Y.;

Electrophoresis 21, 1853-1871, 2000

A>Title: Proteome analysis of mouse brain: Two-dimensional electrophoresis profiles of t

A:Reference number: PC7072

A:Accession: PC7079

A:Molecule type: protein

A:Residues: 1-14 <TSU>

A:Cross-references: UNIPROT:Q8K3J1

A:Experimental source: strain C57BL/6Cr Slc, male; brain, striatum

C:Keywords: brain

Query Match 28.2%; Score 24; DB 2; Length 14;

Best Local Similarity 45.5%; Pred. No. 7.3e+02;

Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 5 YHFVKKHVES 15

DB 2 KYVNKEQES 12

RESULT 3

S74128
 superoxide dismutase (EC 1.15.1.1) 1 (Ni) - Streptomyces coelicolor (fragment)
 C;Species: Streptomyces coelicolor
 C;Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-May-1999
 C;Accession: S74128
 R;Kim, E.J.; Kim, H.P.; Hah, Y.C.; Roe, J.H.
 Eur. J. Biochem. 241, 178-185, 1996
 A;Title: Differential expression of superoxide dismutases containing Ni and Fe/Zn in Streptomyces coelicolor
 A;Reference number: S74128; MUID:97054607; PMID:8898904
 A;Accession: S74128
 A;Molecule type: protein
 A;Residues: 1-14 <KIM>
 A;Experimental source: ATCC 10147
 C;Function:
 A;Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
 C;Keywords: metalloprotein; nickel; oxidoreductase; tetramer

Query Match 27.1%; Score 23; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GGVY 5
 ||||
 Db 6 GGVY 9

RESULT 4
 PLO184
 capsid protein VP-1 - murine poliovirus (fragment)
 C;Species: murine poliovirus, Theiler's encephalomyelitis virus
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Feb-1995
 C;Accession: PLO184
 R;Zurbriggen, A.; Hogle, J.M.; Fujinami, R.S.
 J. Exp. Med. 170, 2037-2049, 1989
 A;Title: Alteration of amino acid 101 within capsid protein VP-1 changes the pathogenicity of murine poliovirus
 A;Reference number: PLO184; MUID:90063468; PMID:2479706
 A;Accession: PLO184
 A;Molecule type: genomic RNA
 A;Residues: 1-8 <ZUR>
 C;Keywords: capsid protein

Query Match 24.7%; Score 21; DB 2; Length 8;
 Best Local Similarity 42.9%; Pred. No. 2.8e+05;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGGVYHF 7
 :||: :
 Db 1 SGGITNF 7

RESULT 5
 PN0662
 dystrophin-associated glycoprotein A3a-I - rabbit (fragment)
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 07-May-1999
 C;Accession: PN0662
 R;Yoshida, M.; Mizuno, Y.; Nonaka, I.; Ozawa, E.
 J. Biochem. 114, 634-639, 1993
 A;Title: A dystrophin-associated glycoprotein, A3a (one of 43DAG doublets), is retained in dystrophin-deficient muscle
 A;Reference number: PN0662; MUID:94156881; PMID:8113213
 A;Accession: PN0662
 A;Molecule type: protein
 A;Residues: 1-15 <YOS>
 C;Comment: This protein is retained in Duchenne type muscular dystrophy muscle.
 C;Keywords: glycoprotein; skeletal muscle

Query Match 24.7%; Score 21; DB 2; Length 15;
 Best Local Similarity 66.7%; Pred. No. 2.5e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 7 FVKGVH 12
 ||||
 Db 5 FIKKGV 10

RESULT 6

PQ0780
 NADH2 dehydrogenase (EC 1.6.99.3) 39K chain - fava bean mitochondrion (fragment)
 N;Alternate names: complex I 39K chain; NADH-ubiquinone reductase 39K chain
 C;Species: mitochondrion Vicia faba (fava bean)
 C;Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
 C;Accession: PQ0780
 R;Letenneur, S.; Boutry, M.
 Plant Physiol. 102, 435-443, 1993
 A;Title: Purification and preliminary characterization of mitochondrial complex I (NADH: NADH-ubiquinone reductase)
 A;Reference number: PQ0775; MUID:94151437; PMID:8108509
 A;Accession: PQ0780
 A;Molecule type: protein
 A;Residues: 1-15 <LET>
 A;Cross-references: UNIPROT:Q7W2F9
 C;Comment: Complex I, mitochondrial NADH-ubiquinone reductase, is the first of the th ranging from 5K to 75K.
 C;Comment: This enzyme catalyzes electron transfer from endogenous NADH to ubiquinone by C;Genetics:
 C;Genome: mitochondrion
 C;Keywords: electron transfer; mitochondrion; oxidoreductase

Query Match 24.7%; Score 21; DB 2; Length 15;
 Best Local Similarity 57.1%; Pred. No. 2.5e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GVVHVFV 9
 ||||
 Db 7 GVGHVLR 13

RESULT 7

PL0142
 carbon-monoxide dehydrogenase (EC 1.2.99.2) medium chain - Pseudomonas carboxydoflava (F)
 C;Species: pseudomonas carboxydoflava
 C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 28-Apr-1993
 C;Accession: PL0142
 R;Kraut, M.; Hugendieck, I.; Herwig, S.; Meyer, O.
 Arch. Microbiol. 152, 335-341, 1989
 A;Title: Homology and distribution of CO dehydrogenase structural genes in carboxydoflora
 A;Reference number: PL0138; MUID:90055678; PMID:2818128
 A;Accession: PL0142
 A;Molecule type: protein
 A;Residues: 1-14 <KRA>
 C;Comment: Carbon-monoxide dehydrogenase consists of three polypeptide chains: large, me
 C;Keywords: oxidoreductase

Query Match 24.1%; Score 20.5; DB 2; Length 14;
 Best Local Similarity 62.5%; Pred. No. 2.8e+03;
 Matches 5; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy 5 YHFKVGHV 12
 ||||
 Db 8 YH-APKHV 14

RESULT 8

NYPG7
 hypothalamic heptapeptide - pig
 C;Species: Sus scrofa domestica (domestic pig)
 C;Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 09-Jul-2004
 C;Accession: A01417
 R;Chang, R.C.C.; Huang, W.Y.; Arimura, A.; Redding, T.W.; Coy, D.H.; Saffran, M.; Kong, Horm. Metab. Res. 13, 228-232, 1981
 A;Title: Isolation, structure and synthesis of a heptapeptide with in vitro ACTH-release
 A;Reference number: A01417; MUID:81213980; PMID:6263778
 A;Accession: A01417
 A;Molecule type: protein
 A;Residues: 1-7 <CHA>
 A;Cross-references: UNIPROT:P01153
 C;Superfamily: hypothalamic heptapeptide

C;Keywords: hypothalamus

Query Match 23.5%; Score 20; DB 1; Length 7;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 VYHVK 9
|||
DB 2 IYHSYK 7

RESULT 9

PQ0733
unidentified 6.0/15K protein [imported] - rice (fragment)
C;Species: Oryza sativa (rice)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: PQ0733
R;Komatsu, S.; Kajiwara, H.; Hirano, H.
Theor. Appl. Genet. 86, 935-942, 1993
A;Title: A rice protein library; a data-file of rice proteins separated by two-dimension
A;Reference number: PQ0696
A;Accession: PQ0733
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11 <KOM>

Query Match 23.5%; Score 20; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 HVH 13
|||
DB 5 HVH 7

RESULT 10

S03530
Ig heavy chain J region (JH-4) - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 21-Nov-1993 #sequence_revision 08-Nov-1996 #text_change 21-Jul-2000
C;Accession: S03530
R;Schwager, J.; Grossberger, D.; du Pasquier, L.
EMBO J. 7, 2409-2415, 1988
A;Title: Organization and rearrangement of immunoglobulin M genes in the amphibian Xenopus
A;Reference number: S01150; MUID:89052653; PMID:2903824
A;Accession: S03530
A;Molecule type: DNA
A;Residues: 1-14 <SCH>
A;Cross-references: EMBL:X14918; NID:G64805; PIDN:CAA33043.1; PID:g1334657

Query Match 23.5%; Score 20; DB 2; Length 14;
Best Local Similarity 75.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 VYHW 7
|||
DB 1 VYHW 4

RESULT 11

S57569
T cell receptor V-J junctional alpha chain region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 05-Nov-1999
C;Accession: S57569
R;Burrows, S.R.; Sillins, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Arguet, V.P.
submitted to the EMBL Data Library, June 1995
A;Description: T cell receptor repertoire for a viral epitope in humans is diversified
A;Reference number: S57494
A;Accession: S57569
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-14 <BUR>

A;Cross-references: EMBL:Z49955; NID:9887482; PIDN:CAA90226.1; PID:9887483
C;Keywords: T-cell receptor

Query Match 23.5%; Score 20; DB 2; Length 14;
Best Local Similarity 42.9%; Pred. No. 3.4e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGGVYHF 7
|||
DB 7 TGNQFYF 13

RESULT 12

S57638
T cell receptor V-J junctional alpha chain region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 05-Nov-1999
C;Accession: S57638
R;Burrows, S.R.; Sillins, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Arguet, V.P.
submitted to the EMBL Data Library, June 1995
A;Description: T cell receptor repertoire for a viral epitope in humans is diversified
A;Reference number: S57494
A;Accession: S57638
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-14 <BUR>

A;Cross-references: EMBL:Z49964; NID:9886676; PIDN:CAA90238.1; PID:9886677
C;Keywords: T-cell receptor

Query Match 23.5%; Score 20; DB 2; Length 14;
Best Local Similarity 42.9%; Pred. No. 3.4e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGGVYHF 7
|||
DB 7 TGNQFYF 13

RESULT 13

A61145
dihydrofolate reductase (EC 1.5.1.3) - Mycobacterium smegmatis (fragment)
C;Species: Mycobacterium smegmatis
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 17-Mar-1999
C;Accession: A61145
R;Sirawaraporn, W.; Sirawaraporn, R.; Chanpongsri, A.; Jacobs Jr., W.R.; Santi, D.V.
Exp. Parasitol. 72, 184-190, 1991
A;Title: Purification and characterization of dihydrofolate reductase from wild-type and
A;Reference number: A61145; MUID:91184314; PMID:2009922

A;Accession: A61145
A;Molecule type: protein
A;Residues: 1-15 <SIR>
C;Keywords: NADP; oxidoreductase

Query Match 23.5%; Score 20; DB 2; Length 15;
Best Local Similarity 75.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGV 4
|||
DB 10 TGGI 13

RESULT 14

PA0093
emiatin synthetase - fungus (Fusarium sporotrichioides) (fragment)
C;Species: Fusarium sporotrichioides
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: PA0093
R;Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Taugita, A.
submitted to JIPID, October 1994
A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichi
A;Reference number: PA0051
A;Accession: PA0093

A;Molecule type: protein
A;Residues: 1-15 <CHO>

A;Cross-References: UNIPROT:Q7M4Z6

Query Match 22.9%; Score 19.5; DB 2; Length 15;
Best Local Similarity 60.0%; Pred. No. 4.4e+03;
Matches 6; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

QY 4 VYHFVKGVH 13
DB 1 VYTFV---VH 7

RESULT 15

C61440

polygalacturonase (EC 3.2.1.15) II b - Aspergillus sp. (fragment)

C;Species: Aspergillus sp.

C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 06-Dec-1996

C;Accession: C61440

R;Stratilova, E.; Markovic, O.; Skrovinova, D.; Rexova-Benkova, L.; Jornvall, H.

J. Protein Chem. 12, 15-22, 1993

A;Title: Pectinase Aspergillus sp. polygalacturonase: multiplicity, divergence, and stru

A;Reference number: A61440; MUID:93151962; PMID:8427629

A;Accession: C61440

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-10 <STR>

C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 22.4%; Score 19; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGVYHF 7
DB 2 GGAFTF 7

Search completed: February 22, 2005, 09:46:29
Job time : 12.1333 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 22, 2005, 08:53:13 ; Search time 52.6 Seconds
(without alignments)
146.030 Million cell updates/sec

Title: US-08-991-628-12

Perfect score: 85

Sequence: 1 TGGVYHFVKKHVHES 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 6622

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	36.5	15	Q64FK1	Q64fk1 homo sapien
2	26	30.6	13	Q6LDM2	Q6ldm2 pseudomonas
3	26	30.6	13	Q7Z2N6	Q7z2n6 xenopus lae
4	25	29.4	11	Q9X9S6	Q9x9s6 streptomyce
5	24	28.2	13	GFAL_RAT	P82808 rattus norv
6	23	27.1	9	Q8QRR5	Q8qrr5 transmissib
7	23	27.1	9	Q8QRR6	Q8qrr6 transmissib
8	23	27.1	10	Q6R7V4	Q6r7v4 carlia zuma
9	23	27.1	11	Q68LE0	Q68le0 pyriglena l
10	23	27.1	11	Q68LE9	Q68le9 myzotherul
11	23	27.1	12	UKA2_HUMAN	P31144 homo sapien
12	23	27.1	12	Q6AV52	Q6av52 oryza sativ
13	23	27.1	14	Q6R7V0	Q6r7v0 carlia viva
14	22	25.9	8	Q70Y68	Q70y68 prostanthor
15	22	25.9	11	Q70Y70	Q70y70 thornicrofti
16	22	25.9	12	Q8GSB9	Q8gsb9 lolium pere
17	22	25.9	13	AU11_LITRA	P82386 litoria ran
18	22	25.9	13	AU12_LITRA	P82387 litoria ran
19	22	25.9	14	ADFA_TENMO	P82965 tenebrio mo
20	22	25.9	15	Q7RHY2	Q7rhy2 plasmodium
21	22	25.9	15	Q6Z274	Q6zz74 lychnis flo
22	22	25.9	15	Q9FS98	Q9fs98 silene laco
23	21.5	25.3	13	Q66NE7	Q66ne7 borrelia bu
24	21	24.7	8	ALJ9_CARMA	P81812 carcinus bu
25	21	24.7	9	Q8W8X4	Q8w8x4 diadema mex
26	21	24.7	10	Q7RSJ0	Q7rsj0 plasmodium
27	21	24.7	13	Q6LCB1	Q6lcb1 rattus norv
28	21	24.7	13	Q90XG9	Q90xg9 gallus gall
29	21	24.7	14	Q85578	Q85578 sigma virus
30	21	24.7	15	UC14_WAIZE	P80620 zea mays (m
31	21	24.7	15	Q7M2F9	Q7m2f9 vicia faba

32 21 24.7 15 2 Q68430
33 20 23.5 7 1 HY7_PIG
34 20 23.5 8 2 Q05403
35 20 23.5 8 2 Q6EGT1
36 20 23.5 8 2 Q6EGV0
37 20 23.5 8 2 Q6EGV3
38 20 23.5 8 2 Q6EGW2
39 20 23.5 12 2 Q9UC29
40 20 23.5 12 2 Q8H6B6
41 20 23.5 15 2 Q7R6W8
42 20 23.5 15 2 Q8TWF3
43 20 23.5 15 2 Q95762
44 20 23.5 15 2 Q54298
45 19.5 22.9 12 2 Q8CJ30

O68430 buchnera ap
P01153 sus scrofa
Q05403 saccharomyc
Q6egt1 stemphylium
Q6egv0 stemphylium
Q6egv3 stemphylium
Q6egw2 stemphylium
Q9uc29 homo sapien
Q8h6e6 hordeum vul
Q7r6w8 plasmodium
Q8twf3 dictyosteli
Q95762 ctenosaura
Q54298 salmonella
Q8cj30 mus musculus

ALIGNMENTS

RESULT 1
Q64FK1 PRELIMINARY; PRT; 15 AA.
AC Q64FK1;
DT 25-OCT-2004 (TREMBLrel. 28, Created)
DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
DE Breast and ovarian cancer susceptibility protein 1 (Fragment).
GN Name=BRCA1;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Soumitra N., Sridevi V., Shanta V., Rajkumar T.;
RT "Mutation analysis of BRCA1 gene";
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY706913; AAU21565.1; -;
FT NON TER 1
SQ SEQUENCE 15 AA; 1905 MW; 6E1A57496E31C01D CRC64;

Query Match 36.5%; Score 31; DB 2; Length 15;
Best Local Similarity 62.5%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 VVHFVKKH 11
||| :||
Db 3 VYKFARKH 10

RESULT 2
Q6LDM2 PRELIMINARY; PRT; 13 AA.
AC Q6LDM2;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical protein (Fragment).
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PAO;
RX MEDLINE=90036723; PubMed=2509433;
RA Hoshino T., Kose K.;
RT "Cloning and nucleotide sequence of brac, the structural gene for the
RT leucine-, isoleucine-, and valine-binding protein of Pseudomonas
RT aeruginosa PAO.";
RL J. Bacteriol. 171:6300-6306(1989).
DR EMBL; M31071; AAA88431.1; -;
KW Hypothetical protein.

FT NON TER 13 13 P275BF6289BE3B51 CRC64;
SQ SEQUENCE 13 AA; 1648 MW; 29.4%; Score 26; DB 2; Length 13;
Best Local Similarity 30.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Query Match 30.6%; Score 26; DB 2; Length 13;
Best Local Similarity 30.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 4 VYHFVKKVHV 13
:||||:|
Db 4 IYHLYQLLVN 13

RESULT 3
Q7ZZN6 PRELIMINARY; PRT; 13 AA.
ID Q7ZZN6
AC Q7ZZN6
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Zinc finger protein (Fragment).
GN Name=Zic3;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cerebellum;
RX MEDLINE=22844363; PubMed=12963115; DOI=10.1016/S0925-4773(03)00082-0;
RA Weber J.R., Sokol S.Y.;
RT "Identification of a phylogenetically conserved activin-responsive
enhancer in the Zic3 gene."
RL Mech. Dev. 120:955-964(2003).
DR EMBL; AF506278; AAP20809.1; -.
FT NON TER 1 1
FT NON TER 13 13
SQ SEQUENCE 13 AA; 1537 MW; 5DDA56257F6DF2C3 CRC64;

Query Match 30.6%; Score 26; DB 2; Length 13;
Best Local Similarity 60.0%; Pred. No. 1.6e+03;
Matches 6; Conservative 2; Mismatches 0; Indels 2; Gaps 1;

QY 8 VKKH--VHES 15
:|||||
Db 1 LRKHKVHES 10

RESULT 4
Q9X9S6 PRELIMINARY; PRT; 11 AA.
ID Q9X9S6
AC Q9X9S6
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Hypothetical protein ORF9 (Fragment).
GN Name=ORF9;
OS Streptomyces lividans.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1916;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TK21;
RX MEDLINE=99328982; PubMed=10400594;
RA Martinez-Costa O.H., Martin-Triana A.J., Martinez E.,
Fernandez-Moreno M.A., Malpartida F.;
RT "An additional regulatory gene for actinorhodin production in
Streptomyces lividans involves a lysr-type transcriptional
regulator."
RL J. Bacteriol. 181:4353-4364(1999).
DR EMBL; Y18818; CAB51138.1; -.
KW Hypothetical protein.

FT NON TER 1 1 D1BABA8EC1EDC412 CRC64;
SQ SEQUENCE 11 AA; 1160 MW; 29.4%; Score 25; DB 2; Length 11;
Best Local Similarity 66.7%; Pred. No. 2e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Query Match 29.4%; Score 25; DB 2; Length 11;
Best Local Similarity 66.7%; Pred. No. 2e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 VKKHVV 13
|:|
Db 4 VRAHVH 9

RESULT 5
GFAL_RAT STANDARD; PRT; 13 AA.
ID GFAL_RAT
AC P82808;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Glucosamine--fructose-6-phosphate aminotransferase [isomerizing] 1
DE (EC 2.6.1.16) (Hexosephosphate aminotransferase 1) (D-fructose-6-
phosphate amidotransferase 1) (GFAT 1) (Fragment).
GN Name=Gfpt1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE, FUNCTION, CATALYTIC ACTIVITY, AND ENZYME REGULATION.
RC STRAIN=Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=20359980; PubMed=10898949; DOI=10.1006/abb1.2000.1895;
RA Huynh Q.K., Gulve E.A., Dian T.;
RT "Purification and characterization of glutamine:fructose 6-phosphate
amidotransferase from rat liver."
RL Arch. Biochem. Biophys. 379:307-313(2000).
CC -|- FUNCTION: Controls the flux of glucose into the hexosamine
pathway. Most likely involved in regulating the availability of
precursors for N- and O-linked glycosylation of proteins.
CC -|- CATALYTIC ACTIVITY: L-glutamine + D-fructose 6-phosphate = L-
glutamate + D-glucosamine 6-phosphate.
CC -|- ENZYME REGULATION: Inhibited by 4,4'-dithiodipyridine.
CC -|- SUBUNIT: Homotetramer (Potential).
CC -|- MISCELLANEOUS: Optimum pH is 7.5.
CC -|- SIMILARITY: Contains 1 type-2 glutamine amidotransferase domain.
DR MEROPS; C44.970; -.
DR InterPro; IPR000583; GATase 2.
DR PROSITE; PS00443; GATASE TYPE II; 1.
KW Aminotransferase; Direct protein sequencing;
KW Glutamine amidotransferase; Transferase.
FT INIT MET 0 0 By similarity.
FT ACT SITE 1 1 GATase (By similarity).
FT DOMAIN 1 >13 Glutamine amidotransferase (Potential).
FT NON TER 13 13
SQ SEQUENCE 13 AA; 1553 MW; 0944F6BB32DB473B CRC64;

Query Match 28.2%; Score 24; DB 1; Length 13;
Best Local Similarity 30.0%; Pred. No. 3.6e+03;
Matches 3; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 GVHFVKKHV 12
|:|:|
Db 2 GIFAYLVHV 11

RESULT 6
Q8QRR5 PRELIMINARY; PRT; 9 AA.
ID Q8QRR5
AC Q8QRR5
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Spike glycoprotein (Fragment).
OS Transmissible gastroenteritis virus.

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
 OC Coronaviridae; Coronavirus; Group 1 species.

OX NCBI_TaxID=111149;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=KT2;
 RL Kim S.J., Kwon H.M.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF481368; AAL89748.1; -.
 FT NON_TER 1
 SQ SEQUENCE 9 AA; 1087 MW; 34E3C1P2C33B1047 CRC64;

Query Match 27.1%; Score 23; DB 2; Length 9;
 Best Local Similarity 80.0%; Pred. No. 1.6e+06;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 KKHVH 13
 DB 5 KKHVH 9

RESULT 7

Q8QRR6 PRELIMINARY; PRT; 9 AA.
 AC Q8QRR6;
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Spike glycoprotein (Fragment).
 OS Transmissible gastroenteritis virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
 OC Coronaviridae; Coronavirus; Group 1 species.
 OX NCBI_TaxID=111149;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HK2;
 RA Kim S.J., Kwon H.M.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF481367; AAL89746.1; -.
 FT NON_TER 1
 SQ SEQUENCE 9 AA; 1087 MW; 34E3C1P2C33B1047 CRC64;

Query Match 27.1%; Score 23; DB 2; Length 9;
 Best Local Similarity 80.0%; Pred. No. 1.6e+06;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 KKHVH 13
 DB 5 KKHVH 9

RESULT 8

Q6R7V4 PRELIMINARY; PRT; 10 AA.
 AC Q6R7V4;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Glyceraldehyde-3-phosphate dehydrogenase (Fragment).
 GN Name=GAPDH;
 OS Carlia zuma.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Scincomorpha; Scincoidea;
 OC Scincidae; Carlia.
 OX NCBI_TaxID=260893;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Dolman G., Phillips B.;
 RA "Single copy nuclear DNA markers characterized for comparative
 phylogeography in Australian wet tropics rainforest skinks.";
 RL Mol. Ecol. Notes 4:185-187(2004).
 DR EMBL; AY508912; AAS09890.1; -.
 FT NON_TER 1

FT NON_TER 10
 SQ SEQUENCE 10 AA; 1171 MW; 9D0ABB2322C9C1EA CRC64;

Query Match 27.1%; Score 23; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 HFVK 9
 DB 4 HFVK 7

RESULT 9

Q68LE0 PRELIMINARY; PRT; 11 AA.
 AC Q68LE0;
 DT 25-OCT-2004 (TREMBLrel. 28, Created)
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
 DE Glyceraldehyde-3-phosphate dehydrogenase (Fragment).
 GN Name=NAPDH;
 OS Pyriglena leuconota.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Passeriformes; Formicariidae;
 OC Pyriglena.
 OX NCBI_TaxID=183187;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=15283860;
 RA Irestedt M., Fjeldea J., Nylander J.A., Ericson P.G.;
 RT "Phylogenetic relationships of typical antbirds (Thamophilidae) and
 test of incongruence based on Bayes factors.";
 RL BMC Evol. Biol. 4:23-23(2004).
 DR EMBL; AY677056; AAT96981.1; -.
 FT NON_TER 1
 FT NON_TER 11
 SQ SEQUENCE 11 AA; 1242 MW; 9D0ABB2622C9C1EA CRC64;

Query Match 27.1%; Score 23; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 4.5e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 HFVK 9
 DB 5 HFVK 8

RESULT 10

Q68LE9 PRELIMINARY; PRT; 11 AA.
 AC Q68LE9;
 DT 25-OCT-2004 (TREMBLrel. 28, Created)
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
 DE Glyceraldehyde-3-phosphate dehydrogenase (Fragment).
 GN Name=NAPDH;
 OS Myrmotherula fulviventris.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Passeriformes; Thamophilidae;
 OC Myrmotherula.
 OX NCBI_TaxID=288045;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=15283860;
 RA Irestedt M., Fjeldea J., Nylander J.A., Ericson P.G.;
 RT "Phylogenetic relationships of typical antbirds (Thamophilidae) and
 test of incongruence based on Bayes factors.";
 RL BMC Evol. Biol. 4:23-23(2004).
 DR EMBL; AY677047; AAT96972.1; -.
 FT NON_TER 1
 FT NON_TER 11
 SQ SEQUENCE 11 AA; 1242 MW; 9D0ABB2622C9C1EA CRC64;

Query Match 27.1%; Score 23; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 4.9e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 HFVK 9
 ||||
 Db 5 HFVK 8

RESULT 11
 UKA2 HUMAN
 ID UKA2 HUMAN STANDARD; PRT; 12 AA.
 AC P31144;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Unknown protein from 2D-PAGE of epidermal keratinocytes (Spot 1617) (Fragments).
 DE (Fragments).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Keratinocytes;
 RX MEDLINE=93162043; PubMed=1286667;
 RA Rasmussen H.H., van Damme J., Puyte M., Geisser B., Celis J.E.,
 RA Vandeckerkhove J.;
 RT "Microsequences of 145 proteins recorded in the two-dimensional gel
 protein database of normal human epidermal keratinocytes.";
 RL Electrophoresis 13:960-969(1992).
 CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
 protein is: 6.93, its MW is: 81.6 kDa.
 CC Aarhus/Ghent-2DPAGE; 1617; IEF.
 DR Direct protein sequencing.
 KW NON TER 1 1
 FT NON CONS 7 8
 FT UNSURE 8 8
 FT NON TER 12 12
 SQ SEQUENCE 12 AA; 1351 MW; D6CD4A5E75F2C1F6 CRC64;

Query Match 27.1%; Score 23; DB 1; Length 12;
 Best Local Similarity 42.9%; Pred. No. 4.9e+03;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 7 FVKHVV 13
 ::::|||
 Db 2 YLGQHV 8

RESULT 12
 Q6AV52 PRELIMINARY; PRT; 12 AA.
 ID Q6AV52;
 AC Q6AV52;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein OSUNB0101N11.9.
 GN Name=OSUNB0101N11.9;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
 RA Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S.,
 RA Padrosh D.W., Tallon L.J., Koo H., Ziesmann V., Hsiao J., Blunt S.,
 RA Vanaken S.S., Riedmuller S.B., Uterback T.T., Feldblyum T.V.,
 RA Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
 RA White O., Salzberg S.L., Fraser C.M.;
 RT "Oryza sativa chromosome 3 BAC OSUNB0101N11 genomic sequence.";

RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Buell R.;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC105747; AAT76999.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 12 AA; 1323 MW; C9C78EF8E2573B5D CRC64;

Query Match 27.1%; Score 23; DB 2; Length 12;
 Best Local Similarity 57.1%; Pred. No. 4.9e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGVYHFV 8
 ||||:
 Db 3 GGAYLYV 9

RESULT 13
 Q6R7V0 PRELIMINARY; PRT; 14 AA.
 ID Q6R7V0;
 AC Q6R7V0;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Glyceraldehyde-3-phosphate dehydrogenase (Fragment).
 GN Name=GAPDH;
 OS Carlia vivax.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Scincomorpha; Scincoidea;
 OC Scincidae; Carlia.
 OX NCBI_TaxID=124122;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Dolman G., Phillips B.;
 RT "Single copy nuclear DNA markers characterized for comparative
 phylogeography in Australian wet tropics rainforest skinks.";
 RL Mol. Ecol. Notes 4:185-187(2004).
 DR EMBL; AY508916; AAS09894.1; -.
 FT NON TER 1 1
 FT NON TER 14 14
 SQ SEQUENCE 14 AA; 1750 MW; 51923E7F6D0ABB23 CRC64;

Query Match 27.1%; Score 23; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 5.9e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 HFVK 9
 ||||
 Db 4 HFVK 7

RESULT 14
 Q70Y68 PRELIMINARY; PRT; 8 AA.
 ID Q70Y68;
 AC Q70Y68;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Ribosomal protein (Fragment).
 GN Name=rps16;
 OS Prostanthera nivea (snowy mintbush).
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Lamiaceae; Prostantheroideae; Westringiaceae;
 OC Prostanthera.
 OX NCBI_TaxID=39863;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA PubMed=15019625; DOI=10.1016/j.ympev.2003.08.002;
 RA Paton A., Springate D.A., Sudde S., Otieno D., Grayer R., Harley M.M.,
 RA Willis F., Simonds M.S.J., Powell M.P., Savolainen V.;

RT "Phylogeny and evolution of basils and allies (Ocimeae, Labiatae)
 RT based on three plastid DNA regions."
 RL Mol. Phylogenet. Evol. 31:277-299(2004).
 DR EMBL; AJ505403; CAD45523.1; -
 DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
 KW Ribosomal protein.
 FT NON_TER 1
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 838 MW; C821P2C058786415 CRC64;

Query Match 25.9%; Score 22; DB 2; Length 8;
 Best Local Similarity 60.0%; Pred. No. 1.6e+06;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGVYH 6
 ||:
 Db 3 GGIVH 7

RESULT 15

Q70Y70
 ID Q70Y70 PRELIMINARY; PRT; 11 AA.
 AC Q70Y70;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Ribosomal protein (Fragment).
 GN Name=rpel6;
 GN Thorncroftia longiflora.
 OS Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Thorncroftia.
 OX NCBI_TaxID=204202;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=15019625; DOI=10.1016/j.ympev.2003.08.002;
 RA Paton A., Springate D.A., Sudde S., Otieno D., Grayer R., Harley M.M.,
 RA Willis P., Simonds M.S.J., Powell M.P., Savolainen V.;
 RT "Phylogeny and evolution of basils and allies (Ocimeae, Labiatae)
 RT based on three plastid DNA regions."
 RL Mol. Phylogenet. Evol. 31:277-299(2004).
 DR EMBL; AJ505401; CAD45521.1; -
 DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
 KW Ribosomal protein.
 FT NON_TER 1
 FT NON_TER 11
 SQ SEQUENCE 11 AA; 1201 MW; 396BE78821F2C058 CRC64;

Query Match 25.9%; Score 22; DB 2; Length 11;
 Best Local Similarity 60.0%; Pred. No. 6.7e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGVYH 6
 ||:
 Db 3 GGIVH 7

Search completed: February 22, 2005, 09:38:02
 Job time : 53.6667 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 22, 2005, 08:52:23 ; Search time 65.6667 Seconds
(without alignments)
88.346 Million cell updates/sec

Title: US-08-991-628-12

Perfect score: 85

Sequence: 1 TGGVYHFVKGVHES 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 632537

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85	100.0	15	2	Aaw04852 Internal
2	37	43.5	13	5	Abb74425 Karyophil
3	36	42.4	15	5	Abj10692 Japanese
4	36	42.4	15	5	Abj10696 Japanese
5	35	41.2	15	2	Aaw04855 Internal
6	32	37.6	12	2	Aaw80378 Peptide e
7	32	37.6	15	5	Aau78249 Polypepti
8	31	36.5	7	4	Aau03943 Human GDN
9	31	36.5	13	7	Adb81184 Human pan
10	30	35.3	11	2	Aaw11603 Linear Zn
11	30	35.3	12	8	Adp83191 ICAM-5 PG
12	30	35.3	13	8	Adi32280 Cosmetic
13	30	35.3	15	3	Abi13485 C. tracho
14	30	35.3	15	4	Aag83161 Chlamydia
15	30	35.3	15	5	Abb94132 Chlamydia
16	30	35.3	15	6	Abc32837 Human can
17	30	35.3	15	6	Abc32881 Human can
18	30	35.3	15	6	Abc33030 Human can
19	30	35.3	15	6	Abc32938 Human can
20	30	35.3	15	6	Abc33038 Human can
21	29	34.1	10	6	Abj20765 162P1E6 c
22	29	34.1	10	6	Abj23568 162P1E6 c
23	29	34.1	10	6	Abj22816 162P1E6 c
24	29	34.1	10	6	Abu22415 162P1E6 c
25	29	34.1	10	6	Abj21424 162P1E6 c

26	29	34.1	10	6	ABJ24945	Abj24945 162P1E6 c
27	29	34.1	10	6	ABJ22137	Abj22137 162P1E6 c
28	29	34.1	12	2	AAR63394	Aar63394 Peptide f
29	29	34.1	12	2	AAR96448	Aar96448 Hepatitis
30	29	34.1	12	2	AAR96449	Aar96449 Hepatitis
31	29	34.1	14	3	AAJ78374	Aaj78374 H. pylori
32	29	34.1	15	2	AAJ30497	Aaj30497 Mutant se
33	29	34.1	15	5	AAU76497	Aau76497 Ribosomal
34	29	34.1	15	8	ADP26532	Adp26532 Plasmodiu
35	28	32.9	9	2	AAV45437	Aav45437 Immunogen
36	28	32.9	9	4	AAB98468	Aab98468 HLA class
37	28	32.9	9	4	AAB96047	Aab96047 HLA-A11 b
38	28	32.9	9	4	AAG84524	Aag84524 Human leu
39	28	32.9	9	4	AAU06283	Aau06283 Human leu
40	28	32.9	9	4	AAG88276	Aag88276 Human leu
41	28	32.9	9	4	ABP11505	Abp11505 HLA class
42	28	32.9	9	4	AAG89372	Aag89372 Human leu
43	28	32.9	9	4	AAJ00060	Aaj00060 Hepatitis
44	28	32.9	9	5	ABJ05792	Abj05792 Hepatitis
45	28	32.9	9	8	ADK39622	Adk39622 Hepatitis

ALIGNMENTS

RESULT 1
AAW04852
ID AAW04852 standard; peptide; 15 AA.
AC AAW04852;
XX
DT 16-OCT-2003 (revised)
DT 18-FEB-1997 (first entry)
XX
DE Internal fragment of Epstein-Barr virus DNA polymerase.

XX
KW Tolerisation; self-epitope; antigen; autoimmune disease; autoantigen;
KW HLA; human leukocyte antigen; T-cell; thymocyte; pemphigus vulgaris;
KW desmoglein; multiple sclerosis; herpes simplex virus; adenovirus;
KW phosphomannomutase; human papillomavirus; Epstein-Barr virus;
KW DNA polymerase; influenza; haemagglutinin; reovirus; sigma protein.
XX
OS Human herpesvirus 4.

XX
PN WO9627387-A1.

XX
PD 12-SEP-1996.

XX
PF 07-MAR-1996; 96WO-US003182.

XX
PR 07-MAR-1995; 95US-00400796.

XX
PA (HARD) HARVARD COLLEGE.

XX
PI Strominger JL, Wuchterfennig KW;

XX
DR WPI; 1996-425218/42.

XX
PT Pemphigus vulgaris auto-antigens and multiple sclerosis non-self antigens
PT - useful in disease treatment, and method for identification of other
PT self and non-self antigens implicated in auto-immune disease.

XX
PS Claim 2; Page 45; 58pp; English.

XX
CC Pharmaceutical preparations for tolerisation to antigens comprise either
CC an isolated human non-collagen or non-mysin basic protein (MBP)
CC polypeptide which is capable of tolerising an individual to an
CC autoantigen; or an isolated human pathogen polypeptide capable of
CC tolerising an individual to that polypeptide. In both cases, the
CC polypeptide (whether self or non-self) includes an amino acid sequence
CC corresponding to a sequence motif for a MHC class II protein, such as HLA
CC -DR, which is associated with a human autoimmune disease and which binds
CC to the polypeptide to activate autoreactive T-cells in individuals with

CC the autoimmune disease. This peptide is an internal peptide of Epstein-
CC Barr virus DNA polymerase and is implicated as a foreign epitope involved
CC in the aetiology or in remissions of multiple sclerosis. It has been
CC shown capable of inducing the proliferation of autoreactive T-cell clones
CC isolated from multiple sclerosis patients. (Updated on 16-OCT-2003 to
CC standardise OS field)

XX Sequence 15 AA;

Query Match 100.0%; Score 85; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGGVYHFVKKHVHES 15

Db 1 TGGVYHFVKKHVHES 15

RESULT 2

ID ABB74425 standard; peptide; 13 AA.

XX AC ABB74425;

XX DT 18-APR-2002 (first entry)

XX DE Karyophilic peptide SEQ ID NO:189.

XX Fucogenic; nuclear localisation signal; NLS; encapsulation; lipogene;
KW liposome; micelle; karyophilic; cytostatic; antitumour; solid tumour;
KW peptide-lipid-polynucleotide complex; neoplastic disease; gene therapy;
KW breast carcinoma; prostate carcinoma.

XX OS Schizosaccharomyces pombe.

XX PN WO200193836-A2.

XX PD 13-DEC-2001.

XX PF 08-JUN-2001; 2001WO-US018657.

XX PR 09-JUN-2000; 2000US-0210925P.

XX PA (BOUL/) BOULIKAS T.

XX PI Boulikas T;

XX PS WPI; 2002-164295/21.

XX Encapsulation of plasmid DNA (Lipogenes) and therapeutic agents with
PT nuclear localization signal/fucogenic peptide conjugates into targeted
PT liposome complexes.

XX Claim 14; Page 66; 107pp; English.

XX The present invention describes a method for producing micelles with
CC entrapped therapeutic agents. The method comprises: (1) combining
CC negatively charged agent with a cationic lipid in a ratio where 30-90 %
CC of the negatively charged atoms are neutralised by positive charges on
CC lipid molecules to form an electrostatic micelle complex in 20-80 %
CC ethanol; and (2) combining the micelle complex of (a) with fucogenic-
CC karyophilic peptide conjugates in a 0.0-0.3 ratio, therefore producing
CC micelles with entrapped therapeutic agents. Also described is a method
CC for delivering a therapeutic agent in vivo, comprising the administration
CC of the micelle. ABB74256 to ABB74858 represent specifically claimed
CC nuclear localisation signal (NLS) peptides for use in the method as the
CC fucogenic-karyophilic peptides. The micelles produced can have cytostatic
CC and antitumour activities. The peptide-lipid-polynucleotide complexes
CC produced are useful for inhibiting the progression of neoplastic
CC diseases. The invention relates to the field of gene therapy and is
CC directed toward methods for producing peptide-lipid-polynucleotide
CC complexes suitable for delivery of polynucleotides. The encapsulated
CC molecules display therapeutic efficacy in eradicating solid tumours

CC including but not limited to breast carcinoma or prostate carcinoma.
CC ABB74235 to ABB74255 are used in the exemplification of the present
CC invention

XX Sequence 13 AA;

Query Match 43.5%; Score 37; DB 5; Length 13;
Best Local Similarity 40.0%; Pred. No. 24;
Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGVYHFVKKH 11

Db 2 GELFHYIRKH 11

RESULT 3

ID ABBJ0692 standard; peptide; 15 AA.

XX AC ABBJ0692;

XX DT 28-NOV-2002 (first entry)

XX DE Japanese encephalitis virus vaccine related peptide #87.

XX KW Virucide; Japanese encephalitis viral infection; protective immunity;
KW chimeric synthetic peptide; viral infection; envelope glycoprotein;
KW vaccine; neutralising antibody.

XX OS Unidentified.

XX OS Chimeric.

XX PN WO200253182-A1.

XX PD 11-JUL-2002.

XX PF 04-JAN-2002; 2002WO-IN000003.

XX PR 05-JAN-2001; 2001IN-DE000013.

XX PA (BIOT-) SEC DEPT BIOTECHNOLOGY.

XX PA (NAVI-) NAT INST VIROLOGY.

XX PA (UVPU-) UNIV PUNE.

XX PI Gore MM, Kolaskar AS, Dewasthaly SS, Kale UDK;

XX PS WPI; 2002-548046/58.

XX Vaccine composition for inducing protective immunity against Japanese
PT encephalitis viral infection, has synthetic peptide e.g. envelope
PT glycoprotein of virus, or neutralizing antibody inducing glycoprotein
PT sequences.

XX Disclosure; Page 28; 44pp; English.

XX The invention relates to a vaccine composition for humans and animals
CC against Japanese encephalitis viral infection. The composition comprises
CC a chimeric synthetic peptide, especially an envelope glycoprotein of the
CC Japanese encephalitis virus, to induce protective immunity against the
CC viral infection, or a neutralising antibody inducing peptide sequences
CC from the envelope glycoproteins of Japanese encephalitis virus. The
CC vaccine composition is useful for inducing a protective immunity against
CC Japanese encephalitis viral infection. This sequence represents a
CC Japanese encephalitis virus vaccine peptide of the invention

XX Sequence 15 AA;

Query Match 42.4%; Score 36; DB 5; Length 15;
Best Local Similarity 46.2%; Pred. No. 41;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 2 GGVYHFVKKHVHE 14

||||:|

Db 3 GGVFNSIGKAVHQ 15

RESULT 4
ABJ10696

ID ABJ10696 standard; peptide; 15 AA.

XX
AC
XX
XX
DT
XX
XX
DE
XX
XX
KW
KW
KW
XX
OS
OS
XX
PN
XX
PD
XX
PF
XX
PR
XX
PA
XX
PI
XX
DR
XX
PT
XX
PT
XX
PS
XX
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
CC
SQ

Unidentified.
Chimeric.
WO200253182-A1.
11-JUL-2002.
04-JAN-2002; 2002WO-IN000003.
05-JAN-2001; 2001IN-DE000013.
(BIOT-) SEC DEPT BIOTECHNOLOGY.
(NAVI-) NAT INST VIROLOGY.
(UYPU-) UNIV PUNE.
Gore MM, Kolaskar AS, Dewasthaly SS, Kale UDK;
WPI; 2002-548046/58.
Vaccine composition for inducing protective immunity against Japanese encephalitis viral infection, has synthetic peptide e.g. envelope glycoprotein of virus, or neutralizing antibody inducing glycoprotein sequences.
Disclosure; Page 29; 44pp; English.
The invention relates to a vaccine composition for humans and animals against Japanese encephalitis viral infection. The composition comprises a chimeric synthetic peptide, especially an envelope glycoprotein of the Japanese encephalitis virus, to induce protective immunity against the viral infection, or a neutralising antibody inducing peptide sequences from the envelope glycoproteins of Japanese encephalitis virus. The vaccine composition is useful for inducing a protective immunity against Japanese encephalitis viral infection. This sequence represents a Japanese encephalitis virus vaccine peptide of the invention

Query Match 42.4%; Score 36; DB 5; Length 15;
Best Local Similarity 46.2%; Pred. No. 41;
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGVFHFVKKVHVE 14
|||::|||
Db 3 GGVFNSIGKAVHQ 15

RESULT 5
AAW04855
ID AAW04855 standard; peptide; 15 AA.
AC
XX
XX
DT
XX
DE

Internal fragment of herpes simplex virus DNA polymerase.

XX
KW
KW
KW
KW
XX
OS
XX
PN
XX
PD
XX
PF
XX
PR
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PA
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PI
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PT
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PT
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PS
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CC
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SQ

Tolerisation; self-epitope; antigen; autoimmune disease; autoantigen; HLA; human leukocyte antigen; T-cell; thymocyte; pemphigus vulgaris; desmoglein; multiple sclerosis; herpes simplex virus; adenovirus; phosphomannomutase; human papillomavirus; Epstein-Barr virus; DNA polymerase; influenza; haemagglutinin; reovirus; sigma protein.
Herpes simplex virus.
W09627387-A1.
12-SEP-1996.
07-MAR-1996; 96WO-US003182.
07-MAR-1995; 95US-00400796.
(HARD) HARVARD COLLEGE.
Strominger JL, Wuchterfennig KW;
WPI; 1996-425218/42.
Pemphigus vulgaris auto-antigens and multiple sclerosis non-self antigens - useful in disease treatment, and method for identification of other self and non-self antigens implicated in auto-immune disease.
Claim 2; Page 47; 58pp; English.
Pharmaceutical preparations for tolerisation to antigens comprise either an isolated human non-collagen or non-mysin basic protein (MBP) polypeptide which is capable of tolerising an individual to an autoantigen; or an isolated human pathogen polypeptide capable of tolerising an individual to that polypeptide. In both cases, the polypeptide (whether self or non-self) includes an amino acid sequence corresponding to a sequence motif for a MHC class II protein, such as HLA -DR, which is associated with a human autoimmune disease and which binds to the polypeptide to activate autoreactive T-cells in individuals with the autoimmune disease. This peptide is an internal peptide of herpes simplex virus DNA polymerase and is implicated as a foreign epitope involved in the aetiology or in remissions of multiple sclerosis. It has been shown capable of inducing the proliferation of autoreactive T-cell clones isolated from multiple sclerosis patients

Query Match 41.2%; Score 35; DB 2; Length 15;
Best Local Similarity 77.8%; Pred. No. 60;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 FVKKXVHVS 15
|||::|||
Db 7 FVKAHVRES 15

RESULT 6
AAW80378
ID AAW80378 standard; peptide; 12 AA.
XX
AC
XX
XX
DT
XX
DE
XX
KW
KW
XX
OS
XX
PN
XX
PD

Peptide eluted after biopanning against maltose binding protein.
Intervening protein sequence; IVPS; protein splicing; protein production; maltose binding protein.
Synthetic.
US5834247-A.
10-NOV-1998.

XX PF 05-MAR-1997; 97US-00811492.
 XX PR 09-DEC-1992; 92US-00004139.
 XX PR 03-NOV-1993; 93US-00146885.
 XX PR 28-JUN-1995; 95US-00496247.
 XX PR 29-DEC-1995; 95US-00580555.
 XX (NEWSE) NEW ENGLAND BIOLABS INC.
 XX PI Hodges RA, Ferler FB, Comb DG, Southworth M, Adam E, Noren CJ;
 XX PI Xu M, Chong SSC, Jack WE;
 XX WPI; 1999-008713/01.
 XX New modified target proteins - which have controllable intervening
 PT protein sequence which can facilitate production, purification, labelling
 PT or isolation of target proteins.
 XX Example 22; Fig 36; 123pp; English.
 XX AA080372-93 represent peptides eluted after biopanning against maltose
 CC binding protein, in the course of the invention. The specification
 CC describes IVPS (intervening protein sequence) regions which encode
 CC peptides which are removed via protein splicing to form the native
 CC protein. The specification describes a modified protein comprising a
 CC target protein or portion, fused either internally or terminally, to a
 CC IVPS, or to an amino- or carboxyl-terminal element of a IVPS. The IVPS
 CC are capable of excision from or cleavage of the modified protein upon
 CC predetermined conditions, in cis or trans, e.g. temperature increase,
 CC deglycosylation, unblocking of amino acid residues, treatment with
 CC chemical reagents. The methods can be used for modifying, producing,
 CC purifying, labelling or isolating target proteins such as enzymes,
 CC toxins, cytokines, glycoproteins and growth factors
 XX Sequence 12 AA;
 SQ
 Query Match 37.6%; Score 32; DB 2; Length 12;
 Best Local Similarity 62.5%; Pred. No. 1.5e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 6 HFVKKHVH 13
 ||| |||
 Db 5 HHRVPHVH 12
 RESULT 7
 AAU78249
 ID AAU78249 standard; peptide; 15 AA.
 XX AC AAU78249;
 XX DT 18-JUN-2002 (first entry)
 XX DE Polypeptide-calcium ion binding 14 N-terminus.
 XX KW Polypeptide-calcium ion binding 14; cancer; HIV;
 KW human immunodeficiency virus infection.
 XX OS Unidentified.
 XX PN CNI327999-A.
 XX PD 26-DEC-2001.
 XX PF 12-JUN-2000; 2000CN-00116458.
 XX PR 12-JUN-2000; 2000CN-00116458.
 XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.
 XX MAO Y, Xie Y;

DR WPI; 2002-270051/32.
 XX New polypeptide-calcium ion binding 14 and polynucleotide encoding it,
 PT for treating diseases such as cancer, and human immunodeficiency virus
 PT infection.
 XX Example 5; Page 19 (Disclosure); 33pp; Chinese.
 XX The invention relates to a new polypeptide-calcium ion binding 14, the
 CC polynucleotide encoding it, preparing the polypeptide by DNA
 CC recombination, application of the polypeptide in treating diseases such
 CC as cancer, human immunodeficiency virus (HIV) infection, the antagonist
 CC to the polynucleotide and its medical action, and the application of the
 CC polynucleotide are disclosed. The present sequence represents the
 CC polypeptide-calcium ion binding 14 N-terminus, used in an ELISA (enzyme-
 CC linked immunosorbent assay) experiment
 XX Sequence 15 AA;
 SQ
 Query Match 37.6%; Score 32; DB 5; Length 15;
 Best Local Similarity 62.5%; Pred. No. 1.9e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 6 HFVKKHVH 13
 ||| |||
 Db 3 HFNKIKIH 10
 RESULT 8
 AAU03943
 ID AAU03943 standard; peptide; 7 AA.
 XX AC AAU03943;
 XX DT 23-OCT-2001 (first entry)
 XX DE Human GDNF F2c region peptide.
 XX KW Persephin; F2a; F2c; GDNF; neurturin; artemin; human; mouse; rat; AIDS;
 KW growth factor receptor alpha1-RET protein tyrosine kinase; GFRalpha1-RET;
 KW trophic support; peripheral neuropathy; amyotrophic lateral sclerosis;
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease; diabetes;
 KW acquired immunodeficiency syndrome; ischaemic stroke; acute brain injury;
 KW acute spinal cord injury; multiple sclerosis; nervous system tumour;
 KW neuroblastoma; enteric disease; idiopathic constipation; eosinopaenia;
 KW basopaenia; lymphopaenia; monocytopenia; neutropaenia; anaemia;
 KW cardiac muscle degeneration; congestive heart failure; thrombocytopaenia.
 XX OS Homo sapiens.
 XX PN WO200147946-A2.
 XX PD 05-JUL-2001.
 XX PF 21-DEC-2000; 2000WO-US034852.
 XX PR 28-DEC-1999; 99US-00473551.
 XX (UNIW) UNIV WASHINGTON.
 XX PI Milbrandt JD, Baloh RH;
 XX WPI; 2001-425618/45.
 XX New growth factor that activates growth factor receptor alpha1-Ret
 PT protein-tyrosine kinase, for providing trophic support to a mammalian
 PT cell and producing differentiation of a mammalian cell in a patient.
 XX Claim 6; Page 47; 73pp; English.
 XX The sequence represents a human GDNF F2c region peptide. Residues from
 CC the F2a and/or F2c regions can substitute those of the F2a and F2c
 CC regions of the growth factor protein persephin. The substitutions can be

PN WO200121189-A1.
XX
PD 29-MAR-2001.
XX
PF 19-JUL-2000; 2000WO-US019774.
XX
PR 19-JUL-1999; 99US-00357737.
XX
PA (EPIM-) EPIMUNE INC.
XX
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX
DR WPI; 2001-308046/32.
XX
PT A new composition useful as a vaccines against hepatitis C virus.
XX
PS Disclosure; Page 131; 214pp; English.
XX
CC The present invention describes a composition comprising a prepared
CC hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
CC These are derived from HCV HLA-binding motifs. They are useful in
CC vaccines for the prevention and treatment of HCV infection in humans. The
CC present sequence is an epitope used in the disclosure of the invention
XX
SQ Sequence 9 AA;
Query Match 35.1%; Score 27; DB 4; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 GGRRLFF 7
Db 3 GGRHLIF 9
Search completed: February 22, 2005, 09:24:57
Job time : 67.6667 secs

PS Claim 2; Page 2995; 3148pp; English.

XX This invention describes novel antibodies that immunospecifically bind to

CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the

CC tumour necrosis factor (TNF) super family and induces B cell

CC proliferation and differentiation. The antibodies of the invention have

CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,

CC antirheumatic and antiAIDS activity and can be used in vaccines to

CC inhibit the expression and activity of Blys. The antibodies bind to Blys

CC and so may be used to detect and quantitate the presence of Blys in

CC biological samples and may be used in this way to diagnose disease

CC associated with aberrant expression of Blys. They may also be

CC administered to treat diseases associated with aberrant Blys expression

CC and activity such as cancer, immune, and autoimmune disorders and

CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,

CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and

CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent

CC the antibodies and fragments of the antibodies described in the method of

XX the invention

SQ Sequence 14 AA;

Query Match 36.4%; Score 28; DB 5; Length 14;

Best Local Similarity 55.6%; Pred. No. 5.5e+02;

Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 5 LFFVKAHVR 13

Db 5 LLFPRAHLR 13

|||:|

|||:|

RESULT 11

ADG97285

ID ADG97285 standard; peptide; 14 AA.

XX

AC ADG97285;

XX

DT 11-MAR-2004 (first entry)

XX

DE scFV VHCDR3 peptide that immunospecifically binds Blys SeqID 2469.

XX

KW antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;

KW B cell proliferation; differentiation; scFv; myasthenia gravis;

KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;

KW carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;

KW antiinflammatory; antiasthmatic; antiallergic; cytostatic.

XX

OS Unidentified.

XX

XX WO2003055979-A2.

XX

PD 10-JUL-2003.

XX

PF 14-NOV-2002; 2002WO-US036496.

XX

XX 16-NOV-2001; 2001US-0331469P.

PR 19-DEC-2001; 2001US-0340817P.

XX

XX (HUMA-) HUMAN GENOME SCI INC.

PA

XX Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;

PI

XX WPI; 2003-505530/47.

DR

XX

XX Novel antibody that immunospecifically binds to a B lymphocyte stimulator

PT (Blys), useful for detecting and treating diseases or disorders e.g.

PT rheumatoid arthritis, asthma and leukemia.

XX

XX Example 1; SEQ ID NO 2469; 394pp; English.

PS

XX This invention relates to novel antibodies that immunospecifically bind

CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to

CC chromosome 13q34 and encodes a protein that is a member of the tumour

CC

CC necrosis factor superfamily and induces both in vivo and in vitro B cell

CC proliferation and differentiation. Specifically, it refers to single

CC chain antibody molecules (scFvs) derived, preferably, from the variable

CC heavy CDR3 region that immunospecifically bind to a polypeptide, or

CC fragment thereof, of either human, murine, rat or monkey Blys. The

CC present invention refers to the use of such antibodies in various methods

CC for the detection, diagnosis and prognosis of diseases related to the

CC aberrant expression or inappropriate function of Blys or its receptor. As

CC such, these compositions are useful for identifying immune disorders

CC including myasthenia gravis and multiple sclerosis, inflammatory

CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such

CC as AIDS and proliferative disorders including leukaemia, carcinoma and

CC lymphoma. Accordingly, they can be described as exhibiting various

CC activities such as antirheumatic, antiallergic and neuroprotective,

CC antiinflammatory, antiasthmatic, antiarthritic and cytostatic. This

CC peptide sequence is a single chain antibody variable heavy CDR3 peptide

CC that immunospecifically binds Blys of the invention.

XX

SQ Sequence 14 AA;

Query Match 36.4%; Score 28; DB 7; Length 14;

Best Local Similarity 55.6%; Pred. No. 5.5e+02;

Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 5 LFFVKAHVR 13

Db 5 LLFPRAHLR 13

|||:|

|||:|

RESULT 12

AAR93674

ID AAR93674 standard; peptide; 15 AA.

XX

AC AAR93674;

XX

DT 27-APR-1996 (first entry)

XX

DE HIV principal neutralisation epitope binding to 588 antibody.

XX

KW SPNE; selected principal neutralisation epitope; vaccine; HIV;

KW outer membrane proteosome; Neisseria; OMPC; AIDS; 588 antibody.

XX

OS Synthetic.

XX

PN GB2282381-A.

XX

FD 05-APR-1995.

XX

XX 23-SEP-1994; 94GB-00019257.

PF

XX 30-SEP-1993; 93US-00129723.

PR

XX (MERI) MERCK & CO INC.

PA

XX Arnold BA, Conley AJ, Keller PM;

PI

XX WPI; 1995-125268/17.

DR

XX New antigenic conjugate useful as vaccine for AIDS - comprising HIV

PT principal neutralisation epitope covalently linked to outer membrane

PT proteosome of Neisseria.

XX

XX Claim 14; Page 9; 69pp; English.

PS

XX An antigenic conjugate, useful as a vaccine for AIDS, has the formula

CC (SPNE)n-OMPC, where SPNE is a selected principal neutralisation epitope

CC of HIV, which is one of 17 specified polypeptides (including the present

CC sequence) or their fragments containing at least 5 amino acids and

CC including the EWG region or its homologue in the sequence; OMPC is

CC purified outer membrane proteosome of Neisseria (pref. N. meningitidis);

CC and n is 1-200, indicating the number of SPNE moieties covalently linked

CC to the OMPC. The conjugates may be substituted by anions, and conjugation

CC may be via a bigeneric spacer. The SPNE polypeptides bind an HIV broadly

DE 101P3A11 protein derived peptide, SEQ ID No 3586.
 XX transgenic animal; cytotoxic; cancer; immune; 101P3A11; cytostatic;
 KW stomach; cervix; uterus; rectum; prostate; colon; kidney; breast.
 XX Unidentified.
 XX WO200292842-A2.
 XX 21-NOV-2002.
 XX 15-MAY-2002; 2002WO-US015520.
 XX 15-MAY-2001; 2001US-0291118P.
 XX 31-OCT-2001; 2001US-00001469.
 XX 14-DEC-2001; 2001US-00017666.
 XX (AGEN-) AGENSYS INC.
 XX Jakobovits A, Faris M, Raitano AB, Morrison RK, Saffran D, Ge W;
 PI Challita-Eid PM;
 PI WPI; 2003-129310/12.
 XX New composition comprising 101P3A11-related protein, useful for
 PT preventing or treating cancer e.g., stomach, cervix, uterus, rectum,
 PT prostate, colon, kidney or breast cancer.
 XX Claim 13; SEQ ID NO 3586; 327pp; English.
 XX The invention relates to a novel composition comprising: a substance that
 CC modulates the status of a protein comprising a sequence with a fully
 CC defined 2466 or 3136 amino acid sequence given in the specification; or a
 CC molecule that is immobilised by a protein comprising a sequence with a
 CC fully defined 2466 or 3136 amino acids, where the status of a cell
 CC expressing the protein is modulated. The invention further relates to: an
 CC antibody; a non-human transgenic animal or hybridoma that produces the
 CC cell that expresses the protein; a polynucleotide that encodes the
 CC protein; a method for generating a mammalian immune response directed
 CC to the protein; a method for detecting in a sample the presence of a 101P3A11
 CC -related protein or polynucleotide; and a method for monitoring one or
 CC more 101P3A11 gene products in a biological sample from a patient having
 CC or suspected of having cancer. The novel composition has cytostatic
 CC activity. The composition is useful for preventing or treating cancer
 CC e.g., stomach, cervix, uterus, rectum, prostate, colon, kidney or breast
 CC cancer. This sequence represents a peptide derived from the 101P3A11
 XX protein of the invention.
 XX Sequence 15 AA;

Query Match 37.7%; Score 29; DB 7; Length 15;
 Best Local Similarity 54.5%; Pred. No. 3.9e+02;
 Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 4 RLFFVKAHVRE 14
 |||||
 Db 4 RLFFVKAHVRE 14

RESULT 7
 ADI09519
 ID ADI09519 standard; peptide; 15 AA.
 XX ADI09519;
 XX 22-APR-2004 (first entry)
 XX 101P3A11 protein derived peptide, SEQ ID No 3705.
 XX transgenic animal; cytotoxic; cancer; immune; 101P3A11; cytostatic;
 KW stomach; cervix; uterus; rectum; prostate; colon; kidney; breast.

XX Unidentified.
 XX WO200292842-A2.
 XX 21-NOV-2002.
 XX 15-MAY-2002; 2002WO-US015520.
 XX 15-MAY-2001; 2001US-0291118P.
 XX 31-OCT-2001; 2001US-00001469.
 XX 14-DEC-2001; 2001US-00017666.
 XX (AGEN-) AGENSYS INC.
 XX Jakobovits A, Faris M, Raitano AB, Morrison RK, Saffran D, Ge W;
 PI Challita-Eid PM;
 PI WPI; 2003-129310/12.
 XX New composition comprising 101P3A11-related protein, useful for
 PT preventing or treating cancer e.g., stomach, cervix, uterus, rectum,
 PT prostate, colon, kidney or breast cancer.
 XX Claim 13; SEQ ID NO 3705; 327pp; English.
 XX The invention relates to a novel composition comprising: a substance that
 CC modulates the status of a protein comprising a sequence with a fully
 CC defined 2466 or 3136 amino acid sequence given in the specification; or a
 CC molecule that is immobilised by a protein comprising a sequence with a
 CC fully defined 2466 or 3136 amino acids, where the status of a cell
 CC expressing the protein is modulated. The invention further relates to: an
 CC antibody; a non-human transgenic animal or hybridoma that produces the
 CC cell that expresses the protein; a polynucleotide that encodes the
 CC protein; a method for generating a mammalian immune response directed
 CC to the protein; a method for detecting in a sample the presence of a 101P3A11
 CC -related protein or polynucleotide; and a method for monitoring one or
 CC more 101P3A11 gene products in a biological sample from a patient having
 CC or suspected of having cancer. The novel composition has cytostatic
 CC activity. The composition is useful for preventing or treating cancer
 CC e.g., stomach, cervix, uterus, rectum, prostate, colon, kidney or breast
 CC cancer. This sequence represents a peptide derived from the 101P3A11
 XX protein of the invention.
 XX Sequence 15 AA;

Query Match 37.7%; Score 29; DB 7; Length 15;
 Best Local Similarity 54.5%; Pred. No. 3.9e+02;
 Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 4 RLFFVKAHVRE 14
 |||||
 Db 5 RLFFVKAHVRE 15

RESULT 8
 ADI09704
 ID ADI09704 standard; peptide; 15 AA.
 XX ADI09704;
 XX 22-APR-2004 (first entry)
 XX 101P3A11 protein derived peptide, SEQ ID No 3890.
 XX transgenic animal; cytotoxic; cancer; immune; 101P3A11; cytostatic;
 KW stomach; cervix; uterus; rectum; prostate; colon; kidney; breast.
 XX Unidentified.
 XX WO200292842-A2.

SQ Sequence 14 AA;

Query Match 40.3%; Score 31; DB 4; Length 14;
Best Local Similarity 42.9%; Pred. No. 1.6e+02; Mismatches 6; Indels 0; Gaps 0;

QY 2 GRRLFFVKAHVRES 15
| | | | |
Db 1 GAMLNLSGHVRES 14

RESULT 4

ABG76689
ID ABG76689 standard; peptide; 15 AA.

XX AC ABG76689;

XX DT 05-NOV-2002 (first entry)

XX DE Hepatitis C virus (HCV)-specific ligand #20.

XX KW Binding specificity; anti-antigen antibody; serum; ADAM;
XX KW antigen detection by antigen mimic; Hepatitis C virus infection; HCV;
XX KW HCV-specific ligand; human.

XX OS Homo sapiens.

XX PN WO200237115-A1.

XX PD 10-MAY-2002.

XX PF 03-NOV-2000; 2000WO-IT000442.

XX PR 03-NOV-2000; 2000WO-IT000442.

XX PA (KENT-) KENTON SRL.

XX PI Felici P, Gargano N, Minenkova O, Monaci P;

XX DR WPI; 2002-599299/64.

XX PT Making diagnosis of antigen, by identifying binding specificity of anti-
XX PT antigen antibody molecules in serum by antibody detection by antigen
XX PT mimics methodology, and identifying antibodies associated with antigen.

XX PS Claim 26; Page 42; 86pp; English.

CC The present invention relates to a method for making a diagnosis of an
CC antigen. The method involves identifying the binding specificity of the
CC anti-antigen antibody molecules in serum by the antibody detection by
CC antigen mimics (ADAM) methodology. The method comprises screening phage
CC libraries using sera from antigen-infected and non-infected individuals,
CC and identifying peptides binding antibodies (ligands) specifically
CC associated with the antigen. The method of the invention can be used for
CC the detection of infectious agents, particularly Hepatitis C virus (HCV).
CC The invention provides HCV-specific ligands which are useful for the
CC preparation of a diagnostic assay for detecting HCV infection in a
CC subject. The HCV-specific ligands are also useful for the preparation of
CC vaccines against HCV. ABG76670-ABG76743 represent HCV-specific ligands
CC identified from human sera

SQ Sequence 15 AA;

Query Match 40.3%; Score 31; DB 5; Length 15;
Best Local Similarity 58.3%; Pred. No. 1.7e+02;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 RLFFVKAHVRES 15
| | | | |
Db 3 RTFLMKAHGIES 14

RESULT 5

ABB56587

ID ABB56587 standard; peptide; 14 AA.

XX AC ABB56587;

XX DT 05-MAR-2002 (first entry)

XX DE Human SNP related amino acid sequence SEQ ID NO:1152.

XX KW Human; single nucleotide polymorphism; SNP; polymorphism; cytostatic;
XX KW immunosuppressive; antiinflammatory; neuroprotective; antimicrobial;
XX KW autoimmune disease; inflammation; cancer; nervous system disease;
XX KW infection; polymorphic protein.

XX OS Homo sapiens.

XX PN WO200138586-A2.

XX PD 31-MAY-2001.

XX PF 22-NOV-2000; 2000WO-US032311.

XX PR 24-NOV-1999; 99US-0167383P.

XX PA (CURA-) CURAGEN CORP.

XX PI Shimkets RA, Leach M;

XX DR WPI; 2001-355949/37.

XX PT Isolated human nucleic acids comprising one or more single nucleotide
XX PT polymorphisms, useful for treating a subject suffering from a pathology,
XX PT e.g. autoimmune diseases, ascribed to the presence of a sequence
XX PT polymorphism.

XX PS Claim 1; Page 597; 674pp; English.

CC ABL00010 to ABL01104 represent human nucleic acid oligonucleotides
CC comprising one or more single nucleotide polymorphisms (SNPs). ABB56531
CC to ABB56903 represent human peptides encoded by some of the SNP
CC oligonucleotides. The sequences from the present invention can have
CC immunosuppressive, cytostatic, antiinflammatory, neuroprotective and
CC antimicrobial activities. Nucleic acids, polypeptides, oligonucleotides
CC and antibodies from the present invention can be used for treating a
CC subject suffering from, at risk for, or suspected of, suffering from a
CC pathology ascribed to the presence of a sequence polymorphism. The
CC pathology may be autoimmune diseases, inflammation, cancer, diseases of
CC the nervous system, and infection by pathogenic microorganisms. The SNPs
CC are also useful for determining which forms of a characterised
CC polymorphism are present in individuals. The antibodies may be used in
CC the detection, quantitation and/or cellular or tissue localisation of a
CC polymorphic protein (e.g., for use in measuring levels of the polymorphic
CC protein within appropriate physiological samples)

SQ Sequence 14 AA;

Query Match 39.0%; Score 30; DB 4; Length 14;
Best Local Similarity 62.5%; Pred. No. 2.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GRRLFFVK 9
| | | | |
Db 1 GRRLFFVK 8

RESULT 6

ADI09400
ID ADI09400 standard; peptide; 15 AA.

XX AC ADI09400;

XX DT 22-APR-2004 (first entry)

CC simplex virus DNA polymerase and is implicated as a foreign epitope
 CC involved in the aetiology or in remissions of multiple sclerosis. It has
 CC been shown capable of inducing the proliferation of autoreactive T-cell
 CC clones isolated from multiple sclerosis patients

XX Sequence 15 AA;

Query Match 100.0%; Score 77; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 9.7e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGRLLFFVKAHVRES 15
 Db 1 GGRLLFFVKAHVRES 15

RESULT 2

AAW04852
 ID AAW04852 standard; peptide; 15 AA.

XX AAW04852;

DT 16-OCT-2003 (revised)

DT 18-FEB-1997 (first entry)

XX Internal fragment of Epstein-Barr virus DNA polymerase.

XX Tolerisation; self-epitope; antigen; autoimmune disease; autoantigen;
 KW HLA; human leukocyte antigen; T-cell; thymocyte; pemphigus vulgaris;
 KW demoglein; multiple sclerosis; herpes simplex virus; adenovirus;
 KW phosphomannomutase; human papillomavirus; Epstein-Barr virus;
 KW DNA polymerase; influenza; haemagglutinin; reovirus; sigma protein.

OS Human herpesvirus 4.

XX W09627387-A1.

XX 12-SEP-1996.

XX 07-MAR-1996; 96WO-US003182.

XX 07-MAR-1995; 95US-00400796.

XX (HARD) HARVARD COLLEGE.

PI Strominger JL, Wucherpfennig KW;

XX WPI; 1996-425218/42.

XX Pemphigus vulgaris auto-antigens and multiple sclerosis non-self antigens
 PT - useful in disease treatment, and method for identification of other
 PT self and non-self antigens implicated in auto-immune disease.

PS Claim 2; Page 45; 58pp; English.

XX Pharmaceutical preparations for tolerisation to antigens comprise either
 CC an isolated human non-collagen or non-mysin basic protein (MBP)
 CC polypeptide which is capable of tolerising an individual to an
 CC autoantigen; or an isolated human pathogen polypeptide capable of
 CC tolerising an individual to that polypeptide. In both cases, the
 CC polypeptide (whether self or non-self) includes an amino acid sequence
 CC corresponding to a sequence motif for a MHC class II protein, such as HLA
 CC -DR, which is associated with a human autoimmune disease and which binds
 CC to the polypeptide to activate autoreactive T-cells in individuals with
 CC the autoimmune disease. This peptide is an internal peptide of Epstein-
 CC Barr virus DNA polymerase and is implicated as a foreign epitope involved
 CC in the aetiology or in remissions of multiple sclerosis. It has been
 CC shown capable of inducing the proliferation of autoreactive T-cell clones
 CC isolated from multiple sclerosis patients. (Updated on 16-OCT-2003 to
 CC standardise OS field)

XX Sequence 15 AA;

Query Match 45.5%; Score 35; DB 2; Length 15;
 Best Local Similarity 77.8%; Pred. No. 33;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 FVKXHVRES 15
 Db 7 FVKXHVRES 15

RESULT 3

AAG98020
 ID AAG98020 standard; peptide; 14 AA.

XX AAG98020;

DT 19-SEP-2001 (first entry)

DE Human SNP associated peptide SEQ ID NO. 662.

XX Human; single nucleotide polymorphism; SNP; angiotensin;
 KW 4-hydroxybutyrate; dehydrogenase; protein therapy;
 KW adenosine triphosphate-dependent RNA helicase;
 KW major histocompatibility complex Class I histocompatibility antigen; MHC;
 KW phosphoglycerate kinase; immunosuppressive; immunostimulatory;
 KW antirheumatic; antisclerotic; antidiabetic; antiinflammatory; cytostatic;
 KW antileukemic; neuroprotective; antimicrobial; gene therapy; vaccine.

OS Homo sapiens.

XX W0200148245-A2.

XX 05-JUL-2001.

XX 27-DEC-2000; 2000WO-US035346.

XX 27-DEC-1999; 99US-00472688.

XX (CURA-) CURAGEN CORP.

XX Shimkets RA, Leach M;

XX WPI; 2001-418297/44.

XX Polymorphic nucleic acids encoding e.g. angiotensin, dehydrogenase,
 PT adenosine triphosphate-dependent RNA helicase and/or phosphoglycerate
 PT kinase, useful for diagnosing and treating, e.g. cancer, autoimmune
 PT diseases and infections.

PS Disclosure; Page 436; 484pp; English.

XX The invention relates to nucleic acids (AAH79386-AAH80036) encoding
 CC polymorphic variants of proteins (AAG98010-AAG98238) related to
 CC angiotensin, 4-hydroxybutyrate, dehydrogenase, adenosine triphosphate
 CC (ATP)-dependent RNA helicase, major histocompatibility complex (MHC)
 CC Class I histocompatibility antigen and/or phosphoglycerate kinase. These
 CC nucleic acid single nucleotide polymorphisms (SNPs) and the encoded
 CC proteins have potential immunosuppressive, immunostimulatory,
 CC antirheumatic, antisclerotic, antidiabetic, antiinflammatory, cytostatic,
 CC antileukemic, neuroprotective and antimicrobial activity and may be
 CC useful in gene/protein therapy, vaccines, modulation of the expression
 CC and activity of proteins related to angiotensin, 4-hydroxybutyrate,
 CC dehydrogenase, adenosine triphosphate (ATP)-dependent RNA helicase, major
 CC histocompatibility complex (MHC) Class I histocompatibility antigen
 CC and/or phosphoglycerate kinase. Disorders that may be prevented,
 CC diagnosed and/or treated by the above methods include multifactorial
 CC diseases with a genetic component, such as autoimmune diseases (e.g.
 CC rheumatoid arthritis, multiple sclerosis, diabetes, systemic lupus
 CC erythematosus and Grave's disease), inflammation, cancer (e.g. cancers of
 CC the bladder, brain, breast, colon and kidney, leukemia), diseases of the
 CC nervous system, an infection of pathogenic organisms. They may also be
 CC used to alter phenotypic traits such as longevity, appearance, strength,
 CC speed and endurance

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 22, 2005, 08:52:23 ; Search time 65.6667 Seconds
(without alignments)
88.346 Million cell updates/sec

Title: US-08-991-628-15

Perfect score: 77

Sequence: 1 GGRLLFFVKAHVRES 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 632537

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	77	100.0	15	2 AAW04855	Internal
2	35	45.5	15	2 AAW04852	Internal
3	31	40.3	14	4 AAG98020	Human SNP
4	31	40.3	15	5 ABG76689	Hepatitis
5	30	39.0	14	4 ABB56587	Human SNP
6	29	37.7	15	7 ADT09400	101P3A11
7	29	37.7	15	7 ADI09519	101P3A11
8	29	37.7	15	7 ADI09704	Dictyoste
9	28	36.4	10	5 AAU77504	Dictyoste
10	28	36.4	14	5 ABP46458	Human Bly
11	28	36.4	14	7 ADG97285	scfV VHCD
12	28	36.4	15	2 AAR93674	HIV princ
13	28	36.4	15	5 ABG76687	Hepatitis
14	27	35.1	8	4 AAJ02281	Hepatitis
15	27	35.1	9	4 AAJ01219	Hepatitis
16	27	35.1	9	4 AAJ02683	Hepatitis
17	27	35.1	9	4 AAJ02187	Hepatitis
18	27	35.1	10	4 AAJ02282	Hepatitis
19	27	35.1	10	4 AAJ02744	Hepatitis
20	27	35.1	11	4 AAJ02684	Hepatitis
21	27	35.1	11	4 AAJ02188	Hepatitis
22	27	35.1	11	6 ABP76436	Peptidomi
23	27	35.1	12	8 ADJ34590	AKT subat
24	27	35.1	13	4 AAG84591	MAGE3 DR
25	27	35.1	13	4 AAG84606	MAGE3 DR

26	27	35.1	13	4 AAG84613	MAGE3 DR
27	27	35.1	13	4 AAG84618	MAGE3 DR
28	27	35.1	14	4 AAG98022	Human SNP
29	27	35.1	15	5 ABG76686	Hepatitis
30	27	35.1	15	7 ADE86173	Antennape
31	27	35.1	15	7 ADE78445	Peptide t
32	27	35.1	15	8 ADI35013	Hepatitis
33	27	35.1	15	8 ADI35012	Hepatitis
34	27	35.1	15	8 ADL26316	Synthetic
35	26	33.8	7	2 AAW10790	Ferritin
36	26	33.8	7	2 AAW10763	Ferritin
37	26	33.8	7	2 AAW10808	Ferritin
38	26	33.8	7	5 ABG77576	Targettin
39	26	33.8	8	2 AAW31837	Peptide 3
40	26	33.8	8	4 AAU05710	p21 C-ter
41	26	33.8	9	2 AAR89238	LN clone
42	26	33.8	9	4 AAE11956	Mammalian
43	26	33.8	9	6 ABP76390	Peptidomi
44	26	33.8	9	8 ADK04523	Hepatitis
45	26	33.8	9	8 ADK04077	Hepatitis

ALIGNMENTS

RESULT 1

AAW04855
ID AAW04855 standard, peptide; 15 AA.

XX AC AAW04855;

DT 18-FEB-1997 (first entry)

XX DE Internal fragment of herpes simplex virus DNA polymerase.

XX KW Tolerisation; self-epitope; antigen; autoimmune disease; autoantigen;
KW HLA; human leukocyte antigen; T-cell; thymocyte; pemphigus vulgaris;
KW desmoglein; multiple sclerosis; herpes simplex virus; adenovirus;
KW phosphomannomutase; human papillomavirus; Epstein-Barr virus;
KW DNA polymerase; influenza; haemagglutinin; reovirus; sigma protein.

XX OS Herpes simplex virus.

XX PN WO9627387-A1.

XX PD 12-SEP-1996.

XX PF 07-MAR-1996; 96WO-US003182.

XX PR 07-MAR-1995; 95US-00400796.

XX PA (HARD) HARVARD COLLEGE.

XX PI Strominger JL, Wucherpfennig KW;

XX DR WPI; 1996-425218/42.

XX PT Pemphigus vulgaris auto-antigens and multiple sclerosis non-self antigens
PT - useful in disease treatment, and method for identification of other
PT self and non-self antigens implicated in auto-immune disease.

XX PS Claim 2; Page 47; 58pp; English.

XX CC Pharmaceutical preparations for tolerisation to antigens comprise either
CC an isolated human non-collagen or non-mysin basic protein (MBP)
CC polypeptide which is capable of tolerising an individual to an
CC autoantigen; or an isolated human pathogen polypeptide capable of
CC tolerising an individual to that polypeptide. In both cases, the
CC polypeptide (whether self or non-self) includes an amino acid sequence
CC corresponding to a sequence motif for a MHC class II protein, such as HLA
CC -DR, which is associated with a human autoimmune disease and which binds
CC to the polypeptide to activate autoreactive T-cells in individuals with
CC the autoimmune disease. This peptide is an internal peptide of herpes
CC the autoimmune disease.

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OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Moniliformes; Filicophyta; Marattiopsida; Marattiales;
 OC Marattiaceae; Archangiopteris.
 OX NCBI_TaxID=203826;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Chiang T., Chiang Y., Chou C., Cheng Y., Chiou W.;
 RT "Phylogeography and conservation of Archangiopteris somai and A. itoi
 RT (Marattiaceae, Pteridophyta) based on nucleotide variation of cpDNA
 RT atpB-rbcL intergenic spacer.";
 RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
 RN [2]

RP SEQUENCE FROM N.A.
 RA Chiang Y.C.;
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ505259; CAD44048.1; -;
 DR GO; GO:0009507; C:chloroplast; IEA.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 KW Chloroplast; Hydrolase.
 FT NON_TER 10
 SQ SEQUENCE 10 AA; 1195 MW; 9E2AF0C9C7376451 CRC64;
 Query Match 26.0%; Score 20; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LFFV 8
 Db ||||
 6 LFFV 9

RESULT 15
 O39952 PRELIMINARY; PRT; 10 AA.
 AC O39952;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE E1 protein (Fragment).
 OS GB virus C/Hepatitis G virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC GBV-C/HGV group.
 OX NCBI_TaxID=54290;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97368412; PubMed=9225026;
 RA Smith D.B., Cuccianu N., Davidson F., Jarvis L.M., Mokili J.L.,
 RA Hamid S., Ludlam C.A., Simmonds P.;
 RT "Discrimination of hepatitis G virus/GBV-C geographical variants by
 RT analysis of the 5' non-coding region.";
 RL J. Gen. Virol. 78:1533-1542(1997).
 DR EMBL; AF003170; AAC57981.1; -;
 FT NON_TER 10
 SQ SEQUENCE 10 AA; 1152 MW; CC88F0C9C7272732 CRC64;

Query Match 26.0%; Score 20; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1e+04;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LFFV 8
 Db ||||
 6 LFFV 9

Search completed: February 22, 2005, 09:38:06
 Job time : 53.6667 secs

SQ SEQUENCE 11 AA; 1370 MW; 592BC02D12C9DB57 CRC64;

Query Match 27.3%; Score 21; DB 2; Length 11;
 Best Local Similarity 50.0%; Pred. No. 7.1e+03;
 Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 4 RLFFVK 9
 :|||:
 Db 3 KLYFVR 8

RESULT 11

G6PD MAIZE
 ID G6PD MAIZE STANDARD; PRT; 15 AA.
 AC P80619;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Glucose-6-phosphate 1-dehydrogenase, cytoplasmic isoform (EC 1.1.1.49)
 DE (G6PD) (20-page of etiological coleoptile spot 243) (Fragment).
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACAD clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]

RP SEQUENCE.

RC TISSUE=Coleoptile;
 RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
 RA Pernollet J.-C., Zivy M., de Vienne D.;
 RT "The maize two dimensional gel protein database: towards an integrated
 genome analysis program.";
 RL Theor. Appl. Genet. 93:997-1005 (1996).
 CC -1- CATALYTIC ACTIVITY: D-glucose 6-phosphate + NADP(+) = D-glucono-
 1,5-lactone 6-phosphate + NADPH.
 CC -1- SUBUNIT: Pentose phosphate pathway; first step.
 CC -1- PATHWAY: Pentose phosphate pathway; first step.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the glucose-6-phosphate dehydrogenase
 family.
 DR Maize-ZDPAGE; P80619; COLEOPTILE.
 DR MaizeDB; 123946; -.
 DR InterPro; IPR001282; G6PD.
 DR PROSITE; PS00069; G6P DEHYDROGENASE; PARTIAL.
 KW Carbohydrate metabolism; Direct protein sequencing;
 KW Glucose metabolism; NADP; Oxidoreductase.
 FT NON_TER 1
 FT NON_TER 15
 SQ SEQUENCE 15 AA; 1739 MW; 02038EE7471AE038 CRC64;

Query Match 27.3%; Score 21; DB 1; Length 15;
 Best Local Similarity 28.6%; Pred. No. 9.7e+03;
 Matches 4; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 2 GRRLLFFVKVHRES 15
 :|||:
 Db 2 GRNEFVIRLQXSEA 15

RESULT 12

O84887
 ID O84887 PRELIMINARY; PRT; 15 AA.
 AC O84887;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Truncated GTP-binding protein.
 GN Name=lepa;
 OS Salmonella typhimurium.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Salmonella.
 OX NCBI_TaxID=602;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=LT2;
 RA Figueroa-Bossi N., Bossi L.;
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF001386; AAC26066.1; -.
 DR PIR; T03000; T03000.
 SQ SEQUENCE 15 AA; 1786 MW; 9DC811919C7EA87C CRC64;

Query Match 27.3%; Score 21; DB 2; Length 15;
 Best Local Similarity 44.4%; Pred. No. 9.7e+03;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 RLFFVKARV 12
 :|||:
 Db 5 RNFSIIAH 13

RESULT 13

TPIS NICPL
 ID TPIS NICPL STANDARD; PRT; 10 AA.
 AC P19118;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Triosephosphate isomerase, cytosolic (EC 5.3.1.1) (TIM) (Triose-
 phosphate isomerase) (Fragment).
 OS Nicotiana glauca (Leadwort-leaved tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC lamids; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4092;
 RN [1]

RP SEQUENCE.

RA Bauw G., de Loose M., Inze D., van Montagu M., Vandekerckhove J.;
 RT "Alterations in the phenotype of plant cells studied by NH2-terminal
 amino acid-sequence analysis of proteins electrophoretically separated from two-
 dimensional gel-separated total extracts.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:4806-4810 (1987).
 CC -1- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate = glycerone
 phosphate.
 CC -1- PATHWAY: Plays an important role in several metabolic pathways.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
 CC -1- MISCELLANEOUS: In plants, there are two types of TPIS, cytosolic
 and plastid.
 CC -1- SIMILARITY: Belongs to the triosephosphate isomerase family.
 DR PIR; A27617; A27617.
 DR InterPro; IPR000652; Triophos_ismrse.
 DR PROSITE; PS00171; TIM; PARTIAL.
 KW Direct protein sequencing; Fatty acid biosynthesis; Gluconeogenesis;
 KW Glycolysis; Isomerase; Pentose shunt.
 FT NON_TER 10
 FT NON_TER 10
 SQ SEQUENCE 10 AA; 1140 MW; 80B9D37862C9C9D1 CRC64;

Query Match 26.0%; Score 20; DB 1; Length 10;
 Best Local Similarity 80.0%; Pred. No. 1e+04;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 RLFFV 8
 :|||:
 Db 2 RTFFV 6

RESULT 14

Q6A3T0
 ID Q6A3T0 PRELIMINARY; PRT; 10 AA.
 AC Q6A3T0;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE ATP synthase beta subunit (EC 3.6.3.14) (Fragment).
 GN Name=atpB;
 OS Archaegiopteris somai.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=95079448; PubMed=7527301;
RT Okada H., Yoshida J., Seo H., Wakabayashi T., Sugita K., Hagiwara M.;
RT "Anti-(glioma surface antigen) monoclonal antibody G-22 recognizes
RT overexpressed CD44 in glioma cells.";
RL Cancer Immunol. Immunother. 39:313-317(1994).
FT NON_TER 1
FT NON_TER 12
SQ SEQUENCE 12 AA; 1337 MW; 2E0F6CE9D9D2C1E8 CRC64;

Query Match 28.6%; Score 22; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 FVKAHV 12
DB 2 FIEGHV 7
|::||
|::||

RESULT 7
Q7M2Q3 PRELIMINARY; PRT; 14 AA.
AC Q7M2Q3;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Probursin tetradecapeptide.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=91133172; PubMed=1671611; DOI=10.1016/0024-3205(91)90092-P;
RA Audhya T., King R., Goldstein G.;
RT "Bovine probursin tetradecapeptide contains amino acid sequence from
RT somatostatin, tuftsin and bursin.";
RL Life Sci. 48:773-780(1991).
DR PIR: JH0328; JH0328.
SQ SEQUENCE 14 AA; 1801 MW; 2CF3549CEC6BFA17 CRC64;

Query Match 28.6%; Score 22; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GQRR 4
DB 11 GGR 14
||||
||||

RESULT 8
Q95949 PRELIMINARY; PRT; 15 AA.
AC Q95949;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE NADH dehydrogenase subunit 4 (Fragment).
GN Name=ND4;
OS Sauromalus ater (Common chuckwalla) (Sauromalus obesus).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Iguaninae; Sauromalus.
OX NCBI_TaxID=65995;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97019047; PubMed=8865663;
RA Sites J.W. Jr., Davis S.K., Guerra T., Iverson J.B., Snell H.L.;

RT "Character congruence and phylogenetic signal in molecular and
RT morphological data sets: a case study in the living Iguanas (Squamata,
RT Iguanidae).";
RL Mol. Biol. Evol. 13:1087-1105(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Sites J.W., Davis S.K., Guerra T., Iverson J.B., Snell H.L.;
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U66232; AA807479.1; -.
DR GO; GO:0005739; Mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 15 AA; 1896 MW; 8327179CFC353901 CRC64;

Query Match 28.6%; Score 22; DB 2; Length 15;
Best Local Similarity 30.8%; Pred. No. 6.2e+03;
Matches 4; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 3 RRLPFVKAHVRES 15
DB 3 RRLHSTRRLTKT 15
||| |::||
||| |::||

RESULT 9
Q37854 PRELIMINARY; PRT; 8 AA.
AC Q37854;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Coliphage gene of unknown function, 5'end. (Fragment).
OS Bacteriophage R17.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Levivirus.
OX NCBI_TaxID=12026;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=73224987; PubMed=4352721;
RA Rensing U.F.E.;
RT "A sequence of seventy-three nucleotides from the coliphage R17
RT genome.";
RL Biochem. J. 131:593-604(1973).
DR EMBL; M24820; AAA72755.1; -.
FT NON_TER 8
SQ SEQUENCE 8 AA; 969 MW; ECB45412C1E72726 CRC64;

Query Match 27.3%; Score 21; DB 2; Length 8;
Best Local Similarity 80.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 HVRES 15
DB 4 HVRNS 8
||| |::||
||| |::||

RESULT 10
Q6RUX9 PRELIMINARY; PRT; 11 AA.
AC Q6RUX9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Induced stolon tip protein PJ-2.
OS Capsicum annuum (Bell pepper).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Capsicum.
OX NCBI_TaxID=4072;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim S., Lee K.-W.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY496132; AAR83870.1; -.


```

GN Name=ctrA;
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NMB;
RA MEDLINE=96312345; PubMed=8763931;
RX Swartley J.S., Ahn J.H., Liu L.J., Kahler C.M., Stephens D.S.;
RT "Expression of sialic acid and polysialic acid in serogroup B
RT Neisseria meningitidis: divergent transcription of biosynthesis and
RT transport operons through a common promoter region.";
RL J. Bacteriol. 178:4052-4059(1996).
DR EMBL; U40741; AAB17456.1; -
FT NON_TER
SQ SEQUENCE 11 AA; 1440 MW; DB2075394B59C322 CRC64;

Query Match 29.9%; Score 23; DB 2; Length 11;
Best Local Similarity 36.4%; Pred. No. 2.9e+03;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 5 LFFVKVHVRES 15
Db 1 MFKVKFYIRHA 11

RESULT 5
ID Q9X9S6 PRELIMINARY; PRT; 11 AA.
AC Q9X9S6;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Hypothetical protein ORF9 (Fragment).
GN Name=ORF9;
OS Streptomyces lividans.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1916;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TK21;
RX MEDLINE=99328982; PubMed=10400594;
RA Martinez-Costa O.H., Martin-Triana A.J., Martinez E.,
RA Fernandez-Moreno M.A., Malpartida F.;
RT "An additional regulatory gene for actinorhodin production in
RT Streptomyces lividans involves a lyrA-type transcriptional
RT regulator.";
RL J. Bacteriol. 181:4353-4364(1999).
DR EMBL; Y18818; CAB51138.1; -
KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 11 AA; 1160 MW; D1BAB8EC1EDC412 CRC64;

Query Match 28.6%; Score 22; DB 2; Length 11;
Best Local Similarity 80.0%; Pred. No. 4.5e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VKAHV 12
Db 4 VRAHV 8

RESULT 6
ID Q9UC29 PRELIMINARY; PRT; 12 AA.
AC Q9UC29;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE 85 kDa glioma membrane protein/CD44 homolog (Fragment).
OS Homo sapiens (Human).

```

```

GN Name=ctrA;
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NMB;
RA MEDLINE=96312345; PubMed=8763931;
RX Swartley J.S., Ahn J.H., Liu L.J., Kahler C.M., Stephens D.S.;
RT "Expression of sialic acid and polysialic acid in serogroup B
RT Neisseria meningitidis: divergent transcription of biosynthesis and
RT transport operons through a common promoter region.";
RL J. Bacteriol. 178:4052-4059(1996).
DR EMBL; U40741; AAB17456.1; -
FT NON_TER
SQ SEQUENCE 11 AA; 1440 MW; DB2075394B59C322 CRC64;

Query Match 29.9%; Score 23; DB 2; Length 11;
Best Local Similarity 36.4%; Pred. No. 2.9e+03;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 5 LFFVKVHVRES 15
Db 1 MFKVKFYIRHA 11

RESULT 5
ID Q9X9S6 PRELIMINARY; PRT; 11 AA.
AC Q9X9S6;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Hypothetical protein ORF9 (Fragment).
GN Name=ORF9;
OS Streptomyces lividans.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1916;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TK21;
RX MEDLINE=99328982; PubMed=10400594;
RA Martinez-Costa O.H., Martin-Triana A.J., Martinez E.,
RA Fernandez-Moreno M.A., Malpartida F.;
RT "An additional regulatory gene for actinorhodin production in
RT Streptomyces lividans involves a lyrA-type transcriptional
RT regulator.";
RL J. Bacteriol. 181:4353-4364(1999).
DR EMBL; Y18818; CAB51138.1; -
KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 11 AA; 1160 MW; D1BAB8EC1EDC412 CRC64;

Query Match 28.6%; Score 22; DB 2; Length 11;
Best Local Similarity 80.0%; Pred. No. 4.5e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VKAHV 12
Db 4 VRAHV 8

RESULT 6
ID Q9UC29 PRELIMINARY; PRT; 12 AA.
AC Q9UC29;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE 85 kDa glioma membrane protein/CD44 homolog (Fragment).
OS Homo sapiens (Human).

```

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OM protein - protein search, using sw model

Run on: February 22, 2005, 08:53:13 ; Search time 52.6 Seconds
(without alignments)
146.030 Million cell updates/sec

Title: US-08-991-628-15
Perfect score: 77
Sequence: 1 GGRLLFFVKAHVRES 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 6622

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	37.7	12	1 YZPY_ECOLI	P17776 escherichia
2	28	36.4	15	2 Q6QQR3	Q6QQR3 helicobacte
3	24	31.2	14	2 Q945F2	Q945f2 cicer ariet
4	23	29.9	11	2 Q79CEB7	Q79CE7 neisseria m
5	22	28.6	11	2 Q9X9S6	Q9X9S6 streptomyce
6	22	28.6	12	2 Q7UC29	Q9UC29 homo sapien
7	22	28.6	14	2 Q7M2Q3	Q7M2Q3 bos taurus
8	22	28.6	15	2 Q95949	Q95949 saurosalus
9	21	27.3	8	2 Q37854	Q37854 bacterioph
10	21	27.3	11	2 Q6RUX9	Q6RUX9 capsicum an
11	21	27.3	15	1 G6PD_WA1ZE	P80619 zea mays (m
12	21	27.3	15	2 Q84887	Q84887 salmonella
13	20	26.0	10	1 TPTS_NICPL	P19118 nicotiana p
14	20	26.0	10	2 Q6A3T0	Q6A3T0 archangiot
15	20	26.0	10	2 Q39952	Q39952 gb virus c/
16	20	26.0	10	2 Q8WLE4	Q8WLE4 gb virus c/
17	20	26.0	11	2 Q8MER8	Q8MER8 dombeya til
18	20	26.0	11	2 Q9RBV0	Q9RBV0 pseudomonas
19	20	26.0	11	2 Q39951	Q39951 gb virus c/
20	20	26.0	14	2 Q96Q50	Q96Q50 homo sapien
21	20	26.0	15	1 RM12_YEAST	P36522 saccharomyc
22	20	26.0	15	2 Q9TR46	Q9TR46 bos taurus
23	19	24.7	8	2 Q6EGT1	Q6EGT1 stemphylium
24	19	24.7	8	2 Q6EGV0	Q6EGV0 stemphylium
25	19	24.7	8	2 Q6EGV3	Q6EGV3 stemphylium
26	19	24.7	8	2 Q6EGW2	Q6EGW2 stemphylium
27	19	24.7	10	2 Q7M4X7	Q7M4X7 fusarium sp
28	19	24.7	11	2 Q7KYZ8	Q7KYZ8 homo sapien
29	19	24.7	12	2 Q7RHA4	Q7RHA4 plasmodium
30	19	24.7	12	2 Q945C3	Q945C3 crypthecodi
31	19	24.7	14	1 SAP2_ARBPU	P11760 arabacia pun

32	19	24.7	14	2	Q61864	Q61864 mus musculu
33	19	24.7	15	2	Q9TWF3	Q9TWF3 dictyosteli
34	19	24.7	15	2	Q842L7	Q842L7 salmonella
35	18	23.4	9	2	Q8MEM3	Q8MEM3 howittia tr
36	18	23.4	9	2	Q95GN1	Q95GN1 pelargonium
37	18	23.4	10	2	Q7SA62	Q7SA62 neurospora
38	18	23.4	10	2	Q71UL3	Q71UL3 hallois ru
39	18	23.4	10	2	Q8HUB4	Q8HUB4 anomobryum
40	18	23.4	10	2	Q67B22	Q67B22 bacterioph
41	18	23.4	10	2	Q7LZJ7	Q7LZJ7 carcharinu
42	18	23.4	11	1	ASL2_BACSE	P8147 bacteroides
43	18	23.4	11	1	MLG_THETS	P41989 theromyzon
44	18	23.4	11	2	O77880	O77880 oreochromis
45	18	23.4	11	2	O77907	O77907 oreochromis

ALIGNMENTS

RESULT 1

YZPY_ECOLI
ID YZPY_ECOLI STANDARD; PRT; 12 AA.
AC P17776;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Hypothetical pyrE leader peptide.
GN Name=pyrL; Synonyms=pyrE-LP;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85003588; PubMed=6207018;
RA Poulsen P., Bonekamp F., Jensen K.F.;
RT "Structure of the Escherichia coli pyrE operon and control of pyrE expression by a UTP modulated intercistronic attenuation.";
RL EMEQ J. 3:1783-1790 (1984).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=83287414; PubMed=6349999;
RA Poulsen P., Jensen K.F., Valentin-Hansen P., Carlsson P.,
RA Lundberg L.G.;
RT "Nucleotide sequence of the Escherichia coli pyrE gene and of the DNA in front of the protein-coding region.";
RL Eur. J. Biochem. 135:223-229 (1983).
CC -!- CAUTION: This sequence, according to the EcoSeq database (K. Rudd) is probably not a real protein; therefore this entry will probably be deleted in future releases.

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CC EMBL; X00781; -; NOT ANNOTATED CDS.

DR EMBL; V01578; -; NOT_ANNOTATED_CDS.

DR PIR; A30400; LPECPD.

KW Hypothetical protein.

SQ SEQUENCE 12 AA; 1542 MW; C4291FA437A2C9C9 CRC64;

Query Match 37.7%; Score 29; DB 1; Length 12;
Best Local Similarity 70.0%; Pred. No. 2.2e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 RLFFVKAHVR 13

DB 3 RLFFVCKVR 12

Query Match 26.0%; Score 20; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GRRLLFF 7
| : |||
DB 6 GQEVFF 11

RESULT 14

PH1466
T-cell receptor beta chain (clone A3/74.1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 15-Mar-2004
C;Accession: PH1466
R;Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; K
J. Exp. Med. 177, 811-820, 1993
A;Title: T cell receptor selection by and recognition of two class I major histocompatib
A;Reference number: PH1430; MUID:93171821; PMID:8436911
A;Accession: PH1466
A;Molecule type: mRNA
A;Residues: 1-12 <CAS>
A;Experimental source: cytolytic T-lymphocyte
C;Keywords: receptor; T-cell

Query Match 26.0%; Score 20; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GRRLLFF 7
| : |||
DB 6 GQEVFF 11

RESULT 15

S22761
Ig lambda-2 chain J region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 16-Aug-1996
C;Accession: S22761
R;Weiss, S.; Wu, G.E.
EMBO J. 6, 927-932, 1987
A;Title: Somatic point mutations in unrearranged immunoglobulin gene segments encoding b
A;Reference number: S22759; MUID:87246527; PMID:3109891
A;Accession: S22761
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-13 <WEI>
A;Cross-references: EMBL:X58422
C;Keywords: heterotetramer; immunoglobulin

Query Match 26.0%; Score 20; DB 2; Length 13;
Best Local Similarity 80.0%; Pred. No. 2.9e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGRRL 5
| : |||
DB 4 GGTRL 8

Search completed: February 22, 2005, 09:46:30
Job time : 11.1333 secs

C:Species: Bos primigenius taurus (cattle)
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 16-Aug-2004
C:Accession: JH0328
R:Audhya, T.; King, R.; Goldstein, G.
Life Sci. 48, 773-780, 1991
A:Title: Bovine probursin tetradecapeptide contains amino acid sequence from somatostatin
A:Reference number: JH0328; MUID:91133172; PMID:1671611
A:Accession: JH0328
A:Molecule type: protein
A:Residues: 1-14 <AUD>
A:Cross-references: UNIPROT:Q7M203
C:Comment: Intact probursin has the biological activity of both somatostatin and bursin.
C:Keywords: amidated carboxyl end; hormone
F:5-8/Product: tufsein #status predicted <TUF>
F:9-11/Product: bursin #status predicted <BUR>
F:Fill/Modified site: amidated carboxyl end (Gly) (amide in mature form from following gly

Query Match 28.6%; Score 22; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.3e+03; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 0;

QY 1 GGRR 4
| | | |
DB 11 GGRR 14

RESULT 9
S57577
T cell receptor V-J junctional alpha chain region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 05-Nov-1999
C:Accession: S57577
R:Burrows, S.R.; Silins, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Argæt, V.P.
submitted to the EMBL Data Library, June 1995
A:Description: T cell receptor repertoire for a viral epitope in humans is diversified b
A:Reference number: S57494
A:Accession: S57577
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-15 <BUR>
A:Cross-references: EMBL:249945; NID:g887492; PIDN:CAA90216.1; PID:g887493
C:Keywords: T-cell receptor

Query Match 28.6%; Score 22; DB 2; Length 15;
Best Local Similarity 57.1%; Pred. No. 1.4e+03; Mismatches 3; Indels 0; Gaps 0;
Matches 4; Conservative 0;

QY 1 GGRRLLFF 7
| | | | |
DB 8 GANNLFF 14

RESULT 10
T03000
GTP-binding protein, truncated - Salmonella typhimurium
C:Species: Salmonella typhimurium
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C:Accession: T03000
R:Figueroa-Bossi, N.; Bossi, L.
submitted to the EMBL Data Library, June 1998
A:Reference number: Z14818
A:Accession: T03000
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-15 <FIG>
A:Cross-references: UNIPROT:O84887; EMBL:AF001386; NID:g3294471; PIDN:AAC26066.1; PID:g3
C:Genetics:
A>Note: lepA

Query Match 27.3%; Score 21; DB 2; Length 15;
Best Local Similarity 44.4%; Pred. No. 2.2e+03; Mismatches 4; Conservative 2; Indels 0; Gaps 0;

QY 4 RLFFVKAHV 12
| | | | |
DB 5 RNFSIIAH 13

RESULT 11
A27617
triose-phosphate isomerase (EC 5.3.1.1) - curled-leaved tobacco (fragment)
C:Species: Nicotiana glauca (curled-leaved tobacco)
C:Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 09-Jul-2004
C:Accession: A27617
R:Bauw, G.; De Loose, M.; Inze, D.; Van Montagu, M.; Vandekerckhove, J.
Proc. Natl. Acad. Sci. U.S.A. 84, 4806-4810, 1987
A:Title: Alterations in the phenotype of plant cells studied by NH2-terminal amino acid
A:Reference number: A94167
A:Accession: A27617
A:Molecule type: protein
A:Residues: 1-10 <BAU>
A:Cross-references: UNIPROT:P19118
C:Keywords: gluconeogenesis; glycolysis; intramolecular oxidoreductase; isomerase; pent

Query Match 26.0%; Score 20; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 2.3e+03; Mismatches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 RLFFV 8
| | | | |
DB 2 RTFFV 6

RESULT 12
S57575
T cell receptor V-J junctional alpha chain region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 05-Nov-1999
C:Accession: S57575
R:Burrows, S.R.; Silins, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Argæt, V.P.
submitted to the EMBL Data Library, June 1995
A:Description: T cell receptor repertoire for a viral epitope in humans is diversified i
A:Reference number: S57494
A:Accession: S57575
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-11 <BUR>
A:Cross-references: EMBL:249953; NID:g887510; PIDN:CAA90224.1; PID:g887511
C:Keywords: T-cell receptor

Query Match 26.0%; Score 20; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 2.5e+03; Mismatches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGRRLLF 6
| | | | |
DB 5 GGKLLF 10

RESULT 13
S26559
T-cell receptor beta chain (clone Cw3/Cas15) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 17-Apr-1998 #text_change 17-Mar-1999
C:Accession: S26559
R:Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wi
J. Exp. Med. 176, 439-447, 1992
A:Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor
A:Reference number: S26512; MUID:92364546; PMID:1380061
A:Accession: S26559
A:Molecule type: mRNA
A:Residues: 1-12 <CAS>
A:Cross-references: EMBL:X68009
A:Experimental source: cytolytic T-lymphocyte, clone Cw3/Cas15
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor

Query Match 35.1%; Score 27; DB 2; Length 12;
 Best Local Similarity 83.3%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GRRLLFF 7
 Db 6 GERLFF 11

RESULT 3
 S26554
 T-cell receptor beta chain (clone Cw3/Cas7) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 13-Jan-1995 #sequence_revision 17-Apr-1998 #text_change 17-Mar-1999
 C:Accession: S26554
 R:Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid
 J. Exp. Med. 176, 439-447, 1992
 A:Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor
 A:Reference number: S26512; MUID:92364546; PMID:1380061
 A:Accession: S26554
 A:Molecule type: mRNA
 A:Residues: 1-12 <CAS>
 A:Cross-references: EMBL:X68004
 A:Experimental source: cytolytic T-lymphocyte, clone Cw3/Cas7
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: T-cell receptor

Query Match 35.1%; Score 27; DB 2; Length 12;
 Best Local Similarity 83.3%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GRRLLFF 7
 Db 6 GERLFF 11

RESULT 4
 S26555
 T-cell receptor beta chain (clone Cw3/1B4) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 13-Jan-1995 #sequence_revision 17-Apr-1998 #text_change 17-Mar-1999
 C:Accession: S26555
 R:Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid
 J. Exp. Med. 176, 439-447, 1992
 A:Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor
 A:Reference number: S26512; MUID:92364546; PMID:1380061
 A:Accession: S26555
 A:Molecule type: mRNA
 A:Residues: 1-12 <CAS>
 A:Cross-references: EMBL:X68005
 A:Experimental source: cytolytic T-lymphocyte, clone Cw3/1B4
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: T-cell receptor

Query Match 35.1%; Score 27; DB 2; Length 12;
 Best Local Similarity 83.3%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GRRLLFF 7
 Db 6 GERLFF 11

RESULT 5
 PH0804
 T-cell receptor alpha chain (L4) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C:Accession: PH0804
 R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
 J. Exp. Med. 174, 1371-1383, 1991
 A:Title: T cell receptor genes in a series of class I major histocompatibility complex-

allelic exclusion and antigen-specific repertoire.
 A:Reference number: PH0746; MUID:92078846; PMID:1836010
 A:Accession: PH0804
 A:Molecule type: mRNA
 A:Residues: 1-14 <CAS>
 A:Cross-references: EMBL:X60913
 A:Experimental source: T lymphocyte
 C:Keywords: T-cell receptor

Query Match 33.8%; Score 26; DB 2; Length 14;
 Best Local Similarity 71.4%; Pred. No. 2.3e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGRRLFF 7
 Db 7 GGRALIF 13

RESULT 6

PH0762
 T-cell receptor beta chain (K1) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
 C:Accession: PH0762
 R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
 J. Exp. Med. 174, 1371-1383, 1991
 A:Title: T cell receptor genes in a series of class I major histocompatibility complex-

allelic exclusion and antigen-specific repertoire.
 A:Reference number: PH0746; MUID:92078846; PMID:1836010
 A:Accession: PH0762
 A:Molecule type: mRNA
 A:Residues: 1-14 <CAS>
 A:Cross-references: EMBL:X60856; NID:952768; PIDN:CAA43246.1; PID:952769
 A:Experimental source: T lymphocyte
 C:Keywords: T-cell receptor

Query Match 31.2%; Score 24; DB 2; Length 14;
 Best Local Similarity 57.1%; Pred. No. 5.5e+02;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGRRLFF 7
 Db 7 GGTVEVF 13

RESULT 7

PT0245
 Ig heavy chain CRD3 region (clone 2-103C) - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C:Accession: PT0245
 R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
 J. Exp. Med. 173, 395-407, 1991
 A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and

A:Reference number: PT0222; MUID:91108337; PMID:1899102
 A:Accession: PT0245
 A:Molecule type: DNA
 A:Residues: 1-10 <YAM>
 A:Experimental source: B lymphocyte
 C:Keywords: heterotetramer; immunoglobulin

Query Match 28.6%; Score 22; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 9.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGRR 4
 Db 2 GGRR 5

RESULT 8

JH0328
 probrusin tetradecapeptide - bovine

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 22, 2005, 09:08:09 ; Search time 11.1333 Seconds
(without alignments)
129.633 Million cell updates/sec

Title: US-08-991-628-15

Perfect score: 77
Sequence: 1 GGRRLFFVKAHVRES 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 2523

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	37.7	12	1 LFECPE	pyrE leader peptid
2	27	35.1	12	2 S26556	T-cell receptor be
3	27	35.1	12	2 S26554	T-cell receptor be
4	27	35.1	12	2 S26555	T-cell receptor al
5	26	33.8	14	2 PH0804	T-cell receptor be
6	24	31.2	14	2 PH0762	Ig heavy chain CVD
7	22	28.6	10	2 PT0245	probursin tetradec
8	22	28.6	14	2 JH0328	T cell receptor V-
9	22	28.6	15	2 S57577	GRP-binding protei
10	21	27.3	15	2 T03000	triose-phosphate i
11	20	26.0	10	2 A27617	T cell receptor V-
12	20	26.0	11	2 S57575	T-cell receptor be
13	20	26.0	12	2 S26559	T-cell receptor be
14	20	26.0	12	2 PH1466	Ig lambda-2 chain
15	20	26.0	13	2 S22761	T-cell antigen rec
16	20	26.0	15	2 S47387	T-cell receptor al
17	19	24.7	10	2 PH0807	triose-phosphate i
18	19	24.7	10	2 PN0165	CCK-B gastrin rece
19	19	24.7	11	2 I65231	hydrin 1 - African
20	19	24.7	12	2 A33900	Ig heavy chain DJ
21	19	24.7	14	2 PH1332	Ig H chain V-D-J r
22	19	24.7	14	2 PH1617	TSH protein beta c
23	19	24.7	15	2 S55312	serum heterodimer,
24	18	23.4	10	2 B56899	T-cell receptor be
25	18	23.4	11	2 PT0218	translation elonga
26	18	23.4	11	2 PD0441	gamma-MSH-like pro
27	18	23.4	11	2 S45698	T-cell receptor be
28	18	23.4	12	2 S26552	T-cell receptor be
29	18	23.4	12	2 S26549	T-cell receptor be

30	18	23.4	12	2 S26553	T-cell receptor be
31	18	23.4	12	2 PH1467	T-cell receptor be
32	18	23.4	12	2 PH1463	T-cell receptor be
33	18	23.4	12	2 PH1464	T-cell receptor be
34	18	23.4	12	2 PH1469	T-cell receptor be
35	18	23.4	12	2 PH1468	T-cell receptor be
36	18	23.4	13	2 JQ2309	hypothetical 1.6K
37	18	23.4	13	2 JQ2319	corticostatic pept
38	18	23.4	13	2 JH0460	T-cell receptor be
39	18	23.4	14	2 PH0753	T-cell receptor al
40	18	23.4	15	2 PH0808	phosphonoacetaldeh
41	17	22.1	7	2 A28709	T-cell receptor be
42	17	22.1	7	2 PT0520	fibrinogen beta ch
43	17	22.1	9	2 D24180	fibrinopeptide B -
44	17	22.1	9	2 F28854	
45	17	22.1	9	2 F28854	

ALIGNMENTS

RESULT 1

LFECPE
pyrE leader peptide - Escherichia coli
C:Species: Escherichia coli
C>Date: 31-Mar-1990 #sequence revision 31-Mar-1990 #text_change 09-Jul-2004
C:Accession: A30400; A05110; Q00495
R:Poulsen, P.; Bonekamp, P.; Jensen, K.F.
EMBO J. 3, 1783-1790, 1984

A>Title: Structure of the Escherichia coli pyrE operon and control of pyrE expression by
A:Reference number: A30400; MUID:85003588; PMID:6207018

A:Accession: A30400

A:Molecule type: DNA

A:Residues: 1-12 <POU1>

A:Cross-references: UNIPROT:P17776

R:Poulsen, P.; Jensen, K.F.; Valentin-Hansen, P.; Carleson, P.; Lundberg, L.G.

Eur. J. Biochem. 135, 223-229, 1983

A>Title: Nucleotide sequence of the Escherichia coli pyrE gene and of the DNA in front

A:Reference number: A05110; MUID:83287414; PMID:634999

A:Accession: A05110

A:Molecule type: DNA

A:Residues: 1-12 <POU2>

C:Genetics:

A:Gene: pyrE-LP

A:Map position: 82 min

C:Superfamily: pyrE leader peptide

Query Match 37.7%; Score 29; DB 1; Length 12;
Best Local Similarity 70.0%; Pred. No. 54;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 RLFFVKAHVR 13
|||
DB 3 RLFFVCKVR 12

RESULT 2

S26556

T-cell receptor beta chain (clone Cw3/2C3) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 13-Jan-1995 #sequence_revision 17-Apr-1998 #text_change 17-Mar-1999

C:Accession: S26556

R:Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wi

J. Exp. Med. 176, 439-447, 1992

A>Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor

A:Reference number: S26512; MUID:92364546; PMID:1380061

A:Accession: S26556

A:Molecule type: mRNA

A:Residues: 1-12 <CAS>

A:Cross-references: EMBL:X68006

A:Experimental source: cytolytic T-lymphocyte, clone Cw3/2C3

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: T-cell receptor

XX Example 1; Page 7; 19pp; English.

PS The present invention relates to a method for identifying compounds for

CC treating disorders mediated by deregulation of the Mitogen Activated

CC Protein Kinase (MAPK) pathway, related to structural and/or functional

CC alterations of the endosomal/lysosomal system. The compounds are tested

CC for their ability to inhibit, on late endosomes/lysosomes, the

CC interaction of p14 with MPI or the interaction of p14/MPI complex with

CC components of MAPK pathway. The method is useful for identifying

CC compounds for treating disorders such as lysosomal storage/transport

CC diseases, e.g., cystic fibrosis, Nieman-Pick-disease and diseases that

CC affect lysosomal secretion, e.g., asthma or Chediak-Higashi syndrome. The

CC present sequence is a peptide fragment of murine p14 protein, which was

CC obtained in an example from the invention

XX Sequence 10 AA;

SQ Query Match 36.8%; Score 28; DB 5; Length 10;

Best Local Similarity 83.3%; Pred. No. 3.9e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 9 KTVGFG 14

Db :|||||

2 ETVGFG 7

RESULT 15

AA49625

ID AAR49625 standard; peptide; 15 AA.

XX

AC AAR49625;

XX

DT 25-MAR-2003 (revised)

DT 22-AUG-1994 (first entry)

XX

DE Camel immunoglobulin variable heavy chain CDR3 peptide.

XX

KW Immunoglobulin; heavy chain; variable region; Camelid.

XX

OS Camelus dromedarius.

XX

PN WO9404678-A1.

XX

PD 03-MAR-1994.

XX

PF 18-AUG-1993; 93WO-EP002214.

XX

PR 21-AUG-1992; 92EP-00402326.

PR 21-MAY-1993; 93EP-00401310.

XX

PA (CAST/) CASTERMAN C.

PA (HAME/) HAMERS R.

XX

PI Casterman C, Hamers R;

PI WPI; 1994-083195/10.

DR

XX

PT Immunoglobulins devoid of light chains - also processes for their

PT preparation, and protein and nucleotide sequence encoding them.

XX

FS Claim 10; Page 60; 87pp; English.

XX

CC A novel immunoglobulin (Ig) is claimed which comprises two heavy (H)

CC polypeptide chains sufficient for the formation of a complete antigen

CC binding site or several such chains. The Ig is devoid of light (L)

CC polypeptide chains. The Ig may be obtd. from prokaryotic cells, esp. E.

CC coli, by: cloning a DNA or cDNA sequence coding for the VH domain of an

CC Ig devoid of L chains obtainable from e.g. lymphocytes of Camelids;

CC recovering the cloned fragment after amplification using a 5' primer

CC contg. an Xho site and a 3' primer contg. the Spe site having the

CC sequence in AAQ44383; cloning the recovered fragment is a vector;

CC transforming host cells; and recovering the expression product of the VHH

CC coding sequence. A claimed Ig comprises 4 frameworks in its variable (V)

CC region selected from: sequences in AAR49611-16 and AAR49720 for the

CC framework 1 domain; AAR49617-21 for the framework 4 domain; and/or

CC AAR49622-39 for the CDR3 domain; and/or that its constant region

CC comprises CH2 and CH3 domains comprising AA sequences selected from, for

CC the CH2 domain AAR49640-3, and for the CH3 domain AAR49444-48; and/or that

CC its hinge region comprises 0-50 AAs, esp. a sequence selected from

CC AAR49649 or AAR49650. (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 15 AA;

Query Match 36.8%; Score 28; DB 2; Length 15;

Best Local Similarity 50.0%; Pred. No. 5.9e+02;

Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 6 FLFKTVGFGG 15

Db :|||||

1 FCYSTAGDGG 10

Search completed: February 22, 2005, 09:24:55

Job time : 66.6667 secs

PS Disclosure; Page 30; 588pp; English.

XX The present invention describes a single chain polypeptide comprising
 CC clostridial neurotoxin light and heavy chains. The single chain
 CC polypeptide comprises 2 domains: the first domain is a clostridial
 CC neurotoxin light chain, or its fragment or variant, which is capable of
 CC cleaving one or more vesicle or plasma membrane associated proteins
 CC essential to exocytosis; the second domain is a clostridial neurotoxin
 CC heavy chain H-N portion, or its fragment or variant, which is capable of
 CC translocating the polypeptide into a cell and/or increasing the
 CC solubility of the polypeptide compared to the solubility of the first
 CC domain on its own. The second domain lacks a functional C-terminal part
 CC of a clostridial neurotoxin heavy chain, designated H-C, which renders
 CC the polypeptide incapable of binding to cell surface receptors that are
 CC the natural cell surface receptors to which native clostridial neurotoxin
 CC binds. Also described is a nucleic acid molecule encoding the single
 CC chain polypeptide described above. The single chain polypeptide has
 CC antibacterial activity, and can be used in vaccines. The single chain
 CC polypeptides can be used as positive controls for toxin assays, as
 CC reagent components for the synthesis of therapeutic molecules, or for
 CC developing vaccines against clostridial toxin. The polypeptides are also
 CC useful as non-toxic standards for the assessment and development of in
 CC vitro assays for detection of functional botulinum or tetanus neurotoxins
 CC in foodstuffs or environmental samples. The present sequence is used in
 CC the exemplification of the present invention.

XX Sequence 11 AA;

Query Match 38.2%; Score 29; DB 8; Length 11;
 Best Local Similarity 62.5%; Pred. No. 2.8e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 LFKTVGFG 14
 |:| |||
 Db 3 LYKXAGFG 10

RESULT 13

ADL90463
 ID ADL90463 standard; peptide; 15 AA.

AC ADL90463;

DT 17-JUN-2004 (first entry)

XX N-terminal extension peptide.

XX single chain polypeptide; clostridial neurotoxin light chain;
 KW clostridial neurotoxin heavy chain; Clostridium; neurotoxin; exocytosis;
 KW antibacterial; vaccine; toxin assay; clostridial toxin; detection;
 KW botulinum; tetanus.

XX Synthetic.

OS WO2004024909-A2.

PN 25-MAR-2004.

PD 12-SEP-2003; 2003WO-GB003824.

PF 12-SEP-2002; 2002US-00241596.

PR (HEAL-) HEALTH PROTECTION AGENCY.

PA Shone CC, Foster KA, Chaddock J, Marks P, Sutton MJ, Stancombe P;
 PI Wayne J;

XX WPI; 2004-270039/25.

XX New single chain polypeptides comprising clostridial neurotoxin light and
 PT heavy chains, useful as positive controls for toxin assays, or for
 PT developing vaccines against clostridial toxin.

PS Disclosure; Page 30; 588pp; English.

XX The present invention describes a single chain polypeptide comprising
 CC clostridial neurotoxin light and heavy chains. The single chain
 CC polypeptide comprises 2 domains: the first domain is a clostridial
 CC neurotoxin light chain, or its fragment or variant, which is capable of
 CC cleaving one or more vesicle or plasma membrane associated proteins
 CC essential to exocytosis; the second domain is a clostridial neurotoxin
 CC heavy chain H-N portion, or its fragment or variant, which is capable of
 CC translocating the polypeptide into a cell and/or increasing the
 CC solubility of the polypeptide compared to the solubility of the first
 CC domain on its own. The second domain lacks a functional C-terminal part
 CC of a clostridial neurotoxin heavy chain, designated H-C, which renders
 CC the polypeptide incapable of binding to cell surface receptors that are
 CC the natural cell surface receptors to which native clostridial neurotoxin
 CC binds. Also described is a nucleic acid molecule encoding the single
 CC chain polypeptide described above. The single chain polypeptide has
 CC antibacterial activity, and can be used in vaccines. The single chain
 CC polypeptides can be used as positive controls for toxin assays, as
 CC reagent components for the synthesis of therapeutic molecules, or for
 CC developing vaccines against clostridial toxin. The polypeptides are also
 CC useful as non-toxic standards for the assessment and development of in
 CC vitro assays for detection of functional botulinum or tetanus neurotoxins
 CC in foodstuffs or environmental samples. The present sequence is used in
 CC the exemplification of the present invention.

XX Sequence 15 AA;

Query Match 38.2%; Score 29; DB 8; Length 15;
 Best Local Similarity 62.5%; Pred. No. 3.9e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 LFKTVGFG 14
 |:| |||
 Db 4 LYKXAGFG 11

RESULT 14

ABB98511
 ID ABB98511 standard; peptide; 10 AA.

AC ABB98511;

DT 25-NOV-2002 (first entry)

XX Murine p14 peptide fragment #1.

XX Murine; antiasthmatic; immunomodulator; asthma;
 KW Mitogen Activated Protein Kinase; MAPK; endosome; lysosome; p14;
 KW lysosomal storage disease; lysosomal transport disease; cystic fibrosis;
 KW Nieman-Pick-disease; lysosomal secretion; Chediak-Higashi syndrome.

XX Mus musculus.

OS EP1233271-A1.

PN 21-AUG-2002.

PD 16-FEB-2001; 2001EP-00103792.

PR 16-FEB-2001; 2001EP-00103792.

XX (HUBER) HUBER L.

PA (WUNDERLICH) WUNDERLICH W.

XX (FIALKA) FIALKA I.

PI Huber L, Wunderlich W, Fialka I;

XX WPI; 2002-668424/72.

XX Identifying compounds for treating disorders mediated by deregulation of
 PT mitogen activated protein kinase pathway related to structural and/or
 PT functional alterations of endosomal/lysosomal system.

XX Analyzing cleavage of polymer, by providing polymer sample, incubating
PT the sample with labeled isotope for cleavage at potential cleavage site,
XX and analyzing the masses of any uncleaved fragments by mass spectrometry.
XX
PS Example 8; Page 33; 73pp; English.
XX
CC The present invention describes a method (M1) for analysing cleavage of a
CC polymer. M1 comprises: (a) providing a sample of the polymer, a portion
CC of the polymer molecules having been labeled at a position on one side of
CC the potential cleavage site with a first isotopic label and a portion of
CC the polymer molecules having been labeled at a position on the opposite
CC side of the potential cleavage site with a second isotopic label; (b)
CC incubating the sample under conditions suitable for cleavage at the
CC potential cleavage site; and (c) analysing the mass(es) of any cleaved
CC fragments by mass spectrometry and thereby determining whether and/or
CC where cleavage has taken place. M1 is useful for analysing cleavage of a
CC polymer, where the polymer is a linear polymer, and comprises a peptide
CC or protein. Methods from the present invention can be used in discovering
CC new or improved synthetic substrates for both known and unknown enzymes,
CC e.g. enzymes identified from the human genome. The methods are also
CC useful to identify the sequence origin, and in screening methods to
CC identify new substrates for enzymes, in positional peptide scanning
CC libraries, in *in vivo/ex vivo* in vitro peptide, and in assaying methods
CC for oligonucleotide or peptide sequencing and in measuring differential
CC protein expression. The methods are useful for monitoring the cleavage of
CC polypeptides or polynucleotides, and for determining optimal polymer
CC substrates. ABP57505 to ABP57605 represent peptides used in the
CC exemplification of the present invention
XX
SQ Sequence 10 AA;
Query Match 38.2%; Score 29; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 AAFLEPK 9
DB 1 AAFLEPK 6
RESULT 11
ABP57592
ID ABP57592 standard; peptide; 11 AA.
AC
XX ABP57592;
XX
DT 28-APR-2003 (first entry)
XX
DE Differentially isotopically labelled (DiMas) peptide #78.
XX
KW Mass spectrometry; polymer; analysis; cleavage; substrate specificity;
KW isotope; protease.
XX
OS Synthetic.
XX
XX WO2003001206-A1.
XX
PD 03-JAN-2003.
XX
PF 25-JUN-2002; 2002WO-GB002921.
XX
PR 26-JUN-2001; 2001GB-00015581.
XX
PA (GLAXO) GLAXO GROUP LTD.
XX
XX Mckewen SC;
XX
XX WPI; 2003-184066/18.
XX
DR Analyzing cleavage of polymer, by providing polymer sample, incubating
PT the sample with labeled isotope for cleavage at potential cleavage site,
PT and analyzing the masses of any uncleaved fragments by mass spectrometry.
PT

XX Example 8; Page 36; 73pp; English.
PS
XX
CC The present invention describes a method (M1) for analysing cleavage of a
CC polymer. M1 comprises: (a) providing a sample of the polymer, a portion
CC of the polymer molecules having been labeled at a position on one side of
CC the potential cleavage site with a first isotopic label and a portion of
CC the polymer molecules having been labeled at a position on the opposite
CC side of the potential cleavage site with a second isotopic label; (b)
CC incubating the sample under conditions suitable for cleavage at the
CC potential cleavage site; and (c) analysing the mass(es) of any cleaved
CC fragments by mass spectrometry and thereby determining whether and/or
CC where cleavage has taken place. M1 is useful for analysing cleavage of a
CC polymer, where the polymer is a linear polymer, and comprises a peptide
CC or protein. Methods from the present invention can be used in discovering
CC new or improved synthetic substrates for both known and unknown enzymes,
CC e.g. enzymes identified from the human genome. The methods are also
CC useful to identify the sequence origin, and in screening methods to
CC identify new substrates for enzymes, in positional peptide scanning
CC libraries, in *in vivo/ex vivo* in vitro peptide, and in assaying methods
CC for oligonucleotide or peptide sequencing and in measuring differential
CC protein expression. The methods are useful for monitoring the cleavage of
CC polypeptides or polynucleotides, and for determining optimal polymer
CC substrates. ABP57505 to ABP57605 represent peptides used in the
CC exemplification of the present invention
XX
SQ Sequence 11 AA;
Query Match 38.2%; Score 29; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 AAFLEPK 9
DB 2 AAFLEPK 7
RESULT 12
ADL90462
ID ADL90462 standard; peptide; 11 AA.
XX
AC ADL90462;
XX
DT 17-JUN-2004 (first entry)
XX
DE N-terminal extension peptide.
XX
KW single chain polypeptide; clostridial neurotoxin light chain;
KW clostridial neurotoxin heavy chain; Clostridium; neurotoxin; exocytosis;
KW antibacterial; vaccine; toxin assay; clostridial toxin; detection;
KW botulinum; tetanus.
XX
XX Synthetic.
XX
XX WO2004024909-A2.
XX
PD 25-MAR-2004.
XX
PF 12-SEP-2003; 2003WO-GB003824.
XX
PR 12-SEP-2002; 2002US-00241596.
XX
XX (HEAL-) HEALTH PROTECTION AGENCY.
XX
XX Shone CC, Foster KA, Chaddock J, Marks P, Sutton MJ, Stancombe P;
PI Wayne J;
XX
XX WPI; 2004-270039/25.
XX
PT New single chain polypeptides comprising clostridial neurotoxin light and
PT heavy chains, useful as positive controls for toxin assays, or for
PT developing vaccines against clostridial toxin.
XX

CC polynucleotides and specific antibodies. Immunotherapy; Anti-HIV. The
CC compounds are useful for inducing an immune response and administering
CC immunotherapy to a subject with AIDS. The present sequence represents a
CC specific example of a HIV S19 peptide epitope derived compound.
XX
SQ Sequence 9 AA;

Query Match

Best Local Similarity 39.5%; Score 30; DB 8; Length 9;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 FLFKTVG 12

DB 1 FLYRTVG 7

RESULT 8

ID ABR44302 standard; peptide; 15 AA.

AC ABR44302;

DT 27-JUN-2003 (first entry)

DE Human L-asparaginase 24.53 N-terminal peptide sequence #SEQ ID 7.
KW Human; L-asparaginase; 24.53; diabetes; tumour.
XX

OS Homo sapiens.

XX CN1360049-A.

PN 24-JUL-2002.

PD 20-DEC-2000; 2000CN-00135126.

PF 20-DEC-2000; 2000CN-00135126.

PR (BODE-) BODE GENE DEV CO LTD SHANGHAI.
PA Mao Y, Xie Y;
PI WPI; 2002-733674/80.

DR A human L-asparaginase 24.53 polypeptide L-asparaginase 24.53 and the
PT polynucleotide encoding it.
PS Example 6; Page 18 (disclosure); 32pp; Chinese.

XX The invention relates to a human L-asparaginase polypeptide designated
CC 24.53, and the polynucleotide encoding it. Also disclosed is the method
CC for preparing the polypeptide using DNA recombination techniques. The
CC application of the polypeptide is in treating diseases including diabetes
CC and tumours. The current sequence represents the human L-asparaginase N-
CC terminal peptide sequence
XX

SQ Sequence 15 AA;

Query Match

Best Local Similarity 39.5%; Score 30; DB 5; Length 15;

Matches 8; Conservative 1; Mismatches 1; Indels 4; Gaps 1;

QY 1 MARAAFLFKTVGFG 14

DB 1 MVRAA----TVGYG 10

RESULT 9

ID ABP55159 standard; peptide; 15 AA.

AC ABP55159;

XX

XX

DT 05-FEB-2003 (first entry)
XX Mouse myoglobulin I-111-18.48 N-terminal peptide.
DE Mouse; myoglobulin I-111-18.48; diabetes; tumour; antidiabetic;
XX antitumour.
KW Mus sp.
XX CN1343726-A.

PN 10-APR-2002.

PP 19-SEP-2000; 2000CN-00125213.

PR 19-SEP-2000; 2000CN-00125213.

PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.

PI Mao Y, Xie Y;

XX WPI; 2002-548994/59.

DR A novel mouse myoglobulin I-111-18.48 polypeptide, useful for treating
XX several diseases e.g. diabetes and tumors.
PS Example 6; Page 19 (disclosure); 31pp; Chinese.
XX The present invention relates to novel mouse myoglobulin I-111-18.48 (see
CC ABP55159) and to a polynucleotide (see ABV75939) encoding it. The protein
CC is useful for the treatment of several diseases, e.g. diabetes and
CC tumours. The present sequence is an N-terminal peptide fragment of the
CC myoglobulin, which was used in an example from the invention
XX

SQ Sequence 15 AA;

Query Match

Best Local Similarity 39.5%; Score 30; DB 5; Length 15;

Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 MARAAFLFKTVGFG 14

DB 1 MVEKALLYRTVATG 14

RESULT 10

ID ABP57556 standard; peptide; 10 AA.

AC ABP57556;

DT 28-APR-2003 (first entry)

DE Differentially isotopically labelled (DiMas) peptide #42.

XX Mass spectrometry; polymer; analysis; cleavage; substrate specificity;
XX isotope; protease.
XX Synthetic.
XX WO2003001206-A1.

PN 03-JAN-2003.

PP 25-JUN-2002; 2002WO-GB002921.

PR 26-JUN-2001; 2001GB-00015581.

PA (GLAX) GLAXO GROUP LTD.

XX McKeown SC;

XX WPI; 2003-184066/18.

PR 15-JUN-1999; 99WO-IL000329.
 XX (HORN/) HORNIK V.
 PA (APAR/) APARGAN M. M.
 PA (GELL/) GELLERMAN G.
 XX
 PI Hornik V, Afargan MM, Gellerman G;
 XX WPI; 2002-681319/73.
 DR
 XX
 XX New backbone cyclized somatostatin analogs are e.g. useful in the
 PT treatment of atherosclerosis, autoimmune diseases and cancers.
 XX
 PS Disclosure; Page 12; 30pp; English.
 XX
 CC The present invention describes backbone cyclized somatostatin analogues
 CC (I) that incorporates at least one building unit containing one nitrogen
 CC atom of the peptide backbone connected to a bridging group (comprising an
 CC amide, thioether, thioester or disulfide) where at least one building
 CC unit is connected via the bridging group to form a cyclic structure with
 CC a moiety selected from the group consisting of a second building unit,
 CC the side chain of an amino acid residue of the sequence or the N-terminal
 CC amino acid residue. (I) has antiarteriosclerotic, immunosuppressive,
 CC cytostatic, antidiabetic, antiinflammatory and analgesic activities, and
 CC can be used as a somatostatin receptor ligand. (I) are useful in the
 CC treatment of atherosclerosis, autoimmune diseases, cancers, diabetic-
 CC associated complications, endocrine disorders, inflammation,
 CC gastrointestinal disorders, pancreatitis, post-surgical pain, and
 CC restenosis. (I) can also be used in the diagnosis of cancer, by imaging
 CC the existence of metastases, it being labeled with a detectable probe.
 CC The present sequence represents a multiple parallel synthesis
 CC somatostatin analogue from the present invention
 XX
 SQ Sequence 9 AA;
 Query Match 42.1%; Score 32; DB 5; Length 9;
 Best Local Similarity 75.0%; Pred. NO. 1.8e+06;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 6 FLFKTVGF 13
 Db | : || || ||
 2 FAWKTVGF 9
 RESULT 6
 AAW42262
 ID AAW42262 standard; peptide; 15 AA.
 XX AC AAW42262;
 DT 08-APR-1998 (first entry)
 XX
 DE Biotinylated cross-linked interleukin-8 15-mer peptide ligand 2.
 XX
 KW Bacteriophage peptide library; peptide epitope; therapeutic target;
 KW variegated compound library; interleukin-8; IL-8.
 XX
 OS Synthetic.
 XX
 XX WO9735194-A2.
 PN
 XX 25-SEP-1997.
 PD
 XX 21-MAR-1997; 97WO-US0041176.
 PF
 XX 21-MAR-1996; 96US-00622338.
 PR
 XX (HARD) HARVARD COLLEGE.
 PA
 XX Forster AC;
 PI
 XX WPI; 1997-480355/44.
 DR
 XX
 XX
 PT Identifying compounds which interact with target molecules - using
 PT enantiomers of the target molecules and testing of enantiomers of
 XX selected compounds.
 XX
 PS Disclosure; Fig 6; 89pp; English.
 XX
 CC 15-mer peptides AAW42261-77 are identified as ligands of a biotinylated,
 CC cross-linked interleukin-8 (IL-8) target, using the method of the
 CC invention. This novel method identifies compounds which interact with a
 CC target molecule, and comprises contacting a screening molecule with a
 CC variegated compound library, where the screening molecule comprises solid
 CC target molecule, or the enantiomer if the target molecule is chiral.
 CC Compounds which have a desired interaction with the target molecule are
 CC selected, and the ability of their enantiomer to interact with the target
 CC molecule is tested. Ligands for a target protein can be identified by
 CC combining a D-enantiomer of a target protein (a D-target protein), and a
 CC variegated compound library, and then selecting one or more compounds
 CC from the library which have a desired binding interaction with the D-
 CC target protein. The methods can be used for identifying agonists or
 CC antagonists of targets such as receptors, enzymes, DNA binding proteins
 CC or signal transduction proteins. The methods can provide a structurally
 CC selective approach in addition to scoring for interaction of functional
 CC groups. They provide a powerful selection method that allows for the
 CC production of ligands with the same diversity as peptides but with the
 CC greatly improved pharmacokinetic profiles needed for drug activity
 XX
 SQ Sequence 15 AA;
 Query Match 40.8%; Score 31; DB 2; Length 15;
 Best Local Similarity 60.0%; Pred. No. 1.7e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 3 RAFLFKTVG 12
 Db | : || || ||
 5 RSAPRPSVG 14
 RESULT 7
 ADO44298
 ID ADO44298 standard; peptide; 9 AA.
 XX AC ADO44298;
 DT 29-JUL-2004 (first entry)
 XX
 DE HIV SL9 epitope derived compound 4.
 XX
 KW SL9; gag; HIV; immunotherapy; anti-HIV; AIDS; epitope.
 XX
 OS Human immunodeficiency virus 1.
 XX
 XX WO2004039324-A2.
 PN
 XX 13-MAY-2004.
 PD
 XX 24-OCT-2003; 2003WO-US033977.
 PF
 XX 28-OCT-2002; 2002US-0422038P.
 PR
 XX (GENZ) GENZYME CORP.
 PA (MASS-) MASSACHUSETTS GEN HOSPITAL.
 XX
 PI Nicolette CA, Walker BD;
 XX
 DR WPI; 2004-376049/35.
 DR N-PSDB; ADO44299.
 XX
 XX New anti-HIV (SL9) compounds, useful for inducing an immune response and
 PT administering immunotherapy to a subject with AIDS.
 XX
 XX Claim 1; SEQ ID NO 7; 58pp; English.
 PS
 XX The invention relates to anti-HIV (SL9) compounds and encoding
 CC

CC amide, thioether, thioester or disulfide) where at least one building
 CC unit is connected via the bridging group to form a cyclic structure with
 CC a moiety selected from the group consisting of a second building unit,
 CC the side chain of an amino acid residue of the sequence or the N-terminal
 CC amino acid residue. (I) has antiarteriosclerotic, immunosuppressive,
 CC cytostatic, antidiabetic, antiinflammatory and analgesic activities, and
 CC can be used as a somatostatin receptor ligand. (I) are useful in the
 CC treatment of atherosclerosis, autoimmune diseases, cancers, diabetic-
 CC associated complications, endocrine disorders, inflammation,
 CC gastrointestinal disorders, pancreatitis, post-surgical pain, and
 CC restenosis. (I) can also be used in the diagnosis of cancer, by imaging
 CC the existence of metastases, it being labeled with a detectable probe.
 CC The present sequence represents a multiple parallel synthesis
 CC somatostatin analogue from the present invention
 XX
 SQ Sequence 9 AA;

Query Match 43.4%; Score 33; DB 5; Length 9;
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 6 FLFKTVGF 13
 | : |||||
 Db 2 FFWKTVGF 9

RESULT 4
 ABP53382
 ID ABP53382 standard; peptide; 9 AA.
 AC ABP53382;
 DT 19-NOV-2002 (first entry)
 DE Multiple parallel synthesis somatostatin analogue #13.
 KW Backbone cyclised somatostatin analogue; somatostatin; SRIF; analgesic;
 KW somatropin release inhibiting factor; somatostatin receptor subtype;
 KW synthesis; antiarteriosclerotic; immunosuppressive; cytostatic; cancer;
 KW antidiabetic; antiinflammatory; immunosuppressive; cytostatic; cancer;
 KW atherosclerosis; autoimmune disease; somatostatin receptor ligand;
 KW endocrine disorder; inflammation; diabetic-associated complication;
 KW pancreatitis; post-surgical pain.
 XX
 OS Synthetic.

Key Location/Qualifiers
 Modified-site 1
 /label= bala
 /note= "beta-alanine"
 Misc-difference 4
 /note= "D form residue"
 Misc-difference 9
 /note= "D form residue"

US2002052315-A1.
 02-MAY-2002.
 13-DEC-2000; 2000US-00734583.
 19-JUN-1998; 98US-00100360.
 02-DEC-1998; 98US-00203389.
 15-JUN-1999; 99WO-IL000329.
 (HORN/) HORN V.
 (AFAR/) AFARGAN M. M.
 (GELL/) GELLERMAN G.
 Hornik V, Afargan MM, Gellerman G;
 WPI; 2002-681319/73.

PT New backbone cyclized somatostatin analogs are e.g. useful in the
 PT treatment of atherosclerosis, autoimmune diseases and cancers.
 XX
 PS Disclosure; Page 12; 30pp; English.

XX The present invention describes backbone cyclised somatostatin analogues
 CC (I) that incorporates at least one building unit containing one nitrogen
 CC atom of the peptide backbone connected to a bridging group (comprising an
 CC amide, thioether, thioester or disulfide) where at least one building
 CC unit is connected via the bridging group to form a cyclic structure with
 CC a moiety selected from the group consisting of a second building unit,
 CC the side chain of an amino acid residue of the sequence or the N-terminal
 CC amino acid residue. (I) has antiarteriosclerotic, immunosuppressive,
 CC cytostatic, antidiabetic, antiinflammatory and analgesic activities, and
 CC can be used as a somatostatin receptor ligand. (I) are useful in the
 CC treatment of atherosclerosis, autoimmune diseases, cancers, diabetic-
 CC associated complications, endocrine disorders, inflammation,
 CC gastrointestinal disorders, pancreatitis, post-surgical pain, and
 CC restenosis. (I) can also be used in the diagnosis of cancer, by imaging
 CC the existence of metastases, it being labeled with a detectable probe.
 CC The present sequence represents a multiple parallel synthesis
 CC somatostatin analogue from the present invention
 XX

SQ Sequence 9 AA;

Query Match 42.1%; Score 32; DB 5; Length 9;
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 6 FLFKTVGF 13
 | : |||||
 Db 2 FFWKTVGF 9

RESULT 5
 ABP53384
 ID ABP53384 standard; peptide; 9 AA.
 AC ABP53384;
 DT 19-NOV-2002 (first entry)
 DE Multiple parallel synthesis somatostatin analogue #15.
 KW Backbone cyclised somatostatin analogue; somatostatin; SRIF; analgesic;
 KW somatropin release inhibiting factor; somatostatin receptor subtype;
 KW synthesis; antiarteriosclerotic; immunosuppressive; cytostatic; cancer;
 KW antidiabetic; antiinflammatory; immunosuppressive; cytostatic; cancer;
 KW atherosclerosis; autoimmune disease; somatostatin receptor ligand;
 KW endocrine disorder; inflammation; diabetic-associated complication;
 KW pancreatitis; post-surgical pain.
 XX
 OS Synthetic.

Key Location/Qualifiers
 Modified-site 1
 /label= bala
 /note= "beta-alanine"
 Modified-site 3
 /note= "cyclohexyl glycine"
 Misc-difference 4
 /note= "D form residue"
 Misc-difference 9
 /note= "D form residue"

US2002052315-A1.
 02-MAY-2002.
 13-DEC-2000; 2000US-00734583.
 19-JUN-1998; 98US-00100360.
 02-DEC-1998; 98US-00203389.

CC the autoimmune disease. This peptide is an internal peptide of reovirus
 CC type 3 sigma 2 protein and is implicated as a foreign epitope involved in
 CC the aetiology or in remissions of multiple sclerosis. It has been shown
 CC capable of inducing the proliferation of autoreactive T-cell clones
 CC isolated from multiple sclerosis patients. (Updated on 16-OCT-2003 to
 CC standardise OS field)
 XX
 SQ Sequence 15 AA;

Query Match 100.0%; Score 76; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.3e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARAAFLKTVGFGG 15
 |||||
 DB 1 MARAAFLKTVGFGG 15

RESULT 2
 AAY34138
 ID AAY34138 standard; peptide; 15 AA.

XX
 AC AAY34138;

XX
 DT 30-NOV-1999 (first entry)

XX
 DE Variant human potassium channel pore domain peptide sequence 5.

XX
 KW Potassium channel; ataxia; arrhythmia; epilepsy; Bartter's syndrome;
 KW cardiovascular disorder; CNS disorder; renal disorder.

XX
 OS Synthetic.

XX
 OS Homo sapiens.

XX
 PN WO9943696-A1.

XX
 PD 02-SEP-1999.

XX
 PF 22-FEB-1999; 99WO-US003826.

XX
 PR 25-FEB-1998; 98US-0076687P.

PR
 07-AUG-1998; 98US-0095836P.

PR
 19-JAN-1999; 99US-0116448P.

XX
 PA (AXYS-) AXYS PHARM INC.

XX
 PI Miller AP, Curran ME, Hu P, Rutter M, Wang J;

XX
 DR WPI; 1999-527591/44.

XX
 PT New nucleic acids encoding mammalian K+Hnov potassium channel proteins,
 PT useful for the diagnosis and treatment of episodic ataxia with myokymia,
 PT cardiac arrhythmia, epilepsy and Bartter's syndrome.

PS
 Example 1; Page 32; 112pp; English.

XX
 CC This sequence represents a variant human potassium channel pore domain
 CC peptide sequence used in the identification and isolation of human K+Hnov
 CC CDNAS (AA211897-211915). K+Hnov proteins have a high degree of homology
 CC to known potassium channels and may be alpha subunits, which form the
 CC functional channel, or accessory subunits that act to modulate the
 CC channel activity. K+Hnov cDNAs were isolated by extension of expressed
 CC sequence tags (ESTs) which were related but not identical to known human
 CC potassium channels. Potential polymorphisms detected as sequence variants
 CC between multiple independent clones. Potassium channels have critical
 CC roles in various cell types and biochemical pathways. Defective potassium
 CC channels are known to cause four human diseases: episodic ataxia with
 CC myokymia; cardiac arrhythmia (long QT syndrome); epilepsy; and Bartter's
 CC syndrome. As potassium channels are critical components of virtually all
 CC cells, it is likely that abnormal potassium channels are also implicated
 CC in certain renal, cardiovascular and central nervous system (CNS)
 CC disorders. Nucleotides encoding K+Hnov proteins may be used for
 CC identifying homologous or related proteins and the DNA sequences encoding

CC them. They may be used to produce compositions that modulate the
 CC expression and function of the K+Hnov protein and in studying the
 CC biochemical pathways associated with it. They may also be used for the
 CC recombinant production of K+Hnov protein in fermentation cultures.
 CC Additionally, such nucleotides may be used in gene therapy protocols for
 CC the treatment of diseases associated with abnormal potassium channels
 XX
 SQ Sequence 15 AA;

Query Match 46.7%; Score 35.5; DB 2; Length 15;
 Best Local Similarity 53.3%; Pred. No. 26;
 Matches 8; Conservative 1; Mismatches 1; Indels 5; Gaps 1;

QY 6 FLFK-----TVGFGG 15
 |||||
 DB 1 FLFSIEVQVTIGFGG 15

RESULT 3
 ABP53383

ID ABP53383 standard; peptide; 9 AA.

XX
 AC ABP53383;

XX
 DT 19-NOV-2002 (first entry)

XX
 DE Multiple parallel synthesis somatostatin analogue #14.

XX
 KW Backbone cyclised somatostatin analogue; somatostatin; SRIF; analgesic;
 KW somatostatin release inhibiting factor; somatostatin receptor subtype;
 KW synthesis; antiarteriosclerotic; immunosuppressive; cytostatic; cancer;
 KW antidiabetic; antiinflammatory; somatostatin receptor ligand;
 KW atherosclerosis; autoimmune disease; diabetic-associated complication;
 KW endocrine disorder; inflammation; gastointestinal disorder; restenosis;
 KW pancreatitis; post-surgical pain.

XX
 OS Synthetic.

XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /label= bala

FT /note= "beta-alanine"

FT Misc-difference 4 /note= "D form residue"

FT Misc-difference 9 /note= "D form residue"

XX
 US2002052315-A1.

XX
 PD 02-MAY-2002.

XX
 PF 13-DEC-2000; 2000US-00734583.

XX
 PR 19-JUN-1998; 98US-00100360.

PR
 02-DEC-1998; 98US-00203389.

PR
 15-JUN-1999; 99WO-IL000329.

XX
 (HORN/) HORNIK V.

PA (AFAR/) AFARGAN M M.

PA (GELL/) GELLERMAN G.

PI Hornik V, Afargan MM, Gellerman G;

XX
 WPI; 2002-681319/73.

XX
 PT New backbone cyclized somatostatin analogs are e.g. useful in the
 PT treatment of atherosclerosis, autoimmune diseases and cancers.

XX
 PS Disclosure; Page 12; 30pp; English.

XX
 CC The present invention describes backbone cyclised somatostatin analogues
 CC (I) that incorporates at least one building unit containing one nitrogen
 CC atom of the peptide backbone connected to a bridging group (comprising an

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OM protein - protein search, using sw model

Run on: February 22, 2005, 08:52:23 ; Search time 65.6667 Seconds
(without alignments)
88.346 Million cell updates/sec

Title: US-08-991-628-14

Perfect score: 76

Sequence: 1 MARAAFLFKTVGFGG 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 632537

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	76	100.0	15	2 AAW04854	Internal
2	35.5	46.7	15	2 AAY34138	Variant h
3	33	43.4	9	5 ABP53383	Multiple
4	32	42.1	9	5 ABP53382	Multiple
5	32	42.1	9	5 ABP53384	Multiple
6	31	40.8	15	2 AAW42262	Biotinyla
7	30	39.5	9	8 ADO44298	HIV SL9 e
8	30	39.5	15	5 ABR44302	Human L-a
9	30	39.5	15	5 ABP55159	Mouse myo
10	29	38.2	10	6 ABP57556	Different
11	29	38.2	11	6 ABP57592	Different
12	29	38.2	11	8 ADL90462	N-termina
13	29	38.2	15	8 ADL90463	N-termina
14	28	36.8	10	5 ABR98511	Murine p1
15	28	36.8	15	2 AAR49625	Camel Imm
16	27	35.5	7	3 AAB19614	Hepatocyt
17	27	35.5	8	2 AAW56715	Aspergill
18	27	35.5	9	6 ABJ41536	151P3D4 c
19	27	35.5	9	6 ABJ44158	151P3D4 c
20	27	35.5	9	6 ABJ44229	151P3D4 c
21	27	35.5	9	6 ABJ45425	151P3D4 c
22	27	35.5	9	6 ABJ49519	151P3D4 c
23	27	35.5	9	6 ABJ44588	151P3D4 c
24	27	35.5	9	6 ABJ45584	151P3D4 c
25	27	35.5	9	6 ABJ46858	151P3D4 c

26	27	35.5	9	6 ABJ39877	151P3D4 c
27	27	35.5	9	6 ABJ41104	151P3D4 c
28	27	35.5	9	6 ABJ42770	151P3D4 c
29	27	35.5	9	6 ABJ41943	151P3D4 c
30	27	35.5	9	6 ABJ43336	151P3D4 c
31	27	35.5	9	6 ABJ39882	151P3D4 c
32	27	35.5	9	6 ABJ39914	151P3D4 c
33	27	35.5	9	6 ABJ40765	151P3D4 c
34	27	35.5	9	6 ABJ43142	151P3D4 c
35	27	35.5	9	6 ABJ44908	151P3D4 c
36	27	35.5	9	6 ABJ46012	151P3D4 c
37	27	35.5	9	6 ABJ48740	151P3D4 c
38	27	35.5	9	6 ABJ44710	151P3D4 c
39	27	35.5	9	6 ABJ46636	151P3D4 c
40	27	35.5	9	6 ABJ48261	151P3D4 c
41	27	35.5	9	6 ABJ49726	151P3D4 c
42	27	35.5	9	6 ABJ45324	151P3D4 c
43	27	35.5	9	6 ABJ48040	151P3D4 c
44	27	35.5	9	6 ABJ41916	151P3D4 c
45	27	35.5	9	6 ABJ44665	151P3D4 c

ALIGNMENTS

RESULT 1

AAW04854

ID AAW04854 standard; peptide; 15 AA.

XX AC AAW04854;

XX AC

DT 16-OCT-2003 (revised)

DT 18-FEB-1997 (first entry)

XX

DE Internal fragment of reovirus type 3 sigma 2 protein.

XX Tolerisation; self-epitope; antigen; autoimmune disease; autoantigen;
KW HLA; human leukocyte antigen; T-cell; thymocyte; pemphigus vulgaris;
KW desmoglein; multiple sclerosis; herpes simplex virus; adenovirus;
KW phosphomannomutase; human papillomavirus; Epstein-Barr virus;
KW DNA polymerase; influenza; haemagglutinin; reovirus; sigma protein.

XX Reovirus sp.

XX WO9627387-Al.

XX PD 12-SEP-1996.

XX PF 07-MAR-1996; 96WO-US003182.

XX PR 07-MAR-1995; 95US-00400796.

XX PA (HARD) HARVARD COLLEGE.

XX PI Strominger JL, Wucherpfennig KW;

XX DR WPI; 1996-425218/42.

XX

PT Pemphigus vulgaris auto-antigens and multiple sclerosis non-self antigens
PT - useful in disease treatment, and method for identification of other
PT self and non-self antigens implicated in auto-immune disease.
XX Claim 2; Page 46; 58pp; English.

XX

CC Pharmaceutical preparations for tolerisation to antigens comprise either
CC an isolated human non-collagen or non-mysin basic protein (MBP)
CC polypeptide which is capable of tolerising an individual to an
CC autoantigen; or an isolated human pathogen polypeptide capable of
CC tolerising an individual to that polypeptide. In both cases, the
CC polypeptide (whether self or non-self) includes an amino acid sequence
CC corresponding to a sequence motif for a MHC class II protein, such as HLA
CC -DR, which is associated with a human autoimmune disease and which binds
CC to the polypeptide to activate autoreactive T-cells in individuals with

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DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Varanus gilleni (Pygmy mulga monitor).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
OX NCBI_TaxID=169840;
RN [1]
RP SEQUENCE FROM N.A.
RA Ast J.C.;
RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";
RL Cladistics 17:211-226(2001).
DR EMBL; AF407499; AAL10051.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1340 MW; CF6DEE80C733640D CRC64;

Query Match 28.9%; Score 22; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 7.4e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MARAAFLFKT 10
| | | | |
| | | | |
Db 1 MTLARWLFST 10

Search completed: February 22, 2005, 09:38:05
Job time : 54.6667 secs

DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DE 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Cuticle protein 30 (LM-ACP 30) (Fragment).
 OS Locusta migratoria (Migratory locust).
 OC Locusta migratoria; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
 OC Acridoidea; Acrididae; Oedipodinae; Locusta.
 NCBI_TaxID=7004;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86108304; PubMed=3943519;
 RA Hoesjtrup P., Andersen S.O., Roepstorff P.;
 RT "Isolation, characterization, and N-terminal sequence studies of
 RT cuticular proteins from the migratory locust, Locusta migratoria.";
 RL Eur. J. Biochem. 154:153-159(1986).
 CC -!- FUNCTION: Component of the cuticle of migratory locust which
 CC contains more than 100 different structural proteins.
 DR PIR; H24802; H24802.
 KW Cuticle; Direct protein sequencing; Structural protein.
 FT NON TER 10
 SQ SEQUENCE 10 AA; 969 MW; 497383658772877 CRC64;

Query Match 28.9%; Score 22; DB 1; Length 10;
 Best Local Similarity 50.0%; Pred. No. 6.8e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 11 VGFGG 15
 Db 5 LGYGG 9

RESULT 12
 Q85J75 PRELIMINARY; PRT; 10 AA.
 AC Q85J75;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN Name=COI;
 OS Varanus brevicauda (Short-tailed monitor).
 OS Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
 NCBI_TaxID=62038;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ast J.C.;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY264940; AAP22709.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON TER 10
 SQ SEQUENCE 10 AA; 1225 MW; 5DBE80C733640DD7 CRC64;

Query Match 28.9%; Score 22; DB 2; Length 10;
 Best Local Similarity 50.0%; Pred. No. 6.8e+03;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MARAAFLPKT 10
 Db 1 MTLARWLFT 10

RESULT 13
 Q9TG32 PRELIMINARY; PRT; 10 AA.
 AC Q9TG32;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN Name=COI;

OS Ophisaurus ventralis (Eastern glass lizard).
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Anguidae;
 OC Ophisaurus.
 NCBI_TaxID=102195;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99343613; PubMed=10413621; DOI=10.1006/mpev.1999.0615;
 RA Macey J.R., Schulte J.A. II, Larson A., Tuniyev B.S., Orlov N.,
 RA Papenfuss T.J.;
 RT "Molecular phylogenetics, tRNA evolution, and historical biogeography
 RT in anguillid lizards and related taxonomic families.";
 RL Mol. Phylogenet. Evol. 12:250-272(1999).
 DR EMBL; AF085626; AAD51568.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON TER 10
 SQ SEQUENCE 10 AA; 1225 MW; 5DBE80C733640DD7 CRC64;

Query Match 28.9%; Score 22; DB 2; Length 10;
 Best Local Similarity 50.0%; Pred. No. 6.8e+03;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MARAAFLPKT 10
 Db 1 MTLARWLFT 10

RESULT 14
 Q9TG47 PRELIMINARY; PRT; 10 AA.
 ID Q9TG47;
 AC Q9TG47;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN Name=COI;
 OS Ophisaurus koellikeri.
 OS Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Anguidae;
 OC Ophisaurus.
 NCBI_TaxID=102194;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99343613; PubMed=10413621; DOI=10.1006/mpev.1999.0615;
 RA Macey J.R., Schulte J.A. II, Larson A., Tuniyev B.S., Orlov N.,
 RA Papenfuss T.J.;
 RT "Molecular phylogenetics, tRNA evolution, and historical biogeography
 RT in anguillid lizards and related taxonomic families.";
 RL Mol. Phylogenet. Evol. 12:250-272(1999).
 DR EMBL; AF085621; AAD51553.1; -.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON TER 10
 SQ SEQUENCE 10 AA; 1225 MW; 5DBE80C733640DD7 CRC64;

Query Match 28.9%; Score 22; DB 2; Length 10;
 Best Local Similarity 50.0%; Pred. No. 6.8e+03;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MARAAFLPKT 10
 Db 1 MTLARWLFT 10

RESULT 15
 Q94VH7 PRELIMINARY; PRT; 11 AA.
 ID Q94VH7
 AC Q94VH7;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

```

ID Q7CPD2; PRELIMINARY; PRT; 15 AA.
AC Q7CPD2;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Spot 42 RNA, inhibition of DNA synthesis.
GN Name=spf; OrderedLocusNames=STM4000;
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2;
RX MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RA "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2."
RL Nature 413:852-856(2001).
DR EMBL; AE008887; AAL22839.1; -.
KW Complete proteome.
SQ SEQUENCE 15 AA; 1725 MW; 5A51DAF170EA661E CRC64;

Query Match 31.6%; Score 24; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 4.3e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 LFKTVGFG 14
Db 8 LHVIVGFG 15

RESULT 8
Q70F01 PRELIMINARY; PRT; 10 AA.
ID Q70F01;
AC Q70F01;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Calpastatin type 2 (Fragment).
GN Name=CAST;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21531263; PubMed=11673859; DOI=10.1006/abbi.2001.2546;
RA Parr T., Sensky P.L., Bardsley R.G., Buttery P.J.;
RA "Calpastatin expression in porcine cardiac and skeletal muscle and
RT partial gene structure."
RL Arch. Biochem. Biophys. 395:1-13(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC Parr T.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ583410; CAB47431.1; -.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1291 MW; CFF912436365BDD9 CRC64;

Query Match 30.3%; Score 23; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 4.5e+03;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MARAAFLFKT 10
Db 1 MAFASWVWYKT 10
```

```

RESULT 9
Q9TG68 PRELIMINARY; PRT; 10 AA.
ID Q9TG68;
AC Q9TG68;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN Name=COI;
OS Gerhronotus liocephalus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Anguillidae;
OC Gerhronotus.
OX NCBI_TaxID=76654;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99343613; PubMed=10413621; DOI=10.1006/mpsv.1999.0615;
RA Macey J.R., Schulte J.A. II, Larson A., Tunney B.S., Orlov N.,
RA Papenfuss T.J.;
RA "Molecular phylogenetics, tRNA evolution, and historical biogeography
RT in anguillid lizards and related taxonomic families."
RL Mol. Phylogenet. Evol. 12:250-272(1999).
DR EMBL; AF085614; AAD51532.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1213 MW; 85EB80C733640DC1 CRC64;

Query Match 30.3%; Score 23; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 4.5e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MARAAFLFKT 10
Db 1 MTTARWLFST 10

RESULT 10
Q7M4Z7 PRELIMINARY; PRT; 15 AA.
ID Q7M4Z7;
AC Q7M4Z7;
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Cytochrome c2 (Fragment).
OS Fusarium sporotrichioides.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
OX NCBI_TaxID=5514;
RN [1]
RP SEQUENCE.
RA Chow L.P., Fukaya N., Sugiyama Y., Ueno Y., Tabuchi K., Taigita A.;
RL Submitted (OCT-1994) to the PIR data bank.
DR PIR; PA0087; PA0087.
FT NON_TER 1 15
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1576 MW; 37EB5E40C4E886DD CRC64;

Query Match 30.3%; Score 23; DB 2; Length 15;
Best Local Similarity 62.5%; Pred. No. 6.6e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 RAAFLFKT 10
Db 7 KGANLFKT 14

RESULT 11
CU30_LOCOMI
ID CU30_LOCOMI STANDARD; PRT; 10 AA.
AC P11735;
DT 01-OCT-1989 (Rel. 12, Created)
```

```

FT NON TER 14 14
SQ SEQUENCE 14 AA; 1459 MW; 03FA0DCAA88B9A30 CRC64;

Query Match
Best Local Similarity 38.8%; Score 29.5; DB 2; Length 14;
Matches 9; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

Qy 1 MARAAFLKTVGFGG 15
Db 1 MARARSI-KTVGLVG 14

RESULT 3
ID Q9S8Q8 PRELIMINARY; PRT; 15 AA.
AC Q9S8Q8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DB Phospholipase D (BC 3.1.4.4) (Fragment)
OS Ricinus communis (Castor bean)
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Malpighiales; Euphorbiaceae; Acalyphoideae; Acalyphaeae;
OC Ricinus.
OX NCBI_TaxID=3988;
RN [1]
RP SEQUENCE.
RX MEDLINE=94029022; PubMed=8215453; DOI=10.1006/abbi.1993.1541;
RA Wang X., Dyer J.H., Zheng L.;
RT "Purification and immunological analysis of phospholipase D from
RT castor bean endosperm.";
RL Arch. Biochem. Biophys. 306:486-494(1993).
DR GO:0004630; P:phospholipase D activity; IEA.
SQ SEQUENCE 15 AA; 1620 MW; 7C3849DA9B2F50C CRC64;

Query Match
Best Local Similarity 36.8%; Score 28; DB 2; Length 15;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 9 KTVGFG 14
Db 8 ETVGFG 13

RESULT 4
ID P70007 PRELIMINARY; PRT; 14 AA.
AC P70007;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Histone H4-1 (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85160855; PubMed=4039007;
RA Gargiulo G., Razvi F., Ruberti I., Mohr I., Worcel A.;
RT "Chromatin-specific hypersensitive sites are assembled on a Xenopus
RT histone gene injected into Xenopus oocytes.";
RL J. Mol. Biol. 181:333-349(1985).
DR EMBL; M23777; AAA49737.1; -.
DR PIR; I51432; I51432.
FT NON TER 1
FT CHAIN <1 14 Potential.
SQ SEQUENCE 14 AA; 1524 MW; 65A76B0A927B34B4 CRC64;

Query Match
Best Local Similarity 31.6%; Score 24; DB 2; Length 14;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 9 KTVGFG 14
Db 8 ETVGFG 13

RESULT 5
ID Q8TCS7 PRELIMINARY; PRT; 15 AA.
AC Q8TCS7;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DB Complement component C7 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Liver;
RA Gonzalez S., Martinez Borra J., Lopez Larrea C.;
RT "Cloning and characterization of human complement component C7
RT promoter.";
RL Genes Immun. 0:0-0(2002).
DR EMBL; Y11720; CAA72407.1; -.
FT NON TER 15
SQ SEQUENCE 15 AA; 1666 MW; 10984ADCA7B43F19 CRC64;

Query Match
Best Local Similarity 31.6%; Score 24; DB 2; Length 15;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 LFKTVGFGG 15
Db 6 LFILVGFIG 14

RESULT 6
ID Q46963 PRELIMINARY; PRT; 15 AA.
AC Q46963;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Spot 42 RNA.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CF78;
RX MEDLINE=80074983; PubMed=390161;
RA Sahagan B.G., Dahlberg J.B.;
RT "A small, unstable RNA molecule of Escherichia coli: spot 42 RNA.";
RL J. Mol. Biol. 131:573-592(1979).
DR EMBL; X01895; CAA25985.1; -.
DR PIR; A26228; A26228.
SQ SEQUENCE 15 AA; 1725 MW; 5A51DAP170EA661E CRC64;

Query Match
Best Local Similarity 31.6%; Score 24; DB 2; Length 15;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 7 LFKTVGFGG 14
Db 8 LLHVGFIG 15

RESULT 7
ID Q7CPD2

```

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OM protein - protein search, using sw model

Run on: February 22, 2005, 08:53:13 ; Search time 52.6 Seconds
(without alignments)
146.030 Million cell updates/sec

Title: US-08-991-628-14
Perfect score: 76
Sequence: 1 MARAAFLFKTVGFG 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 6622

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	70	92.1	14	2 Q85718	Q85718 reovirus ty
2	29.5	38.8	14	2 Q85662	Q85662 reovirus ty
3	28	36.8	15	2 Q858Q8	Q858Q8 ricinus com
4	24	31.6	14	2 P70007	P70007 xenopus lae
5	24	31.6	15	2 Q8TCS7	Q8TCS7 homo sapien
6	24	31.6	15	2 Q46963	Q46963 escherichia
7	24	31.6	15	2 Q7CPD2	Q7CPD2 salmonella
8	23	30.3	10	2 Q70F01	Q70F01 sus scrofa
9	23	30.3	10	2 Q9TG68	Q9TG68 gerhonotus
10	23	30.3	15	2 Q7M4Z7	Q7M4Z7 fusarium sp
11	22	28.9	10	1 C030_L0CMI	P11735 locusta mlg
12	22	28.9	10	2 Q85J75	Q85J75 varanus bre
13	22	28.9	10	2 Q9TG32	Q9TG32 ophisaurus
14	22	28.9	10	2 Q9TG47	Q9TG47 ophisaurus
15	22	28.9	11	2 Q94VH7	Q94VH7 varanus gil
16	22	28.9	13	2 Q99783	Q99783 caprimulgus
17	22	28.9	15	2 Q85J19	Q85J19 phalarocor
18	22	28.9	15	2 Q6JCR8	Q6JCR8 hemisia arg
19	22	28.9	15	2 Q6QOR3	Q6QOR3 helicobacte
20	21	27.6	10	1 QP2_BOVIN	P1180 bos taurus
21	21	27.6	10	2 QP2LS6	QP2LS6 homo sapien
22	21	27.6	11	2 Q9GH12	Q9GH12 pandorina m
23	21	27.6	11	2 Q86864	Q86864 lymphocytic
24	21	27.6	12	2 Q6AV52	Q6AV52 oryza sativ
25	21	27.6	15	2 Q7M4Z8	Q7M4Z8 fusarium sp
26	20	26.3	10	2 Q8UJ15	Q8UJ15 nephurus w
27	20	26.3	11	2 Q86866	Q86866 lymphocytic
28	20	26.3	11	2 Q86868	Q86868 lymphocytic
29	20	26.3	12	2 Q841R5	Q841R5 agrobacteri
30	20	26.3	12	2 Q91YF5	Q91YF5 mus musculu
31	20	26.3	13	2 Q723E0	Q723E0 homo sapien

32 20 26.3 13 2 Q97122 toxoplasma
33 20 26.3 13 2 Q9U7D6 neospora ca
34 20 26.3 14 1 GLPK_STRGR P25013 streptomyce
35 20 26.3 15 2 Q94IU1 Q94IJ1 zea mays (m
36 20 26.3 15 2 Q7M030 Q7M030 rattus norv
37 20 26.3 15 2 Q8OX05 Q8OX05 mesocricetu
38 19 25.0 10 2 Q7M3T6 Q7M3T6 tripneustes
39 19 25.0 10 2 Q79924 Q79924 elgaria pan
40 19 25.0 10 2 Q8UJ34 Q8UJ34 nephurus l
41 19 25.0 10 2 Q6UJ77 Q6UJ77 carphodacty
42 19 25.0 10 2 Q6UJK6 Q6UJK6 rhynchoedr
43 19 25.0 10 2 Q6UJPS Q6UJPS diploclactyl
44 19 25.0 10 2 Q9TFV5 Q9TFV5 eublepharus
45 19 25.0 10 2 Q9TG50 Q9TG50 elgaria mul

ALIGNMENTS

RESULT 1

Q85718 ID Q85718 PRELIMINARY; PRT; 14 AA.
AC Q85718;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Reovirus serotype 1 S2 (Fragment).
OS Reovirus type 1 (strain Lang) (Til) (Mammalian orthoreovirus 1).
OC Viruses; dsRNA viruses; Reoviridae; Orthoreovirus;
OC Mammalian orthoreoviruses.
OX NCBI_TaxID=10884;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83017877; PubMed=7123853;
RA Gaillard R.K., Li J.K., Keene J.D., Joklik W.K.;
RT "The sequences at the termini of four genes of the three reovirus serotypes.";
RL Virology 121:320-326(1982).
DR EMBL; J02303; AAA47241.1; -.
DR InterPro; IPR004317; Sigma_1_2.
DR Pfam; PF03084; Sigma_1_2; 1.
FT NON_TER 14
SQ SEQUENCE 14 AA; 1516 MW; 52P79D201BF900C7 CRC64;

Query Match Similarity 92.1%; Score 70; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARAAFLFKTVGFG 14
Db 1 MARAAFLFKTVGFG 14

RESULT 2

Q85662 ID Q85662 PRELIMINARY; PRT; 14 AA.
AC Q85662;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Reovirus serotype 2 S2 (Fragment).
OS Reovirus type 2 (strain D5/Jones) (T2J) (Mammalian orthoreovirus 2).
OC Viruses; dsRNA viruses; Reoviridae; Orthoreovirus;
OC Mammalian orthoreoviruses.
OX NCBI_TaxID=10885;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83017877; PubMed=7123853;
RA Gaillard R.K., Li J.K., Keene J.D., Joklik W.K.;
RT "The sequences at the termini of four genes of the three reovirus serotypes.";
RL Virology 121:320-326(1982).
DR EMBL; J02311; AAA47250.1; -.

Db 9 VGAGG 13

RESULT 14

PH0751
T-cell receptor beta chain (P12) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
C;Accession: PH0751
R;Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A;Title: T cell receptor genes in a series of class I major histocompatibility complex-2 allelic exclusion and antigen-specific repertoire.
A;Reference number: PH0746; MUID:92078846; PMID:1836010
A;Accession: PH0751
A;Molecule type: mRNA
A;Residues: 1-15 <CAS>
A;Cross-references: ENBL:X60843; NID:G50931; PIDN:CAA43235.1; PID:G50932
A;Experimental source: T lymphocyte
C;Keywords: T-cell receptor

Query Match 26.3%; Score 20; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 10 TVGFGG 15

Db 3 SIGTGG 8

RESULT 15

C34874
transforming protein (N-rasB) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 09-Jul-2004
C;Accession: C34874
R;McMahon, G.; Davis, E.F.; Huber, L.J.; Kim, Y.; Mogan, G.N.
Proc. Natl. Acad. Sci. U.S.A. 87, 1104-1108, 1990
A;Title: Characterization of c-Ki-ras and N-ras oncogenes in aflatoxin B-1-induced rat
A;Reference number: A34874; MUID:90138946; PMID:2105496
A;Accession: C34874
A;Status: Preliminary
A;Molecule type: protein
A;Residues: 1-15 <MCM>
A;Cross-references: UNIPROT:Q7M030

Query Match 26.3%; Score 20; DB 2; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.2e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 VGFGG 15

Db 2 VGAGG 6

Search completed: February 22, 2005, 09:46:30
Job time : 12.1333 secs

Best Local Similarity 75.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 GFGG 15
|:|
Db 2 GYGG 5

RESULT 9
PA0064
cytochrome C 1 - fungus (Fusarium sporotrichioides) (fragment)
C:Species: Fusarium sporotrichioides
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: PA0064
R:Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JRPID, October 1994
A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichi
A:Reference number: PA0051
A:Accession: PA0064
A:Molecule type: protein
A:Residues: 1-15 <CHO>
A:Cross-references: UNIPROT:Q7M4Z8
C:Keywords: electron transfer; oxidative phosphorylation

Query Match 27.6%; Score 21; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 2.1e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 AFLPKT 10
|:|
Db 9 ANLFKT 14

RESULT 10
S57574
T cell receptor V-J junctional alpha chain region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 19-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 05-Nov-1999
C:Accession: S57574
R:Burrows, S.R.; Sillins, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Arguet, V.P.
submitted to the EMBL Data Library, June 1995
A:Description: T cell receptor repertoire for a viral epitope in humans is diversified b
A:Reference number: S57494
A:Accession: S57574
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-14 <EUR>
A:Cross-references: EMBL:Z49959; NID:g887504; PIDN:CAA90230.1; PID:g887505
C:Keywords: T-cell receptor

Query Match 27.0%; Score 20.5; DB 2; Length 14;
Best Local Similarity 71.4%; Pred. No. 2.4e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 8 PKTVGFG 14
|:|
Db 9 FKTI-FG 14

RESULT 11
S26549
T-cell receptor beta chain (clone Cw3/A8, Cw3/Cas1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 13-Jan-1995 #sequence_revision 17-Apr-1998 #text_change 17-Mar-1999
C:Accession: S26549; S26550
R:Caanaya, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid
J. Exp. Med. 176, 439-447, 1992
A>Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor
A:Reference number: S26512; MUID:92364546; PMID:1380061
A:Accession: S26549
A:Molecule type: mRNA
A:Residues: 1-12 <CAS>
A:Cross-references: EMBL:X67999

A:Experimental source: cytolytic T-lymphocyte, clone Cw3/A8
A:Accession: S26550
A:Molecule type: mRNA
A:Residues: 1-12 <CA2>
A:Cross-references: EMBL:X68000
A:Experimental source: cytolytic T-lymphocyte, clone Cw3/Cas1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: T-cell receptor

Query Match 26.3%; Score 20; DB 2; Length 12;
Best Local Similarity 45.5%; Pred. No. 2.6e+03;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 AAFLEKTVGFG 14
|:|:|:|
Db 2 ASSLETLVFG 12

RESULT 12
PQ0058
glycerol kinase (EC 2.7.1.30) - Streptomyces griseus (fragment)
C:Species: Streptomyces griseus
C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C:Accession: PQ0058
R:Boilotin, A.; Biro, S.
Gene 87, 151-152, 1990
A>Title: Nucleotide sequence of the putative regulatory gene and major promoter region o
A:Reference number: PQ0490; MUID:90236293; PMID:2110096
A:Accession: PQ0058
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-14 <BOL>
A:Cross-references: UNIPROT:P25013; GB:M37327; NID:g153287; PIDN:AAA26751.1; PID:g153289
C:Genetics:
A:Gene: g1YA
A:Start codon: GTG
C:Keywords: phosphotransferase

Query Match 26.3%; Score 20; DB 2; Length 14;
Best Local Similarity 42.9%; Pred. No. 3e+03;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 FLFKTVG 12
|:|:|
Db 7 FIEGTIG 13

RESULT 13
I52734
gene c-Ki-ras protein - hamster (fragment)
C:Species: Cricetinae gen. sp. (hamster)
C>Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 28-May-1999
C:Accession: I52734
R:Takahashi, T.; Moyer, M.P.; Cano, M.; Wang, Q.J.; Mountjoy, C.P.; Sanger, W.; Adrian,
Carcinogenesis 16, 931-939, 1995
A>Title: Differences in molecular biological, biological and growth characteristics betw
A:Reference number: I52734; MUID:95246257; PMID:7728976
A:Accession: I52734
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-15 <RES>
A:Cross-references: GB:S77068; NID:g914176
C:Genetics:
A:Gene: c-Ki-ras
C:Superfamily: ras transforming protein; translation elongation factor Tu homology
C:Keywords: GTP binding

Query Match 26.3%; Score 20; DB 2; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.2e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 VGFGG 15
|:|:|

spot 42 protein - Escherichia coli
C;Species: Escherichia coli
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C;Accession: A26228; A37586; Q00551
R;Joyce, C.M.; Grindley, N.D.F.
J. Bacteriol. 152, 1211-1219, 1982
A;Title: Identification of two genes immediately downstream from the *polA* gene of Escherichia coli.
A;Reference number: A26228; MUID:83056713; PMID:6183253
A;Accession: A26228
A;Molecule type: DNA
A;Residues: 1-15 <JOY2>
A;Cross-references: UNIPROT:Q46963
R;Sahagan, B.G.; Dahlberg, J.E.
J. Mol. Biol. 131, 573-592, 1979
A;Title: A small, unstable RNA molecule of Escherichia coli: spot 42 RNA.
A;Reference number: A37586; MUID:80074983; PMID:390161
A;Accession: A37586
A;Molecule type: DNA
A;Residues: 1-15 <SAH>
A;Cross-references: GB:X01895; NID:g40868; PIDN:CAA25985.1; PID:g40869
C;Genetics:
A;Gene: *spf*
A;Map position: 87 min

Query Match 31.6%; Score 24; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 6e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 LFKTVGFG 14
| : |||
DB 8 LLHVIGFG 15

RESULT 4

PA0087
Cytochrome c2 - fungus (Fusarium sporotrichioides) (fragment)

C;Species: Fusarium sporotrichioides
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: PA0087
R;Chow, L.P.; Fukaya, N.; Sugiyama, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JPIB, October 1994
A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichioides.
A;Reference number: PA0051
A;Accession: PA0087
A;Molecule type: protein
A;Residues: 1-15 <CHO>
A;Cross-references: UNIPROT:Q7M4Z7
C;Keywords: electron transfer; heme; photosynthesis

Query Match 30.3%; Score 23; DB 2; Length 15;
Best Local Similarity 62.5%; Pred. No. 9.1e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 RAAPLTKT 10
: |||||
DB 7 KGANLTKT 14

RESULT 5

A58375
microcin B17 - Escherichia coli (fragment)

C;Species: Escherichia coli plasmid pPV113
C;Date: 19-Mar-1997 #sequence_revision 19-Dec-1997 #text_change 09-Jul-2004
C;Accession: A58375
R;Yorgey, P.; Lee, J.; Koedel, J.; Vivas, E.; Warner, P.; Jebaratnam, D.; Kolter, R.
Proc. Natl. Acad. Sci. U.S.A. 91, 4519-4523, 1994
A;Title: Posttranslational modifications in microcin B17 define an additional class of microcin.
A;Reference number: A58375; MUID:94240167; PMID:8183941
A;Accession: A58375
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-12 <YOR>
A;Cross-references: UNIPROT:P05834

Query Match 28.9%; Score 22; DB 2; Length 12;
Best Local Similarity 80.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 VGFGG 15
| : |||
DB 1 VGIGG 5

RESULT 6

PT0664
T-cell receptor beta chain V-D-J region (121-2L) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0664
R;Peeney, A.J.
J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0664
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-10 <FEE>
A;Experimental source: day 4 postnatal thymus, strain BALB/c

C;Keywords: T-cell receptor

Query Match 27.6%; Score 21; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 TVGFGG 15
| : |||
DB 5 TPGLGG 10

RESULT 7

E33098
214K exoantigen (version 2) - malaria parasite (Plasmodium falciparum) (fragments)
C;Species: Plasmodium falciparum
C;Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000
C;Accession: E33098
R;Nichols, J.H.; Hager, L.P.
submitted to the Protein Sequence Database, May 1990

A;Reference number: A33098

A;Accession: E33098
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-14 <NIC>

Query Match 27.6%; Score 21; DB 2; Length 14;
Best Local Similarity 75.0%; Pred. No. 2e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 GFGG 15
| : |||
DB 1 GYGG 4

RESULT 8

PC4269
unidentified QR310003 protein - rice (fragment)

C;Species: Oryza sativa (rice)
C;Date: 28-May-1997 #sequence_revision 18-Jul-1997 #text_change 18-Jul-1997
C;Accession: PC4269
R;Kawakami, T.; Kamo, M.; Chen, M.C.; Tsugita, A.
submitted to JPIB, April 1997
A;Reference number: PC4267
A;Accession: PC4269
A;Molecule type: protein
A;Residues: 1-15 <KAW>

Query Match 27.6%; Score 21; DB 2; Length 15;

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: February 22, 2005, 09:08:09 ; Search time 11.1333 Seconds
(without alignments)
129.633 Million cell updates/sec

Title: US-08-991-628-14
Perfect score: 76
Sequence: 1 MARAAFLPKTVGFGG 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 2523

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	38.2	14	2 A17150	glucose 1-dehydrog
2	24	31.6	15	2 I51432	histone H4-1 precu
3	24	31.6	15	2 A26228	spot 42 protein -
4	23	30.3	15	2 PA0087	cytochrome c2 - fu
5	22	28.9	12	2 A58375	microcin B17 - Bsc
6	21	27.6	10	2 PT0664	T-cell receptor be
7	21	27.6	14	2 E33098	214K exoantigen (v
8	21	27.6	15	2 PC4269	unidentified Q310
9	21	27.6	15	2 PA0064	cytochrome C 1 - f
10	20.5	27.0	14	2 S57574	T cell receptor V-
11	20	26.3	12	2 S26549	T-cell receptor be
12	20	26.3	14	2 PQ0058	glycerol kinase (E
13	20	26.3	15	2 I52734	gene c-Ki-ras prot
14	20	26.3	15	2 PH0751	T-cell receptor be
15	20	26.3	15	2 C34874	transforming prote
16	19	25.0	10	2 C60527	sperm-activating p
17	19	25.0	11	2 PT0301	ig heavy chain CRD
18	19	25.0	11	2 C58501	42K bile stone pro
19	19	25.0	11	2 D42965	talin - chicken (f
20	19	25.0	12	2 PH1463	T-cell receptor be
21	19	25.0	13	2 B42762	proteasome endopep
22	19	25.0	14	2 B61597	cytochrome P450 AL
23	19	25.0	15	2 S03353	plastocyanin - Mic
24	18	23.7	4	2 A53284	T-cell receptor be
25	18	23.7	7	2 H33098	180K exoantigen
26	18	23.7	7	2 PT0663	T-cell receptor be
27	18	23.7	8	2 PT0725	T-cell receptor be
28	18	23.7	8	2 PC4373	telomeric and tetr
29	18	23.7	8	2 B24749	neuropeptide B - b

30	18	23.7	9	2 D24180	fibrinogen beta ch
31	18	23.7	9	2 F28854	fibrinopeptide B -
32	18	23.7	9	2 PT0225	Ig heavy chain CDR
33	18	23.7	9	2 S10784	enamelin i - bovin
34	18	23.7	9	2 PC7074	translation elonga
35	18	23.7	10	1 ECLQ4M	tachykinin IV - mi
36	18	23.7	10	2 PT0632	T-cell receptor be
37	18	23.7	10	2 S06964	hypothetical prote
38	18	23.7	10	2 I40032	trpE protein - Bac
39	18	23.7	10	2 F60527	sperm-activating p
40	18	23.7	10	2 B60589	sperm-activating p
41	18	23.7	11	2 A44755	20alpha-hydroxyste
42	18	23.7	11	2 A38590	transforming prote
43	18	23.7	12	1 LFECPE	pyrE leader peptid
44	18	23.7	12	2 A49261	coagulation factor
45	18	23.7	13	2 S48210	collagen alpha 1(V

ALIGNMENTS

RESULT 1

AL17150
Glucose 1-dehydrogenase (NAD) (EC 1.1.1.118) - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C>Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 03-Jun-2002
C:Accession: AL17150
R:Franzen, B.; Carubba, C.; Feingold, D.S.; Ashcom, J.; Fransen, J.S.
Biochem. J. 199, 599-602, 1981

A>Title: Amino acid sequence of the tryptic peptide containing the catalytic-site thiol
A:Reference number: AL17150; MUID:82182061; PMID:6896145
A:Accession: AL17150
A:Molecule type: protein
A:Residues: 1-14 <FRA>
C:Keywords: NAD; oxidoreductase

Query Match 38.2%; Score 29; DB 2; Length 14;
Best Local Similarity 83.3%; Pred. No. 68;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 10 TVGFGG 15
:|||||
DB 2 SVGFGG 7

RESULT 2

I51432
histone H4-1 precursor - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: I51432
R:Gargiulo, G.; Razvi, F.; Ruberti, I.; Mohr, I.; Worcel, A.
J. Mol. Biol. 181, 333-349, 1985
A>Title: Chromatin-specific hypersensitive sites are assembled on a Xenopus histone gene
A:Reference number: I51431; MUID:85160855; PMID:4039007
A:Accession: I51432
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-14 <GAR>
A:Cross-references: UNIPROT:P70007; GB:M23777; NID:g214219; PIDN:AAA49737.1; PID:g214222

Query Match 31.6%; Score 24; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 GFGG 15
:|||||
DB 11 GFGG 14

RESULT 3

A26228

DR WPI; 2003-903164/82.
 XX New recombinant bacterial enzymes involved in nucleotide transport and
 PT metabolism, useful for designing potential antibacterial agents.
 XX
 XX Disclosure; Fig 49; 392pp; English.
 XX
 CC This invention relates to novel isolated, recombinant polypeptides that
 CC are involved in nucleotide transport and metabolism. Specifically, it
 CC refers to the identification and functional characterisation of enzymes
 CC that are antimicrobial targets from pathogenic bacteria, namely
 CC *Staphylococcus aureus*, *Pseudomonas aeruginosa*, *Escherichia coli*,
 CC *Enterococcus faecalis*, *Haemophilus influenzae* and *Streptococcus*
 CC *pneumoniae*. These enzymes are deoxyuridine 5' triphosphate
 CC nucleotidohydrolase (dut), guanylate kinase (KGUA), adenine
 CC phosphoribosyltransferase (APR), phosphoribosylpyrophosphate synthetase
 CC (PRSA), thymidylate synthase (thyA), uridylylate kinase (PYRH), ribose
 CC phosphate pyrophosphokinase and cytidine/ deoxycytidylylate deaminase family
 CC protein (YHFC). The present invention describes modulators, inhibitors,
 CC agonists and antagonists against the proteins, which can be used for the
 CC diagnosis and treatment of various diseases and conditions specific to
 CC each bacterial species. Accordingly, the compositions of this invention
 CC can be used in the development of drugs to treat, for example, impetigo,
 CC cystitis, meningitis, osteomyelitis, otitis media and bacteraemia.
 CC Furthermore, determination of the crystalline structure can be useful for
 CC the design of modulators as potential therapeutic agents. This peptide
 CC sequence is an *Enterococcus faecalis* thyA peptide derived from a tryptic
 CC mass spectrum of the invention.
 XX
 XX Sequence 14 AA;
 SQ

Query Match 37.9%; Score 33; DB 7; Length 14;
 Best Local Similarity 55.6%; Pred. No. 1.4e+02;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 4 LVWFIKKNT 12
 |:|:|:|:
 Db 3 LLWFLKGD 11

RESULT 15
 AAR99504
 ID AAR99504 standard; peptide; 10 AA.
 XX
 XX AAR99504;
 AC
 XX
 DT 09-JAN-1997 (first entry)
 XX
 DE B-cell epitope used in construction of chimeric immunoglobulin.
 XX
 KW Chimera; chimeric; immunoglobulin; Ig; B-cell; T-cell; lymphocyte;
 KW epitope; immune response; vaccine; pathogen; antibody; influenza;
 KW measles; hepatitis; foot and mouth disease; tetanus toxoid;
 KW human immunodeficiency virus; HIV; heat shock protein; M protein;
 KW hen egg white lysozyme; nuclease.
 XX
 OS Influenza virus.
 XX
 XX WO9619584-A1.
 PN
 XX 27-JUN-1996.
 FD
 XX 21-DEC-1995; 95WO-US016718.
 XX
 XX 22-DEC-1994; 94US-00363276.
 PR
 XX (MOUN) MOUNT SINAI SCHOOL MEDICINE.
 PA
 XX Bona C, Zaghouani H;
 FI
 XX WPI; 1996-309598/31.
 DR
 XX Chimeric immunoglobulin with CDR loop substd. for T and or B cell epitope
 PT

PT - useful in vaccine composition to enhance immune response to pathogens.
 XX Disclosure; Page 17; 131pp; English.
 XX
 CC Chimeric immunoglobulins (Ig) having a CDR loop of the parent Ig replaced
 CC with a foreign peptide sequence corresponding to a T- or B- cell epitope,
 CC may be used in vaccine compositions to enhance an immune response to a
 CC pathogen. Chimeric Ig comprising a B-cell epitope can also be used to
 CC label B-cells, to test the ability of a subject to mount a humoral
 CC response to a particular B-cell epitope or to collect B-cells which
 CC recognise the epitope. An antibody comprising a chimeric Ig molecule
 CC which comprises an antigen binding site may be used in diagnostic assays
 CC to detect the presence of a particular target antigen, which binds to the
 CC antibody binding site. Sequences of B-cell epitopes are given in AAR99503
 CC -08. Sequences of T-cell epitopes are given in AAR9509-17. The term B-
 CC cell epitope refers to a peptide which is able to bind to an
 CC immunoglobulin receptor of a B-cell and participate in the induction of
 CC antibody production by that B-cell. This peptide is an immunodominant B-
 CC cell epitope in site B of influenza virus HAI haemagglutinin
 XX
 XX Sequence 10 AA;
 SQ

Query Match 36.8%; Score 32; DB 2; Length 10;
 Best Local Similarity 50.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 6 WFIKKNTYYP 15
 |:|:|:|:
 Db 1 WLTKKGDSYP 10

Search completed: February 22, 2005, 09:24:54
 Job time : 67.6667 secs

PT New composition of peptides and nucleic acids capable of binding Major
 PT Histocompatibility Complex molecules, useful for diagnosing, preventing
 PT or treating viral infections or cancer, such as prostate cancer,
 PT hepatitis B or AIDS.

XX Claim 1; SEQ ID NO 2222; 186pp; English.

XX The invention relates to a novel composition comprising one or more
 CC peptides or nucleic acids encoding an HLA binding peptide. The
 CC composition further comprises an HLA epitope. It also comprises a spacer
 CC molecule, a carrier, an MHC targeting sequence or a lipid. The peptides
 CC are incorporated as part of a liposome. The peptide is from an antigen
 CC selected from prostate specific antigen (PSA), prostate specific membrane
 CC antigen (PSM), hepatitis B virus (HBV) antigen, hepatitis C virus (HCV)
 CC antigen, malignant melanoma antigen (MAGE), Epstein Barr virus, human
 CC immunodeficiency type-1 (HIV-1), human immunodeficiency type-2 (HIV-2),
 CC Papilloma virus, Laesa virus, Mycobacterium tuberculosis (MT), p53,
 CC murine p53 (mp53), CEA, HER2/neu, and tyrosine kinase related protein
 CC (TKP). The composition is useful for preventing or treating viral
 CC infections or cancer, such as prostate cancer, hepatitis B, hepatitis C,
 CC AIDS, renal carcinoma, cervical carcinoma, lymphoma, CMV or chondyoma
 CC acuminatum. The composition is also be used for diagnosing such diseases.
 CC This sequence represents a peptide of the invention.

XX Sequence 9 AA;

Query Match 39.1%; Score 34; DB 8; Length 9;
 Best Local Similarity 83.3%; Pred. No. 1.8e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YRNLLW 6
 Db 3 YRNLLW 8
 |||||

RESULT 13

AD R99836
 ID ADR99836 standard; peptide; 13 AA.

XX ADR99836;

XX 02-DEC-2004 (first entry)

XX Human aggrecan peptide P4R as intermediate for citrullination method.

XX immunosuppressive; antiarthritic; antirheumatic; neuroprotective;
 KW antiinflammatory; gene therapy; peptidyl arginine deaminase inhibitor;
 KW citrullinated peptide; major histocompatibility class II molecule;
 KW epitope; myelin basic protein; MBP; glial fibrillary acid protein; GFAP;
 KW diagnosis; autoimmune disorder; rheumatoid arthritis; multiple sclerosis.

XX Homo sapiens.

XX WO2004078098-A2.

XX 16-SEP-2004.

XX 05-MAR-2004; 2004WO-CA000337.

XX 07-MAR-2003; 2003US-0455252P.

XX (LONH-) LONDON HEALTH SCI CENT RES INC.

XX Hill J, Cairns E, Bell D;

XX WPI; 2004-668479/65.

XX New citrullinated myelin basic protein or glial fibrillary acid protein
 PT peptide, for use in preparing a composition for diagnosing or treating
 PT rheumatoid arthritis or multiple sclerosis.

XX Example 2; Page 55; 93pp; English.

CC The invention relates to a citrullinated peptide, binding with increased
 CC affinity to a major histocompatibility (MHC) class II molecule having a
 CC shared epitope comprising an amino acid sequence selected from ADR99775-
 CC ADR99811, given in the specification. The citrullinated myelin basic
 CC protein (MBP) and/or glial fibrillary acid protein (GFAP) peptide is
 CC useful in preparing a composition for diagnosing or treating autoimmune
 CC disorder, e.g., rheumatoid arthritis or multiple sclerosis. This sequence
 CC represents a fragment of the human aggrecan protein (aa 280-292) in which
 CC the Asp residue at position 6 is altered to an Arg residue and used to
 CC generate a citrullinated peptide of the invention.

XX Sequence 13 AA;

Query Match 39.1%; Score 34; DB 8; Length 13;
 Best Local Similarity 40.0%; Pred. No. 85;
 Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 WFIKKNTKYP 15

Db 3 WLRRSVRYP 12

RESULT 14

ADJ62411
 ID ADJ62411 standard; peptide; 14 AA.

XX ADJ62411;

XX 06-MAY-2004 (first entry)

XX Tryptic mass spectrum E_faecalis thyA peptide 11.

XX pathogenic bacteria; deoxyuridine 5' triphosphate nucleotidohydrolase;
 KW dut; guanylate kinase; KGUA; adenine phosphoribosyltransferase; APT;
 KW phosphoribosylpyrophosphate synthetase; PRSA; thymidylate synthase; thyA;
 KW KTHV; uridylylate kinase; PYRH; ribose phosphate pyrophosphokinase;
 KW cytidine/deoxycytidylate deaminase; YHFC; impetigo; cystitis; meningitis;
 KW osteomyelitis; otitis media; bacteraemia; nucleotide transport;
 KW antimicrobial.

XX Enterococcus faecalis.

XX WO2003087354-A2.

XX 23-OCT-2003.

XX 08-APR-2003; 2003WO-CA000485.

XX 09-APR-2002; 2002US-0371067P.

XX 05-JUN-2002; 2002US-0386548P.

XX 06-JUN-2002; 2002US-0386826P.

XX 06-JUN-2002; 2002US-0386869P.

XX 06-NOV-2002; 2002US-0424380P.

XX 08-NOV-2002; 2002US-0425086P.

XX 24-DEC-2002; 2002US-0436243P.

XX 26-DEC-2002; 2002US-0436288P.

XX 26-DEC-2002; 2002US-0436566P.

XX 27-DEC-2002; 2002US-0436708P.

XX 30-DEC-2002; 2002US-0436947P.

XX 30-DEC-2002; 2002US-0436971P.

XX 30-DEC-2002; 2002US-0437038P.

XX 31-DEC-2002; 2002US-0437141P.

XX 31-DEC-2002; 2002US-0437620P.

XX (AFPI-) AFFINIUM PHARM INC.
 XX Edwards A, Dharamsi A, Vedadi M, Domagala M, Mansoury K;
 PI Houston S, Awrey D, Beattie B, Kanagarajah D, Vallee F, Virag C;
 PI Buzadzija K, McDonald M, Tai M, Pinder B, Alam MZ, Ouyang H;
 PI Richards D, Canadien V, Thalakada R, Nethery K;
 XX

PA (KERN/) KERN F.
 XX Kern F, Volk H, Reinke P, Faulhaber N, Surel I, Khatamzas E;
 PI WPI; 2001-557718/62.
 XX
 XX Stimulating CD8 or CD4 T cells for the immuno-stimulation of mammals and
 PT the determination of the response to the antigen comprises using a
 PT synthetic peptide library of the specific antigen.
 XX
 XX Example; Fig 1; 85pp; German.
 XX
 XX This sequence represents a novel method for stimulating CD8 or CD4 T
 CC cells for the immuno-stimulation of mammals and the determination of the
 CC response to an antigen (I). The method comprises (i) dividing the amino
 CC acid sequence of the antigen into protein fragments (II) of at least 9
 CC amino acids, whereby adjacent or neighbouring fragments are in the whole
 CC antigen sequence; (ii) synthesizing a peptide library containing (II);
 CC and (iii) incubating the CD8 and/or CD4 T lymphocytes in a suspension
 CC comprising (II) in a single culture vessel. The method is used to immuno-
 CC stimulate T cells of mammals, particularly humans, and is also useful for
 CC diagnostic purposes to determine if a mammal, especially human, has
 CC previously immunologically responded to a specific protein, and to
 CC determine strength of that response. The method is suitable for in vivo
 CC or in vitro immuno-stimulation of mammalian, more preferably human T
 CC lymphocytes, where the stimulated T lymphocytes are expanded and can be
 CC transfused into a patient. AAB86544-AAB86803 represent fragments of the
 CC human cytomegalovirus IE1 and pp65 lower matrix phosphoprotein which are
 CC used to illustrate the method of the invention
 XX
 XX Sequence 15 AA;
 SQ
 Query Match 39.7%; Score 34.5; DB 4; Length 15;
 Best Local Similarity 46.7%; Pred. No. 81;
 Matches 7; Conservative 4; Mismatches 3; Indels 1; Gaps 1;
 QY 1 YRNLVWFIKKNTRYP 15
 DB 1 YRNIEFF-TKNSAPP 14
 |||: :|||: :||
 RESULT 11
 ADN65655
 ID ADN65655 standard; peptide; 9 AA.
 XX
 XX AC ADN65655;
 XX
 XX DT 01-JUL-2004 (first entry)
 XX
 XX DE HLA binding peptide #2255.
 XX
 XX KW cytostatic; hepatotropic; virucide; antiinflammatory; anti-HIV;
 KW gene therapy; vaccine; HLA binding peptide; HTL epitope; liposome;
 KW prostate specific antigen; prostate specific membrane antigen;
 KW hepatitis B virus antigen; hepatitis C virus antigen;
 KW malignant melanoma antigen; MAGE; Epstein Barr virus; cancer;
 KW prostate cancer; AIDS; renal carcinoma; cervical carcinoma; lymphoma;
 KW chondyloma acuminatum.
 XX
 XX OS Unidentified.
 XX
 XX PN WO2004031211-A2.
 XX
 XX PD 15-APR-2004.
 XX
 XX PF 03-OCT-2003; 2003WO-US031308.
 XX
 XX PR 03-OCT-2002; 2002US-0416207P.
 XX
 XX PR 08-OCT-2002; 2002US-0417269P.
 XX
 XX PA (EPIM-) EPIMMUNE INC.
 XX
 XX PI Sidney J, Southwood S, Sette A;
 XX
 XX DR WPI; 2004-347953/32.
 XX

XX WPI; 2004-347953/32.
 XX
 XX New composition of peptides and nucleic acids capable of binding Major
 PT Histocompatibility Complex molecules, useful for diagnosing, preventing
 PT or treating viral infections or cancer, such as prostate cancer,
 PT hepatitis B or AIDS.
 XX
 XX Claim 1; SEQ ID NO 2255; 186pp; English.
 PS
 XX
 CC The invention relates to a novel composition comprising one or more
 CC peptides or nucleic acids encoding an HLA binding peptide. The
 CC composition further comprises an HLA epitope. It also comprises a spacer
 CC molecule, a carrier, an MHC targeting sequence or a lipid. The peptides
 CC are incorporated as part of a liposome. The peptide is from an antigen
 CC selected from prostate specific antigen (PSA), prostate specific membrane
 CC antigen (PSM), hepatitis B virus (HBV) antigen, hepatitis C virus (HCV)
 CC antigen, malignant melanoma antigen (MAGE), Epstein Barr virus, human
 CC immunodeficiency type-1 (HIV-1), human immunodeficiency type-2 (HIV-2),
 CC Papilloma virus, Lassa virus, Mycobacterium tuberculosis (MT), p53,
 CC murine p53 (mp53), CEA, HER2/neu, and tyrosine kinase related protein
 CC (TRK). The composition is useful for preventing or treating viral
 CC infections or cancer, such as prostate cancer, hepatitis B, hepatitis C,
 CC AIDS, renal carcinoma, cervical carcinoma, lymphoma, CMV or chondyloma
 CC acuminatum. The composition is also be used for diagnosing such diseases.
 CC This sequence represents a peptide of the invention.
 XX
 XX Sequence 9 AA;
 SQ
 Query Match 39.1%; Score 34; DB 8; Length 9;
 Best Local Similarity 83.3%; Pred. No. 1.8e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YRNLVW 6
 DB 3 YRNLW 8
 |||: :|||: :||
 RESULT 12
 ADN65622
 ID ADN65622 standard; peptide; 9 AA.
 XX
 XX AC ADN65622;
 XX
 XX DT 01-JUL-2004 (first entry)
 XX
 XX DE HLA binding peptide #2222.
 XX
 XX KW cytostatic; hepatotropic; virucide; antiinflammatory; anti-HIV;
 KW gene therapy; vaccine; HLA binding peptide; HTL epitope; liposome;
 KW prostate specific antigen; prostate specific membrane antigen;
 KW hepatitis B virus antigen; hepatitis C virus antigen;
 KW malignant melanoma antigen; MAGE; Epstein Barr virus; cancer;
 KW prostate cancer; AIDS; renal carcinoma; cervical carcinoma; lymphoma;
 KW chondyloma acuminatum.
 XX
 XX OS Unidentified.
 XX
 XX PN WO2004031211-A2.
 XX
 XX PD 15-APR-2004.
 XX
 XX PF 03-OCT-2003; 2003WO-US031308.
 XX
 XX PR 03-OCT-2002; 2002US-0416207P.
 XX
 XX PR 08-OCT-2002; 2002US-0417269P.
 XX
 XX PA (EPIM-) EPIMMUNE INC.
 XX
 XX PI Sidney J, Southwood S, Sette A;
 XX
 XX DR WPI; 2004-347953/32.
 XX

PR 21-FEB-2002; 2002US-00082014.
 PR 21-FEB-2003; 2003US-00372076.
 XX (PAGE/) PAGE M.
 PA (FRIE/) FRIEDE M.
 PA (SCHM/) SCHMIDT A E.
 PA (STOB/) STOBER D.
 XX Page M, Friede M, Schmidt AE, Stober D;
 XX WPI; 2004-603322/58.
 DR
 XX
 XX Treating chronic hepatitis, by administering vaccine comprising
 PT immunogenic particles having recombinant hepatitis B core chimeric
 PT protein molecules, that stimulates T cell, to patient chronically
 PT infected with hepatitis B virus.
 XX
 PS Disclosure; SEQ ID NO 14; 117pp; English.
 XX
 CC The invention relates to treating chronic hepatitis, by administering a
 CC vaccine comprising immunogenic particles having recombinant hepatitis B
 CC core (Hbc) chimeric protein molecules (where truncated Hbc molecules are
 CC linked N-terminally or C-terminally to an immunogenic epitope), that
 CC stimulate T cell production, to a patient chronically infected with
 CC hepatitis B virus, and maintaining patient for time sufficient to induce
 CC T cells activated against Hbc. The chimeric proteins are still capable
 CC self-assembling into particles upon expression in a host cell and are
 CC substantially free of binding to nucleic acids, and the particles display
 CC enhanced stability. Also included is enhancing (M2) the production of one
 CC or more of gamma-producing CD8+, CD4+ T cells and cytotoxic T lymphocytes
 CC against hepatitis B virus, involving administering to a patient
 CC chronically infected with hepatitis B virus, a T cell-stimulating amount
 CC of a vaccine comprising immunogenic particles dissolved or dispersed in a
 CC diluent containing one or both of an agonist of toll-like receptor 4 and
 CC receptor 9 (TLR-4 and TLR-9), the immunogenic particles comprising Hbc
 CC chimeric protein molecules and maintaining the patient for a sufficient
 CC time to induce T cells activated against Hbc. The immunogenic epitopes
 CC may be B cell or T cell epitopes. The chimeric vaccine is useful for
 CC treating a patient chronically infected with hepatitis B virus. The
 CC present sequence is a B cell epitope suitable for inclusion in the
 CC chimeric protein of the invention.
 XX
 SQ Sequence 10 AA;
 Query Match 44.8%; Score 39; DB 8; Length 10;
 Best Local Similarity 60.0%; Pred. No. 9;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 YRNLVWFITKK 10
 ||||| :
 DB 1 YRNLWLITEK 10
 RESULT 9
 AAM97704
 ID AAM97704 standard; peptide; 14 AA.
 XX
 AC AAM97704;
 XX
 DT 24-JAN-2002 (first entry)
 XX
 DE Human peptide #979 encoded by a SNP oligonucleotide.
 XX
 KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
 KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KW multifactorial disease; autoimmune disease; infection;
 KW nervous system disease.
 XX
 OS Homo sapiens.

XX WO200147944-A2.
 XX
 XX 05-JUL-2001.
 PD
 XX
 XX 28-DEC-2000; 2000WO-US035498.
 PF
 XX
 XX 28-DEC-1999; 99US-0173419P.
 PR
 XX 27-DEC-2000; 2000US-00173419.
 PR
 XX (CURA-) CURAGEN CORP.
 PA
 XX
 XX Shimkets RA, Leach M;
 PI
 XX
 XX WPI; 2001-465210/50.
 DR
 XX
 XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
 PT autoimmune diseases and infections.
 PT
 XX
 PS Disclosure; Page 3882; 4143pp; English.
 XX
 CC The present invention relates to oligonucleotides (see AAL26793-AAL34659)
 CC encoding polymorphic variants of proteins related to amylases, amyloid
 CC proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,
 CC polymerase, oncogenes, histones, kinases, colony stimulating factors,
 CC complement related proteins, cytochromes, kinesins, cytokines,
 CC interferons, interleukins, G-protein coupled receptors and thioesterases.
 CC The present sequence is a peptide encoded by one such oligonucleotide.
 CC The oligonucleotides and the peptides encoded by them may be used in the
 CC prevention, diagnosis and treatment of diseases associated with
 CC inappropriate expression of the proteins listed above. Disorders that may
 CC be prevented, diagnosed and/or treated include multifactorial diseases
 CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid
 CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus
 CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
 CC brain, breast, colon and kidney, leukaemia), diseases of the nervous
 CC system and an infection of pathogenic organisms
 CC
 XX Sequence 14 AA;
 SQ
 Query Match 41.4%; Score 36; DB 4; Length 14;
 Best Local Similarity 66.7%; Pred. No. 42;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 3 NLVWFIKKN 11
 ||||| :
 DB 6 NAVWLQKN 14
 RESULT 10
 AAB86605
 ID AAB86605 standard; peptide; 15 AA.
 XX
 AC AAB86605;
 XX
 XX 20-NOV-2001 (first entry)
 DT
 XX
 DE Human cytomegalovirus strain AD169 IE1 peptide fragment SEQ ID 62.
 XX
 KW Antigen-specific stimulation; T-lymphocyte; CD8 stimulation; pp65;
 KW CD4 stimulation; immuno-stimulation; IE1; lower matrix phosphoprotein.
 XX
 OS Human cytomegalovirus.
 XX
 XX WO200163286-A2.
 PN
 XX
 XX 30-AUG-2001.
 PD
 XX
 XX 17-FEB-2001; 2001WO-EP001773.
 PF
 XX 22-FEB-2000; 2000DE-01009341.
 PR
 XX

XX DE Recombinant chimera hepatitis B core protein immunogenic epitope #6.
 XX KW Recombinant chimera hepatitis B core protein; HBC; immunogenic epitope;
 XX KW HBC immunodominant loop; immune response.
 XX OS Influenza A virus.
 XX PN US2003185858-A1.
 XX XX
 XX PD 02-OCT-2003.
 XX XX
 XX PF 21-FEB-2002; 2002US-00082014.
 XX XX
 XX PR 15-AUG-2001; 2001US-00930915.
 XX PA (BIRKETT) BIRKETT A J.
 XX XX
 XX PI Birkett AJ;
 XX FI
 XX DR WPI; 2004-031988/03.
 XX XX
 XX PT Recombinant chimera hepatitis B core protein molecule useful for preparing
 PT vaccine or inoculum includes peptide-bonded heterologous immunogenic
 PT epitope at N-terminus in the hepatitis B core immunodominant loop or C-
 PT terminus of the chimera.
 XX PS Disclosure; SEQ ID NO 14; 110pp; English.
 XX CC The invention relates to a recombinant chimera hepatitis B core (HBC)
 CC protein molecule that includes a peptide-bonded heterologous immunogenic
 CC epitope at the N-terminus in the HBC immunodominant loop or the C-
 CC terminus of the chimera, or a heterologous linker residue for a conjugated
 CC epitope present in the loop. The invention also relates to an immunogenic
 CC particle comprising the recombinant hepatitis B core chimeric protein
 CC molecules, a vaccine comprising the immunogenic particles dissolved or
 CC dispersed in a diluent, a nucleic acid that encodes a recombinant HBC
 CC protein molecule or its variant, analogue, or complement and a method for
 CC inducing an immune response in an inoculated host animal comprising
 CC inoculating a host animal with a vaccine and maintaining the inoculated
 CC animal for a period of time sufficient to enable development of an immune
 CC response. The recombinant chimera hepatitis B core protein molecule is
 CC used in an immunogenic particle for preparing a vaccine useful for
 CC inducing an immune response in an inoculated host animal. This sequence
 CC represents an HBC protein immunogenic B cell epitope of the invention.
 XX SQ Sequence 10 AA;

Query Match 44.8%; Score 39; DB 8; Length 10;
 Best Local Similarity 60.0%; Pred. NO. 9;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YRNLVWFIFKK 10
 |||||:
 Db 1 YRNLWLWLEK 10

RESULT 7
 ADP73403
 ID ADP73403 standard; peptide; 10 AA.
 XX AC ADP73403;
 XX XX
 XX DT 09-SEP-2004 (first entry)
 XX DE Influenza virus A8/PR8 B cell epitope of gene HA.
 XX KW transgenic animal; Hepatitis B virus nucleocapsid core protein; HBC;
 KW enhanced stability; hepatotropic; virucide; immunology;
 KW protein engineering; immunogen; vaccine; Hepatitis B infection.
 XX OS Influenza virus.
 XX PR

PN WO2004053091-A2.
 XX PD 24-JUN-2004.
 XX PF 10-DEC-2003; 2003WO-US039164.
 XX XX
 XX PR 10-DEC-2002; 2002US-0432123P.
 XX PA (APOV-) APOVIA INC.
 XX XX
 XX PI Lyons K, Birkett AJ, Haron JA;
 XX DR WPI; 2004-468859/44.
 XX XX
 XX PT New recombinant chimera hepatitis B core (HBC) protein molecules useful in
 PT the fields of immunology and protein engineering, in particular as an
 PT immunogen in a vaccine for Hepatitis B infections.
 XX PS Disclosure; SEQ ID NO 16; 338pp; English.
 XX CC The invention relates to a novel recombinant chimera Hepatitis B virus
 CC nucleocapsid (core) protein (HBC), up to 600 or 380 amino acid residues
 CC in length. The chimera protein is engineered for both enhanced stability
 CC of self-assembled particles and the substantial absence of nucleic acid
 CC binding by the particles. The invention further comprises: a recombinant
 CC HBC protein chimera molecule that has a length of 135-365 amino acid
 CC residues and contains four peptide-linked amino acid residue sequence
 CC domains from the N-terminus that are denominated Domains I, II, III and
 CC IV. The invention also provides nucleic acids, polypeptides, host cells,
 CC vectors and transgenic animals used in the methods of the invention. The
 CC chimeric compositions of the invention have hepatotropic and virucide
 CC activities. The methods and compositions of the present invention are
 CC useful in the fields of immunology and protein engineering, in particular
 CC for using a chimera hepatitis B virus nucleocapsid protein as an
 CC immunogen in a vaccine for Hepatitis B infections. This sequence
 CC represents a Hepatitis B virus nucleocapsid (core) protein related
 CC polypeptide of the invention.
 XX SQ Sequence 10 AA;

Query Match 44.8%; Score 39; DB 8; Length 10;
 Best Local Similarity 60.0%; Pred. NO. 9;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YRNLVWFIFKK 10
 |||||:
 Db 1 YRNLWLWLEK 10

RESULT 8
 ADRI2707
 ID ADRI2707 standard; peptide; 10 AA.
 XX AC ADRI2707;
 XX DT 04-NOV-2004 (first entry)
 XX DE Influenza virus HA B cell epitope.
 XX KW HBV; chronic hepatitis; HBC; nucleocapsid core protein; vaccine;
 KW immunogen; immunogenic epitope; T cell; B cell; CD8+ cell; CD4+ cell;
 KW cytotoxic T lymphocyte; toll-like receptor 4; toll-like receptor 9;
 KW TLR-4; TLR-9; epitope.
 XX OS Influenza virus; strain A8/PR8.
 XX PN US2004156863-A1.
 XX XX
 XX PD 12-AUG-2004.
 XX XX
 XX PF 01-OCT-2003; 2003US-00677074.
 XX PR 21-FEB-2002; 2002US-00080299.

```

Query Match      44.8%; Score 39; DB 5; Length 10;
Best Local Similarity 60.0%; Pred. No. 9;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YRNLVWFYK 10
Db 1 YRNLWLTEK 10

RESULT 4
ADE10780
ID ADE10780 standard; peptide; 10 AA.
XX AC ADE10780;
XX DT 29-JAN-2004 (first entry)
XX DE Chimeric hepatitis B virus related B-cell epitope seqid 14.
KW hepatotropic; virucide; antiinflammatory; chronic hepatitis; vaccine;
KW recombinant hepatitis B core chimeric protein; HBC chimeric protein;
KW hepatitis B infection; T-cell stimulator; B-cell epitope.
XX OS Influenza virus.
XX PN US2003198645-A1.
XX PD 23-OCT-2003.
XX PF 21-FEB-2003; 2003US-00372076.
XX PR 21-FEB-2002; 2002US-00080299.
XX PR 21-FEB-2002; 2002US-00082014.
XX PA (PAGE/) PAGE M.
XX PA (FRIE/) FRIEDE M.
XX PI Page M, Friede M;
XX PI WPI; 2003-852775/79.
XX DR Treating chronic hepatitis B infection by administering a T cell-
PT stimulating vaccine containing immunogenic particles having recombinant
PT carboxy-terminal truncated hepatitis B core (HBC) chimeric protein
PT molecules.
XX PS Disclosure; SEQ ID NO 14; 111pp; English.
XX CC The invention describes a method of treating chronic hepatitis comprising
CC administering to a patient a T cell-stimulating amount of a vaccine
CC comprising immunogenic particles dissolved or dispersed in a diluent,
CC where the immunogenic particles consist of recombinant hepatitis B core
CC (HBC) chimeric protein molecules, and maintaining the patient to induce T
CC cells activated against HBC. The methods and compositions of the present
CC invention are useful for treating chronic hepatitis B infection. This is
CC the amino acid sequence of a chimeric hepatitis B virus related B-cell
CC epitope useful for expression within the HBV chimera at the N-terminus,
CC within the immunogenic loop and/or at the C-terminus.
XX SQ Sequence 10 AA;

Query Match      44.8%; Score 39; DB 7; Length 10;
Best Local Similarity 60.0%; Pred. No. 9;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YRNLVWFYK 10
Db 1 YRNLWLTEK 10

RESULT 5
ADM39685
ID ADM39685 standard; peptide; 10 AA.
XX AC ADM39685;
XX DT 03-JUN-2004 (first entry)
XX DE Influenza A virus B-cell peptide epitope expressed by HBC chimera Seq 17.
KW immunogenic; avian hepatitis B virus; nucleocapsid;
KW self assembled particle; immunogen; inoculum; vaccine; immunostimulant;
KW antibacterial; virucidal; B-cell epitope.
XX OS Influenza A virus.
XX PN WO2003072722-A2.
XX PD 04-SEP-2003.
XX PF 21-FEB-2003; 2003WO-US005315.
XX PR 21-FEB-2002; 2002US-0359129P.
XX PA (APOV-) APOVIA INC.
XX PI Birkett AJ, Peck B;
XX PI WPI; 2003-679948/64.
XX DR New recombinant chimera avian hepatitis B core protein molecule, useful as
PT an immunogen for inducing a B cell or T cell response to produce
PT antibodies, or as a vaccine against pathogens.
XX PS Disclosure; SEQ ID NO 17; 278pp; English.
XX CC This invention relates to novel recombinant immunogenic chimeric avian
CC hepatitis B core (AHBC) nucleocapsid proteins. Specifically, it refers to
CC an AHBC protein that has been engineered to display an immunogenic B cell
CC or T cell epitope, exhibit enhanced stability and an absence of nucleic
CC acid binding as a self assembled particle. The present invention
CC describes the chimeric AHBC protein as truncated at the C-terminus and
CC containing introduced cysteine residues that confers an enhanced
CC stability in aqueous solution, an increased yield and more immunogenicity
CC than similar conjugates that lack N- or C-terminal cysteines.
CC Furthermore, a reduction in the number of positively charged residues
CC (lysine and arginine) towards the C-terminus prepares self-assembled
CC particles that are substantially free of nucleic acid binding. As such,
CC these chimeric particles can be used as immunogens of an inoculum that
CC can also be useful for developing a vaccine to protect against the
CC pathogen from which the heterologous epitope or the haptens is derived.
CC Accordingly, these compositions exhibit immunostimulant, antibacterial
CC and virucidal activities. This peptide sequence is an exemplary B-cell
CC epitope peptide immunogen useful for both linkage to the linker residue
CC after expression of a contemplated chimera and for expression within an
CC HBC chimera of the invention.
XX SQ Sequence 10 AA;

Query Match      44.8%; Score 39; DB 7; Length 10;
Best Local Similarity 60.0%; Pred. No. 9;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YRNLVWFYK 10
Db 1 YRNLWLTEK 10

RESULT 6
ADG63881
ID ADG63881 standard; peptide; 10 AA.
XX AC ADG63881;
XX DT 11-MAR-2004 (first entry)

```

CC the autoimmune disease. This peptide is an internal peptide of influenza
 CC type A haemagglutinin protein and is implicated as a foreign epitope
 CC involved in the aetiology or in remissions of multiple sclerosis. It has
 CC been shown capable of inducing the proliferation of autoreactive T-cell
 CC clones isolated from multiple sclerosis patients. (Updated on 27-AUG-2003
 CC to correct OS field.)
 XX
 SQ Sequence 15 AA;

Query Match

Best Local Similarity 100.0%; Score 87; DB 2; Length 15;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YRNLLWFIKNTYRYP 15
 DB 1 YRNLLWFIKNTYRYP 15

RESULT 2

AAV29685

ID AAV29685 standard; protein; 10 AA.

XX AC AAV29685;

XX DT 08-NOV-1999 (first entry)

XX DE Influenza A8/PR8 antigen HA polypeptide haptens.

XX KW Human hepatitis B core protein; HBC; modified; immunodominant;

XX OS nucleocapsid protein; vaccine; T cell epitope.

XX PN Influenza virus.

XX PW WO9940934-A1.

XX PD 19-AUG-1999.

XX PF 11-FEB-1999; 99WO-US003055.

XX PR 12-FEB-1998; 98US-0074537P.

XX PA (IMMU-) IMMUNE COMPLEX CORP.

XX PI Birkett AJ;

XX DR WPI; 1999-527340/44.

XX PT Conjugate of hepatitis B core protein, modified to increase reactivity
 XX with haptens, used to raise antibodies against the haptens, e.g. in
 XX vaccines.

XX PS Example 3; Page 37; 128pp; English.

XX CC The present invention describes a conjugate (A) comprising a
 CC strategically modified hepatitis B core (HBC) protein (I) attached to a
 CC haptens, where (I) includes amino acids (aa) 10-140 of the wild type HBC
 CC 183 aa sequence (given in AAV29674) and additionally has an insert (II)
 CC in the region corresponding to aa's 50-100, where the insert is of 1 to
 CC about 40 aa's and contains a chemically reactive aa residue linked to the
 CC haptens. A vaccine containing (A), optionally in the form of particles, is
 CC used to induce a protective antibody response against the pathogen from
 CC which the haptens is derived, in humans or other animals. These pathogens
 CC may be bacteria, viruses, rickettsia or protozoa. Insertion of (II)
 CC overcomes the low reactivity of aa side chains in native HBC protein,
 CC increasing the reactivity with haptens and resulting in conjugates of
 CC improved immunogenicity. Modified HBC can be derivatised in the form of
 CC particles by well-defined chemical methods, and is unlikely to cause
 CC immunological side-effects. AAV29675 to AAV29735 represent polypeptide
 CC haptens used in an example from the present invention
 XX
 SQ Sequence 10 AA;

Query Match

44.8%; Score 39; DB 2; Length 10;

Best Local Similarity 60.0%; Pred. No. 9;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 YRNLLWFIK 10
 DB 1 YRNLLWFIK 10

RESULT 3

AAU93809

ID AAU93809 standard; peptide; 10 AA.

XX AC AAU93809;

XX DT 02-JUL-2002 (first entry)

XX DE Influenza virus HA B cell epitope.

XX KW Immunogenic; hepatitis virus nucleocapsid protein; hepatitis B core; HBC;
 XX vaccine; B cell epitope; T cell epitope; immunostimulant.

XX OS Influenza virus.

XX PN WO200214478-A2.

XX PD 21-FEB-2002.

XX PF 16-AUG-2001; 2001WO-US041759.

XX PR 16-AUG-2000; 2000US-0225843P.

XX PR 22-AUG-2000; 2000US-0226867P.

XX PR 15-AUG-2001; 2001US-00930915.

XX PA (APOV-) APOVIA INC.

XX PI Birkett AJ;

XX PW WPI; 2002-257601/30.

XX PT Novel recombinant hepatitis virus nucleocapsid protein, termed as chimeric
 XX hepatitis B core protein, displays immunogenic epitopes at N-terminus,
 XX HBC immunogenic loop with linker for conjugated epitope and C-terminus.

XX PS Disclosure; Page 35; 289pp; English.

XX CC The invention relates to a recombinant hepatitis virus nucleocapsid protein,
 CC i.e. a chimeric hepatitis B core (HBC) protein (I), displaying one or
 CC more immunogenic epitopes at the N-terminus, HBC immunogenic loop (L) or
 CC C-terminus, or having a heterologous linker for a conjugated epitope in
 CC (L), and containing a Cys residue at, or near, the C-terminus that
 CC confers enhanced stability to the particles. A vaccine comprising (I) is
 CC useful for inducing an immune response in an inoculated host animal, by
 CC inoculating a host animal with the vaccine, and maintaining that
 CC inoculated animal for a time period sufficient for that animal to develop
 CC an immune response. The immunogenic particles formed using (I) are
 CC substantially free of binding to nucleic acids, and are most stable than
 CC the particle formed from otherwise identical HBC chimera that lacks the C-
 CC terminal residue or in which a C-terminal Cys is replaced by another
 CC residue. The chimera particles are most stable on storage in aqueous
 CC conditions that are particles of similar sequence that lack any C-
 CC terminal Cys residues. The chimera molecule exhibits the self-assembly not
 CC exhibiting the nucleic acid binding of those native particles, and
 CC excellent B cell and T cell immunogenicities. The chimera particles are
 CC typically prepared in higher yield than similar particles that are free
 CC of a C-terminal Cys. The particles are often far more immunogenic than
 CC the similar conjugates that lack a C-terminal Cys. Immunogenicities of
 CC particles assembled from the chimera molecules are enhanced as compared to
 CC similar particles assembled from chimera molecules lacking at least one C-
 CC terminal Cys. AAU93802-AAU93997 represent immunogenic HBC particles amino
 CC acid sequences and related sequences of the invention
 XX
 SQ Sequence 10 AA;

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OM protein - protein search, using sw model

Run on: February 22, 2005, 08:52:23 ; Search time 65.6667 Seconds
(without alignments)
88.346 Million cell updates/sec

Title: US-08-991-628-13

Perfect score: 87

Sequence: 1 YRNLVFIKKNTRY 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 632537

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	87	100.0	15	2 AAW04853	Internal
2	39	44.8	10	2 AAY29685	Influenza
3	39	44.8	10	5 AAU93809	Influenza
4	39	44.8	10	7 ADE10780	Chimeric
5	39	44.8	10	7 ADM39685	Influenza
6	39	44.8	10	8 ADG63881	Recombina
7	39	44.8	10	8 ADP73403	Influenza
8	39	44.8	10	8 ADR12707	Influenza
9	36	41.4	14	4 AAM97704	Human pep
10	34.5	39.7	15	4 AAB86605	Human cyt
11	34	39.1	9	8 AAB65655	HLA bindi
12	34	39.1	9	8 AAB65622	HLA bindi
13	34	39.1	13	8 ADR99836	Human agg
14	33	37.9	14	7 ADJ62411	Tryptic m
15	32	36.8	10	2 AAR99504	B-cell ep
16	32	36.8	10	2 AAW12228	Influenza
17	32	36.8	10	2 AAW60684	Influenza
18	32	36.8	10	5 ABB79917	Influenza
19	31	35.6	13	2 AAW10481	MHC Class
20	31	35.6	13	4 AAG65616	Amino aci
21	31	35.6	13	8 ADR99837	Citrullin
22	31	35.6	13	8 ADR99835	Human agg
23	30	34.5	10	2 AAR77850	ID-Ala 28
24	30	34.5	10	4 AAM10334	HLA-A1 de
25	30	34.5	10	4 AAM13196	HLA-A26 d

ALIGNMENTS

RESULT 1

AAW04853
ID AAW04853 standard; peptide; 15 AA.

XX AC AAW04853;

XX AC

DT 27-AUG-2003 (revised)

DT 18-FEB-1997 (first entry)

XX Internal fragment of influenza type A haemagglutinin protein.

XX Tolerisation; self-epitope; antigen; autoimmune disease; autoantigen;
KW HLA; human leukocyte antigen; T-cell; thymocyte; pemphigus vulgaris;
KW desmoglein; multiple sclerosis; herpes simplex virus; adenovirus;
KW phosphomannomutase; human papillomavirus; Epstein-Barr virus;
KW DNA polymerase; influenza; haemagglutinin; reovirus; sigma protein.

XX Influenza A virus.

XX WO9627387-A1.

XX 12-SEP-1996.

XX 07-MAR-1996; 96WO-US003182.

XX 07-MAR-1995; 95US-00400796.

XX (HARD) HARVARD COLLEGE.

XX Strominger JL, Wuchterfennig KW;

XX WPI; 1996-425218/42.

XX Pemphigus vulgaris auto-antigens and multiple sclerosis non-self antigens
PT - useful in disease treatment, and method for identification of other
self and non-self antigens implicated in auto-immune disease.

XX Claim 2; Page 46; 58pp; English.

XX Pharmaceutical preparations for tolerisation to antigens comprise either
an isolated human non-collagen or non-mysin basic protein (MBP)
polypeptide which is capable of tolerising an individual to an
autoantigen; or an isolated human pathogen polypeptide capable of
tolerising an individual to that polypeptide. In both cases, the
polypeptide (whether self or non-self) includes an amino acid sequence
corresponding to a sequence motif for a MHC class II protein, such as HLA
-DR, which is associated with a human autoimmune disease and which binds
to the polypeptide to activate autoreactive T-cells in individuals with

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DE Outer surface protein C (Fragment).
GN Name=ospC;
OS Borrelia garinii.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=29519;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=P81;
RX MEDLINE=97426044; PubMed=9282748;
RA Tilly K., Casjens S., Stevenson B., Bono J.L., Samuels D.S., Hogan D.,
RA Rosa P.;
RT "he Borrelia burgdorferi circular plasmid cp26: conservation of
RT plasmid structure and targeted inactivation of the ospC gene.";
RL Mol. Microbiol. 25:361-373(1997).
DR EMBL; U93699; AAC45531.1; -.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1019 MW; 4864C1A731A44333 CRC64;

Query Match 25.3%; Score 22; DB 2; Length 9;
Best Local Similarity 80.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 IKKNT 12
:||||
Db 1 MKKNT 5

RESULT 14

Q9R3T0 PRELIMINARY; PRT; 9 AA.
AC Q9R3T0;
DT 01-WAY-2000 (TrEMBLrel. 13, Created)
DT 01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Outer surface protein C (Fragment).
GN Name=ospC;
OS Borrelia afzelii.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=29518;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PKO, IP21, and J1;
RX MEDLINE=97426044; PubMed=9282748;
RA Tilly K., Casjens S., Stevenson B., Bono J.L., Samuels D.S., Hogan D.,
RA Rosa P.;
RT "he Borrelia burgdorferi circular plasmid cp26: conservation of
RT plasmid structure and targeted inactivation of the ospC gene.";
RL Mol. Microbiol. 25:361-373(1997).
DR EMBL; U93698; AAC45531.1; -.
DR EMBL; U93696; AAC45527.1; -.
DR EMBL; U93697; AAC45529.1; -.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1005 MW; 4864C5B731A44333 CRC64;

Query Match 25.3%; Score 22; DB 2; Length 9;
Best Local Similarity 80.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 IKKNT 12
:||||
Db 1 MKKNT 5

RESULT 15

Q9R792 PRELIMINARY; PRT; 9 AA.
AC Q9R792;
DT 01-WAY-2000 (TrEMBLrel. 13, Created)
DT 01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Outer surface protein C (Fragment).
GN Name=ospC;
OS Borrelia burgdorferi (Lyme disease spirochete).

OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B31;
RX MEDLINE=97426044; PubMed=9282748;
RA Tilly K., Casjens S., Stevenson B., Bono J.L., Samuels D.S., Hogan D.,
RA Rosa P.;
RT "he Borrelia burgdorferi circular plasmid cp26: conservation of
RT plasmid structure and targeted inactivation of the ospC gene.";
RL Mol. Microbiol. 25:361-373(1997).
DR EMBL; U93693; AAC45521.1; -.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1005 MW; 4864C5B731A44333 CRC64;

Query Match 25.3%; Score 22; DB 2; Length 9;
Best Local Similarity 80.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 IKKNT 12
:||||
Db 1 MKKNT 5

Search completed: February 22, 2005, 09:38:03
Job time : 53.6667 secs

OS Bradypodion transvaalense (Transvaal dwarf chameleon).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Acrodonta; Chamaeleonidae;
OC Bradypodion.
OC NCBI_TaxID=179889;
RX [1].
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=22169767; PubMed=12182400; DOI=10.1006/mpev.2001.1076;
RA Townsend T., Larson A.;
RT "Molecular phylogenetics and mitochondrial genomic evolution in the
RT chamaeleonidae (Reptilia, Squamata).";
RL Mol. Phylogenet. Evol. 23:22-36(2002).
RN [2].
RN
RP SEQUENCE FROM N.A.
RX Townsend T.M., Larson A.L.;
RA Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF448731; AAL90475.1;
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
RX NON TER 10
RN SEQUENCE 10 AA; 1353 MW; DC218E2733640059 CRC64;
SQ

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Query Match      27.6%; Score 24; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. NO. 2.8e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      5 VPEIK 9
        :|||:
Db       1 MWEIR 5

RESULT 12
Q79B39
ID      Q79B39      PRELIMINARY;      PRT;      8 AA.
AC      Q79B39,
DT      05-JUL-2004      (TrEMBLrel. 27, Created)
DT      05-JUL-2004      (TrEMBLrel. 27, Last sequence update)
DT      05-JUL-2004      (TrEMBLrel. 27, Last annotation update)
DE      Outer surface protein C (Fragment).

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FT NON TEK 8 8
SQ SEQUENCE 8 AA; 892 MW; F4C5B731A443336 CRC64;
Query Match 25.3%; Score 22; DB 2; Length 8;
Best Local Similarity 80.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DD		1 MKKNT 5	
RESULT 13			
O31363	ID	PRELIMINARY;	PRT; '9 AA.
AC O31363	ID		
DT 01-JAN-1998	(TRENBLREL. 05,	Created)	
DT 01-JAN-1998	(TRENBLREL. 05,	Last sequence update)	
DT 01-DEC-2001	(TRENBLREL. 15,	Last annotation update)	

```

RP SEQUENCE FROM N.A.
RX MEDLINE=21481970; PubMed=11598067;
EI DOI=10.1128/IAI.69.11.6923-6930.2001;
RA Wang L., Qu W., Reeves P.R.;
RT "Sequence analysis of four Shigella boydii O-antigen loci: implication
RL for Escherichia coli and Shigella relationships.";
RL Infect. Immun. 69:6923-6930(2001).
DR EMBL; AF409078; AAL27364.1; -.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1763 MW; 05FA72B5343C1234 CRC64;

Query Match 31.0%; Score 27; DB 2; Length 14;
Best Local Similarity 71.4%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 FIKQNTY 13
Db 3 FIKQNTY 9

RESULT 6
ID Q7SA62 PRELIMINARY; PRT; 10 AA.
AC Q7SA62;
DT 01-MAR-2004 (TREMELrel. 26, Created)
DT 01-MAR-2004 (TREMELrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE Predicted protein.
GN Name=NCU08327.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffé D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Iankiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kamysseilis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
RA Kryzotova S., Rasmussen C., Metzner R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Omani S.A.,
RA DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; ABX0100206; EAA33304.1; -.
SQ SEQUENCE 10 AA; 1284 MW; D6D34CB72DC400S9 CRC64;

Query Match 29.9%; Score 26; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 VNFIKNTY 14
Db 1 VNFIKNTY 10

RESULT 7
ID Q7M110 PRELIMINARY; PRT; 15 AA.
AC Q7M110;
DT 01-MAR-2004 (TREMELrel. 26, Created)
DT 01-MAR-2004 (TREMELrel. 26, Last sequence update)

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DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DS Endo-1,3-beta-glucanase (EC 3.2.1.-), 40k (Fragment).
OS Bacillus circulans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1197;
RN [1]
RP SEQUENCE.
RA Fiske M.J., Tobey-Fincher K.L., Fuchs R.L.;
RT "Cloning of two genes from Bacillus circulans WL-12 which encode 1,3-
RL beta-glucanase activity.";
RL J. Gen. Microbiol. 136:2377-2383(1990).
DR PIR; B60763; B60763.
FT NON_TER 1
FT NON_TER 15
FT NON_TER 15
SQ SEQUENCE 15 AA; 1740 MW; 2C6854FC5CACE1A6 CRC64;

Query Match 28.7%; Score 25; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NLVW 6
Db 5 NLVW 8

RESULT 8
ID Q6LCW3 PRELIMINARY; PRT; 15 AA.
AC Q6LCW3;
DT 05-JUL-2004 (TREMELrel. 27, Created)
DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)
DE Transcription factor AP-2 isoform 2 (Fragment).
GN Name=AP-2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/4;
RX MEDLINE=95269866; PubMed=7750631; DOI=10.1006/dbio.1995.1121;
RA Meier P., Kosedood M., Philipp J., Fontana A., Mitchell P.J.;
RT "Alternative mRNAs encode multiple isoforms of transcription factor
RT AP-2 during murine embryogenesis.";
RL Dev. Biol. 169:1-14(1995).
DR EMBL; U17289; AAA85677.1; -.
DR GO; GO:0005667; C:transcription factor complex; TAS.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0003700; F:transcription factor activity; IDA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IDA.
FT NON_TER 15
FT NON_TER 15
SQ SEQUENCE 15 AA; 1901 MW; 090AE08FEFC6136D CRC64;

Query Match 28.7%; Score 25; DB 2; Length 15;
Best Local Similarity 27.3%; Pred. No. 2.9e+03;
Matches 3; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 4 LVWFIKNTY 14
Db 1 MLWKLTDNIKY 11

RESULT 9
ID Q84156 PRELIMINARY; PRT; 8 AA.
AC Q84156;
DT 01-NOV-1996 (TREMELrel. 01, Created)
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)
DE Similar to Vaccinia virus (Fragment).
OS Orf virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;

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RC STRAIN=LT2;
 RX MEDLINE=8508492; PubMed=6096856;
 RA Sacerdot C., Dessen P., Hershey J.W., Plumbbridge J.A.,
 RA Grunberg-Manago M.;
 RT "Sequence of the initiation factor IF2 gene: unusual protein features
 RT and homologues with elongation factors.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:7787-7791(1984).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LT2;
 RX MEDLINE=94156845; PubMed=8113180;
 RA Craven M.G., Granston A.E., Schauer A.T., Zheng C., Gray T.A.,
 RA Friedman D.I.;
 RT "Escherichia coli-Salmonella typhimurium hybrid nusA genes:
 RT identification of a short motif required for action of the lambda N
 RT transcription antitermination protein.";
 RL J. Bacteriol. 176:1394-1404(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LT2;
 RX MEDLINE=95212911; PubMed=7535280;
 RA Dammel C.S., Noller H.P.;
 RT "Suppression of a cold-sensitive mutation in 16S rRNA by
 RT overexpression of a novel ribosome binding factor, RbFA.";
 RL Genes Dev. 9:626-637(1995).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LT2;
 RA Hedegaard J., Steffensen S.A., Nørskov-Lauritsen N., Mortensen K.K.,
 RA Sperling-Petersen H.O.;
 RT "Identification of Enterobacteriaceae by partial sequencing of the
 RT gene encoding translation initiation factor 2.";
 RL Int. J. Syst. Bacteriol. 48:1531-1538(1999).
 DR EMBL: AJ002552; CAA05548.1; --
 FT NON TER 1
 SQ SEQUENCE 15 AA; 1710 MW; 1C6AD0FD23B00DCC CRC64;
 Query Match 33.3%; Score 29; DB 2; Length 15;
 Best Local Similarity 66.7%; Pred. No. 5.9e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 RNLVWF 7
 DB 6 RNICWF 11
 RESULT 3
 APE_CAPGI STANDARD; PRT; 10 AA.
 AC P80474;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Aminopectidase (EC 3.4.11.-) (Fragment).
 OS Capnocytophaga gingivalis.
 OC Bacteria; Bacteroidetes; Flavobacteria; Flavobacteriales;
 OC Flavobacteriaceae; Capnocytophaga.
 OX NCBI_TaxID=1017;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=ATCC 33624;
 RX MEDLINE=96118234; PubMed=8574402;
 RA Spratt D.A., Greenman J., Schaffer A.G.;
 RT "Capnocytophaga gingivalis aminopeptidase: a potential virulence
 RT factor.";
 RL Microbiology 141:3087-3093(1995).
 CC -1- FUNCTION: Aminopeptidase which hydrolyzes substrates with free N-
 CC terminal amino acid residues but not N-terminal blocked ones.
 CC Optimum activity is measured at pH 7.5. May be important in the
 CC nutrition and pathogenesis of the organism in the human oral
 CC cavity.
 CC -1- COFACTOR: Requires magnesium or calcium.
 KW Aminopeptidase; Calcium; Direct protein sequencing; Hydrolase;

KW Magnesium.
 FT NON TER 1
 FT NON TER 10
 SQ SEQUENCE 10 AA; 1306 MW; 00COA6DB43772694 CRC64;
 Query Match 31.0%; Score 27; DB 1; Length 10;
 Best Local Similarity 25.0%; Pred. No. 8.5e+02;
 Matches 2; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
 QY 3 NLVWFIKK 10
 DB 3 NMLWVYXR 10
 RESULT 4
 Q7RQJ4 PRELIMINARY; PRT; 12 AA.
 ID Q7RQJ4
 AC Q7RQJ4
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein.
 GN Name=PY01103;
 OS Plasmodium yoelii yoelii.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=73239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1YXNL;
 RX PubMed=12368865; DOI=10.1038/nature01099;
 RA Carlton J.M., Arguioli S.V., Suh B.B., Kooij T.W., Portea M.,
 RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
 RA Peterson J.D., Pop M., Kosack D.S., Shumway M.P., Bidwell S.L.,
 RA Shallom S.J., van Aken S.E., Riedmuller S.B., Feidbylum T.V.,
 RA Cho J.K., Quackenbush J., Sedegah M., Shoalbi A., Cummings L.M.,
 RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
 RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
 RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
 RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
 RA Carucci D.J.;
 RT "Genome sequence and comparative analysis of the model rodent malaria
 RT parasite Plasmodium yoelii yoelii.";
 RL Nature 419:512-519(2002).
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AABL01000291; EAA20281.1; --
 KW Hypothetical protein.
 SQ SEQUENCE 12 AA; 1409 MW; 96C174ED7A3059D1 CRC64;
 Query Match 31.0%; Score 27; DB 2; Length 12;
 Best Local Similarity 66.7%; Pred. No. 1e+03; Mismatches 0; Indels 0; Gaps 0;
 Matches 6; Conservative 0;
 QY 3 NLVWFIKK 11
 DB 2 NLSTFIKN 10
 RESULT 5
 Q93C11 PRELIMINARY; PRT; 14 AA.
 ID Q93C11
 AC Q93C11
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE O-antigen polymerase (Fragment).
 GN Name=wzy;
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 22, 2005, 08:53:13 ; Search time 52.6 Seconds
(without alignments)
146.030 Million cell updates/sec

Title: US-08-991-628-13

Perfect score: 87

Sequence: 1 YRNLVWFPIKNTNRY 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 6622

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	33.3	13	2	Q99188 rivulus cau
2	29	33.3	15	2	Q9ZF32 salmone
3	27	31.0	10	1	APR_CAPGI
4	27	31.0	12	2	Q7RQJ4 capnocytoph
5	27	31.0	14	2	Q93C11 plasmodium
6	26	29.9	10	2	Q7SA62 escherichia
7	25	28.7	15	2	Q7M110 neurospora
8	25	28.7	15	2	Q6LCW3 bacillus ci
9	24	27.6	8	2	Q84156 mus musculus
10	24	27.6	10	2	Q84156 orf virus
11	24	27.6	10	2	Q8SHM8 bradypodion
12	22	25.3	8	2	Q8SHM8 bradypodion
13	22	25.3	9	2	Q31363 borrelia ga
14	22	25.3	9	2	Q9R370 borrelia af
15	22	25.3	9	2	Q9R792 borrelia bu
16	22	25.3	10	2	Q83067 bacillus ce
17	22	25.3	10	2	Q9R791 borrelia af
18	22	25.3	11	2	Q9R790 borrelia ga
19	22	25.3	13	2	Q64FK2 homo sapien
20	22	25.3	14	2	Q7RR89 plasmodium
21	22	25.3	14	2	Q9QW75 mus sp. hom
22	22	25.3	15	1	UC16_MAIZE
23	22	25.3	15	2	Q35411 mus musculus
24	21	24.1	10	2	Q79AV7 klebsiella
25	21	24.1	11	2	Q9AIZ7 carsonella
26	21	24.1	13	2	Q6LDS1 bacterioph
27	21	24.1	15	1	UC08_MAIZE
28	21	24.1	15	2	Q9UWM1 methanospir
29	21	24.1	15	2	Q35795 saccharomyc
30	20.5	23.6	14	2	Q89818 murine minu
31	20	23.0	7	2	Q8GL00 borrelia bu

32 20 23.0 7 2 Q8GL04 Q8G104 borrelia bu
33 20 23.0 8 2 Q95M23 Q95M23 sus scrofa
34 20 23.0 8 2 Q8G940 Q8G940 borrelia bu
35 20 23.0 9 2 Q28121 Q28121 bos taurus
36 20 23.0 9 2 Q8GL26 Q8GL26 borrelia bu
37 20 23.0 9 2 Q9R9C4 Q9R9C4 borrelia bu
38 20 23.0 10 2 Q8SHA2 Q8SHA2 brookesia b
39 20 23.0 10 2 P82438 P82438 nicotiana t
40 20 23.0 10 2 Q8G8W5 Q8G8W5 borrelia bu
41 20 23.0 11 2 Q25916 Q25916 plasmodium
42 20 23.0 11 2 Q8GL24 Q8GL24 borrelia bu
43 20 23.0 12 2 Q81VH0 Q81VH0 homo sapien
44 20 23.0 12 2 Q7M1H0 Q7M1H0 leonurus ar
45 20 23.0 13 1 P57104 P57104 rana tempor

ALIGNMENTS

RESULT 1

Q99188 PRELIMINARY; PRT; 13 AA.
ID O99188
AC O99188;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Cytochrome oxidase I (Fragment).
GN Name=COI;
OS Rivulus caudomarginatus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Cyprinodontiformes; Aplocheilidae; Rivulinae; Rivulus.
OX NCBI_TaxID=60318;
RN [1]
RP SEQUENCE FROM N.A.
EX MEDLINE=24072928; PubMed=10603257; DOI=10.1006/mpev.1999.0656;
RA Murphy W.J., Thomson J.E., Collier G.E.;
RT "Phylogeny of the Neotropical killifish family Rivulidae
RT (Cyprinodontiformes, Aplocheiloidei) inferred from mitochondrial DNA
RT sequences.";
RL Mol. Phylogenet. Evol. 13:289-301(1999).
DR EMBL; AF002597; AAD01080.1; -;
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER
SQ SEQUENCE 13 AA; 1705 MW; 404DF35AEFFFE79C7 CRC64;
1

Query Match 33.3%; Score 29; DB 2; Length 13;
Best Local Similarity 57.1%; Pred. No. 5.1e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 YRNLVWF 7

Db 3 YQHLFWP 9

RESULT 2

Q9ZF32 PRELIMINARY; PRT; 15 AA.
ID Q9ZF32
AC Q9ZF32;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE NUSA protein (fragment).
GN Name=nusa;
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.

A;Accession: E60396
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-13 <LIM>
A;Cross-references: GB:M31305

Query Match 23.0%; Score 20; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YRNL 4
|||:
Db 10 YRNI 13

RESULT 15

PN0662

dystrophin-associated glycoprotein A3a-I - rabbit (fragment)

C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 07-May-1999

C;Accession: PN0662

R;Yoshida, M.; Mizuno, Y.; Nonaka, I.; Ozawa, E.

J. Biochem. 114, 634-639, 1993

A;Title: A dystrophin-associated glycoprotein, A3a (one of 43DAG doublets), is retained

A;Reference number: PN0662; MUID:9415681; PMID:8113213

A;Accession: PN0662

A;Molecule type: protein

A;Residues: 1-15 <YOS>

C;Comment: This protein is retained in Duchenne type muscular dystrophy muscle.

C;Keywords: glycoprotein; skeletal muscle

Query Match 23.0%; Score 20; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.7e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 FIKK 10
|||:
Db 5 FIKK 8

Search completed: February 22, 2005, 09:46:29
Job time : 11.1333 secs

Best Local Similarity 75.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 TRYP 15
|:|
Db 6 TKYP 9

RESULT 9
A48372
benzoyl-CoA ligase - Methanospirillum hungatei (fragment)
C:Species: Methanospirillum hungatei
C>Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A48372
R:Auburger, G.; Winter, J.
Appl. Microbiol. Biotechnol. 37, 789-795, 1992
A:Title: Purification and characterization of benzoyl-CoA ligase from a syntrophic, benzotrophic bacterium
A:Reference number: A48372; MUID:93040109; PMID:1369492
C:Accession: A48372
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <AUB>
A:Cross-references: UNIPROT:Q9UWM1
A>Note: sequence extracted from NCBI backbone (NCBIP:118357)

Query Match 24.1%; Score 21; DB 2; Length 15;
Best Local Similarity 42.9%; Pred. No. 3.2e+03;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YRNLVWF 7
|:|
Db 9 YNSADWF 15

RESULT 10
I46023
growth hormone receptor - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C>Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C:Accession: I46023
R:Hauser, S.D.; McGrath, M.F.; Collier, R.J.; Krivi, G.G.
Mol. Cell. Endocrinol. 72, 187-200, 1990
A:Title: Cloning and in vivo expression of bovine growth hormone receptor mRNA.
A:Reference number: I46023; MUID:91146804; PMID:2289631
C:Accession: I46023
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-9 <HAU>
A:Cross-references: UNIPROT:Q28121; EMBL:U24113; NID:g775221; PIDN:AAA91014.1; PID:g775221
C:Genetics:
A:Gene: GHR

Query Match 23.0%; Score 20; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 WFI 8
|:|
Db 5 WVF 7

RESULT 11
B44818
extracellular lipase - Pseudomonas aeruginosa (fragment)
C:Species: Pseudomonas aeruginosa
C>Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 18-Nov-1994
C:Accession: B44818
R:Gilbert, E.J.; Cornish, A.; Jones, C.W.
J. Gen. Microbiol. 137, 2223-2229, 1991
A:Title: Purification and properties of extracellular lipase from Pseudomonas aeruginosa
A:Reference number: A44818; MUID:92085040; PMID:1748875
C:Accession: B44818
A:Status: preliminary

A:Molecule type: protein
A:Residues: 1-12 <GIL>
A:Experimental source: strain EF228
A>Note: sequence extracted from NCBI backbone (NCBIP:70393)

Query Match 23.0%; Score 20; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 3.8e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 TRYP 15
|:|
Db 5 TQYP 8

RESULT 12
S69123
proton-translocating transhydrogenase - Rhodospirillum rubrum (fragment)
C:Species: Rhodospirillum rubrum
C>Date: 10-Mar-1998 #sequence_revision 24-Apr-1998 #text_change 24-Apr-1998
C:Accession: S69123
R:Diggle, C.; Hutton, M.; Jones, G.R.; Thomas, C.M.; Jackson, J.B.
Eur. J. Biochem. 228, 719-726, 1995
A:Title: Properties of the soluble polypeptide of the proton-translocating transhydrogenase
A:Reference number: S69123; MUID:95255277; PMID:7737169
C:Accession: S69123
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-12 <DIG>

Query Match 23.0%; Score 20; DB 2; Length 12;
Best Local Similarity 25.0%; Pred. No. 3.8e+03;
Matches 2; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 3 NLVWFIKK 10
|:| :|
Db 3 DVWVKVQR 10

RESULT 13
JU0356
cycloleoneurin - sagebrush motherwort
C:Species: Leonurus artemisia (sagebrush motherwort)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: JU0356
R:Kinoshita, K.; Tanaka, J.; Kuroda, K.; Koyama, K.; Natori, S.; Kinoshita, T.
Chem. Pharm. Bull. 39, 712-715, 1991
A:Title: Cycloleoneurin, a cyclic peptide from Leonuri fructus.
A:Reference number: JU0356; MUID:91300597; PMID:2070452
C:Accession: JU0356
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-12 <KIN>
A:Cross-references: UNIPROT:Q7MLH0

Query Match 23.0%; Score 20; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 3.8e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 TRYP 15
|:|
Db 7 TQYP 10

RESULT 14
E60396
antigen 7H8/2 - malaria parasite (Plasmodium falciparum) (fragments)
C:Species: Plasmodium falciparum
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jun-2000
C:Accession: E60396
R:Limpaboon, T.; Taylor, D.W.; Jones, G.; Geysen, H.M.; Saul, A.
Southeast Asian J. Trop. Med. Public Health 21, 388-396, 1990
A:Title: Characterization of a Plasmodium falciparum epitope recognized by a monoclonal antibody
A:Reference number: A60396; MUID:91164876; PMID:1706114

PN0649
pullulanase (EC 3.2.1.41) - Bacillus sp. (strain S-1) (fragment)
C;Species: Bacillus sp.
C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 03-Jun-2002
C;Accession: PN0649
B;Kim, C.H.; Choi, H.I.; Lee, D.S.
Biosci. Biotechnol. Biochem. 57, 1632-1637, 1993
A;Title: Purification and biochemical properties of an alkaline pullulanase from alkalophilic bacterium
A;Reference number: PN0649; MUID:94080025; PMID:7764261
A;Accession: PN0649
A;Molecule type: protein
A;Residues: 1-7 <KIM>
C;Comment: This enzyme is used together with glucoamylase to improve the efficiency of starch in high maltose syrups.
C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 27.6%; Score 24; DB 2; Length 7;
Best Local Similarity 42.9%; Pred. No. 2.8e+05;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YRNLVWF 7
: : :
Db 1 FLNWSWF 7

RESULT 4

C48401
ribosomal protein L1 - Thermus aquaticus (fragment)
C;Species: Thermus aquaticus
C;Date: 01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 18-Nov-1994
C;Accession: C48401
R;Garber, M.B.; Agalarov, S.C.; Eliseikina, I.A.; Fomenkova, N.P.; Nikonov, S.V.; Sedelnikova, E.A.;
Biochimie 74, 327-336, 1992
A;Title: Ribosomal proteins from Thermus thermophilus for structural investigations.
A;Reference number: A48401; MUID:92345325; PMID:1637860
A;Accession: C48401
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-15 <GAR>
A;Note: sequence extracted from NCBI backbone (NCBIP:109932)

Query Match 27.6%; Score 24; DB 2; Length 15;
Best Local Similarity 57.1%; Pred. No. 1e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 8 IKKNTRY 14
: : :
Db 1 VKTKRY 7

RESULT 5

PC1215
homeotic protein EghbX5 - tapeworm (Echinococcus granulosus) (fragment)
C;Species: Echinococcus granulosus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 30-Sep-1993
C;Accession: PC1215
R;Oliver, G.; Vispo, M.; Mailhos, A.; Martinez, C.; Sosa-Pineda, B.; Fielitz, W.; Ehrlich, G.;
Gene 121, 337-342, 1992
A;Title: Homeoboxes in flatworms.
A;Reference number: JCL1386; MUID:93077050; PMID:1359988
A;Accession: PC1215
A;Molecule type: DNA
A;Residues: 1-14 <OLI>
A;Cross-references: EMBL:X66821
C;Keywords: homeobox

Query Match 26.4%; Score 23; DB 2; Length 14;
Best Local Similarity 33.3%; Pred. No. 1.4e+03;
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 5 VWFKNTR 13
: : :
Db 1 VWFKNRSK 9

RESULT 6

PH1626
IG H chain V-D-J region (clone B-less 118) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: PH1626
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
A;Reference number: PH1626; MUID:93301609; PMID:8315387
A;Accession: PH1626
A;Molecule type: DNA
A;Residues: 1-14 <LEV>
A;Experimental source: bone marrow pre-B lymphocyte
C;Keywords: immunoglobulin

Query Match 25.3%; Score 22; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YRNLVW 6
: : :
Db 8 YGDLW 13

RESULT 7

A47421
leukotriene B-4 12-hydroxydehydrogenase (EC 1.1.1.-) - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 19-May-1995 #sequence_revision 19-May-1995 #text_change 09-Jul-2004
C;Accession: A47421
R;Yokomizo, T.; Izumi, T.; Takahashi, T.; Kasama, T.; Kobayashi, Y.; Sato, P.; Taketani, J.; Biol. Chem. 269, 18128-18135, 1993
A;Title: Enzymatic inactivation of leukotriene B-4 by a novel enzyme found in the porcine
A;Reference number: A47421; MUID:93352633; PMID:8394361
A;Accession: A47421
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-14 <YOK>
A;Cross-references: UNIPROT:O62642
C;Keywords: oxidoreductase

Query Match 25.3%; Score 22; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 6 WFKKN 11
: : :
Db 6 WTLKKH 11

RESULT 8

A44818
extracellular lipase - Pseudomonas aeruginosa (fragment)
C;Species: Pseudomonas aeruginosa
C;Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A44818
R;Gilbert, E.J.; Cornish, A.; Jones, C.W.
J. Gen. Microbiol. 137, 2223-2229, 1991
A;Title: Purification and properties of extracellular lipase from Pseudomonas aeruginosa
A;Reference number: A44818; MUID:92085040; PMID:1748875
A;Accession: A44818
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-13 <GIL>
A;Cross-references: UNIPROT:Q9L6C7; UNIPROT:P95419
A;Experimental source: strain TE3285
A;Note: sequence extracted from NCBI backbone (NCBIP:70395)
C;Superfamily: Pseudomonas triacylglycerol lipase

Query Match 24.1%; Score 21; DB 2; Length 13;

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: February 22, 2005, 09:08:09 ; Search time 11.1333 Seconds
(without alignments)
129.633 Million cell updates/sec

Title: US-08-991-628-13
Perfect score: 87
Sequence: 1 YRNLVWFIFKNTNRY 15
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 2523

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	28.7	10	2 PT0310	Ig heavy chain CRD
2	25	28.7	15	2 B60763	endo-1,3-beta-gluc
3	24	27.6	7	2 PN0649	pullulanase (EC 3.
4	24	27.6	15	2 C49401	ribosomal protein
5	23	26.4	14	2 PC1215	homeotic protein E
6	22	25.3	14	2 PH1626	Ig H chain V-D-J r
7	22	25.3	14	2 A47421	leukotriene B-4 12
8	21	24.1	13	2 A44818	extracellular lipa
9	21	24.1	15	2 A48372	benzoyl-CoA ligase
10	20	23.0	9	2 I46023	growth hormone rec
11	20	23.0	12	2 B44818	extracellular lipa
12	20	23.0	12	2 S63123	proton-translocati
13	20	23.0	12	2 JU0356	cycloleucorinin -
14	20	23.0	13	2 E60396	antigen 7H8/2 - ma
15	20	23.0	15	2 PN0662	dystrophin-associ
16	19	21.8	7	2 PX0008	glucuronosyltransf
17	19	21.8	10	2 F41839	ribosomal protein
18	19	21.8	11	2 T12264	cytochrome-c oxida
19	19	21.8	11	2 T12253	cytochrome-c oxida
20	19	21.8	11	2 T17081	cytochrome-c oxida
21	19	21.8	12	2 S25056	Ig heavy chain - m
22	19	21.8	15	2 PH1329	Ig heavy chain DJ
23	19	21.8	15	2 PQ0074	T-cell receptor be
24	19	21.8	15	2 B35389	urease (EC 3.5.1.5
25	18	20.7	8	2 S19288	acylase - Kluivera
26	18	20.7	8	2 S43971	tumor-associated a
27	18	20.7	11	2 I54193	Rhesus blood group
28	18	20.7	12	2 I64829	gene HEXA protein
29	18	20.7	13	2 S47358	T-cell antigen rec

ALIGNMENTS

RESULT 1

PT0310
Ig heavy chain CRD3 region (clone 6-97) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0310
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A>Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0310
A:Molecule type: DNA
A:Residues: 1-10 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match 28.7%; Score 25; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LVWF 7
|||
DB 3 LVWF 6

RESULT 2

B60763
endo-1,3-beta-glucanase (EC 3.2.1.1-), 40k - Bacillus circulans (strain WL-12) (fragment)
C:Species: Bacillus circulans
C>Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 09-Jul-2004
C:Accession: B60763
R:Fiske, M.J.; Tobey-Fincher, K.L.; Fuchs, R.L.
J. Gen. Microbiol. 136, 2377-2383, 1990
A>Title: Cloning of two genes from Bacillus circulans WL-12 which encode 1,3-beta-glucan
A:Reference number: A60763; MUID:91178514; PMID:2127800
A:Accession: B60763
A:Molecule type: protein
A:Residues: 1-15 <FIS>
A:Cross-references: UNIPROT:Q7M110
C:Comment: This bacillus produces up to six different 1,3-beta-glucanases for growth on
C:Keywords: glycosidase; hydrolase

Query Match 28.7%; Score 25; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NLVW 6
|||
DB 5 NLVW 8

RESULT 3

CC and methods for the treatment and diagnosis of chlamydial infection. The
CC compounds provided include polypeptides and fusion proteins comprising
CC immunogenic portions of Chlamydia antigens and DNA sequences encoding
CC such polypeptides. They are useful for vaccinating against chlamydial
CC infection, which causes pelvic inflammatory disease, trachoma, acute
CC respiratory tract infections, atherosclerosis and heart disease
SQ Sequence 15 AA;

Query Match 35.3%; Score 30; DB 4; Length 15;
Best Local Similarity 50.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 4 VYHFVKKH 11
| : : : :
Db 2 VWEYIKKH 9

RESULT 15
ABB94132
ID ABB94132 standard; peptide; 15 AA.

AC ABB94132;

DT 05-JUN-2002 (first entry)

DE Chlamydia peptide sequence SEQ ID NO:103.

XX Chlamydial infection; Chlamydia; vaccine; detection; diagnosis; antigen;
KW antibacterial; immunostimulant; immune response;
KW Chlamydia-specific T-cell response.

XX Chlamydia sp.

OS Synthetic.

XX WO200208267-A2.

XX 31-JAN-2002.

XX 20-JUL-2001; 2001WO-US023121.

XX 20-JUL-2000; 2000US-00620412.

PR 23-APR-2001; 2001US-00841132.

XX (CORI-) CORIXA CORP.

XX Fling SP, Skeiky YAW, Probst P, Bhatia A;

XX WPI; 2002-179901/23.

XX Novel compositions comprising Chlamydia CapI protein and its use in the
XX treatment of Chlamydia infection.

XX Disclosure; Page 191; 537pp; English.

XX The present invention describes compositions comprising a Chlamydia CapI
XX protein and methods for the diagnosis and therapy of Chlamydia infection.
XX Chlamydia DNA and protein sequences from the present invention can have
XX antibacterial and immunostimulant activities, and can be used in
XX vaccines. Compounds from the present invention can be used for eliciting
XX an immune response, specifically stimulating a Chlamydia-specific T-cell
XX response or inhibiting the development of a Chlamydia infection in an
XX animal. Methods from the present invention can be used: for detecting the
XX presence of Chlamydia in a patient; to stimulate and/or expand T cells
XX specific for a Chlamydia protein; and for treatment of a Chlamydia
XX infection. ABL92394 to ABL92709 and ABB94096 to ABB94374 represent
XX sequences used in the exemplification of the present invention

XX Sequence 15 AA;

Query Match 35.3%; Score 30; DB 5; Length 15;
Best Local Similarity 50.0%; Pred. No. 4.2e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 4 VYHFVKKH 11
| : : : :
Db 2 VWEYIKKH 9

Search completed: February 22, 2005, 09:24:52
Job time : 67.6667 secs

```
XX 19-JUN-2002; 2002DE-01027238.
XX (WELA ) WELLA AG.
XX
XX Rothe H, Aeby P, Goettel O, Braun H;
XX WPI; 2004-108357/11.
XX
XX Cosmetic composition, especially hair dye, comprises a peptide with high
XX affinity for keratinic materials covalently linked to a cosmetic active
XX agent.
XX
XX Disclosure; Page 20; 30pp; German.
XX
XX This invention describes a novel cosmetic composition which comprises a
XX peptide with high affinity for keratinic materials covalently linked to a
XX cosmetic active agent (including dyes, hair conditioners, combability
XX improvers, surfactants, amidoamines, betaine esters, esterquats, fatty
XX alcohols, moisturisers, vitamins, provitamins, bounce improvers,
XX betaines, sugars and UV filters. Preferred agents include polymers,
XX silicone polyols and chitosan. The composition is useful for cosmetic
XX treatment of human or animal keratinic materials, especially as a hair
XX dye. The peptide targets the active agent to keratinic materials. The
XX invention describes a dye/amino acid conjugate prepared by reacting
XX Reactive Red 2 with DL-lysine hydrochloride. AUI32195-ADI32295 represent
XX peptide linkers used to make the cosmetic constructs described in the
XX invention.
XX
XX Sequence 13 AA;
SQ
    Query Match      35.3%; Score 30; DB 8; Length 13;
    Best Local Similarity 50.0%; Pred. No. 3.6e+02;
    Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 HFVKKHVHES 15
   | | | | |
Db 2 HHKKGHHT 11

RESULT 13
AAB13485
ID AAB13485 standard; peptide; 15 AA.
XX
XX AC AAB13485;
XX
XX 02-FEB-2001 (first entry)
XX
XX C. trachomatis Ct-Swib36-50 peptide.
XX
XX Chlamydial infection; sexually transmitted disease;
XX pelvic inflammatory disease; PID; tubal obstruction; infertility;
XX trachoma; blindness; acute respiratory tract infection; atherosclerosis;
XX coronary heart disease; antibacterial.
XX
XX Chlamydia trachomatis.
XX
XX WO200034483-A2.
XX
XX 15-JUN-2000.
XX
XX 08-DEC-1999; 99WO-US029012.
XX
XX 08-DEC-1998; 98US-00208277.
XX
XX 08-APR-1999; 99US-00288594.
XX
XX 01-OCT-1999; 99US-00410568.
XX
XX 22-OCT-1999; 99US-00426571.
XX
XX (CORI-) CORIXA CORP.
XX
XX Probst P, Bhatia A, Skeiky YAW, Fling SP, Jen S, Stromberg EJ;
XX WPI; 2000-431303/37.

XX Isolated polypeptide for diagnosis and treatment of Chlamydia infection
XX comprises immunogenic portion of Chlamydia antigen, which comprises amino
XX acid sequence encoded by polynucleotide sequence.
XX
XX Claim 2; Page 148; 256pp; English.
XX
XX The present invention relates to new nucleic acid sequences and the
XX proteins encoded by the nucleic acid sequences. The encoded proteins
XX comprise an immunogenic portion of a Chlamydia antigen. The encoded
XX proteins are useful for the serodiagnosis and treatment of Chlamydia
XX infection. Chlamydiae are intracellular bacterial pathogens that are
XX responsible for a wide variety of human infections. C. trachomatis
XX infection is one of the most common sexually transmitted diseases and can
XX lead to pelvic inflammatory disease (PID), resulting in tubal obstruction
XX and infertility. Trachoma due to ocular infection with C. trachomatis is
XX the leading cause of preventable blindness worldwide. C. pneumonia is a
XX major cause of acute respiratory tract infections in humans and is also
XX thought to play a role in the pathogenesis of atherosclerosis and
XX coronary heart disease. The present sequence is a protein isolated in the
XX present invention
XX
XX Sequence 15 AA;
SQ
    Query Match      35.3%; Score 30; DB 3; Length 15;
    Best Local Similarity 50.0%; Pred. No. 4.2e+02;
    Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 VVHFVKKH 11
   | : : : |
Db 2 VVEVIKHH 9

RESULT 14
AAG83161
ID AAG83161 standard; peptide; 15 AA.
XX
XX AC AAG83161;
XX
XX 05-SEP-2001 (first entry)
XX
XX Chlamydia trachomatis Ct-Swib 36-50 peptide.
XX
XX Chlamydia; vaccine; infection; fusion protein; antigen;
XX pelvic inflammatory disease; trachoma; atherosclerosis; heart disease;
XX acute respiratory tract infection; Cap1; CT529; OMCB;
XX polymorphic membrane protein; pmp; thiol specific antioxidant; TSA.
XX
XX Chlamydia trachomatis.
XX
XX WO200140474-A2.
XX
XX 07-JUN-2001.
XX
XX 04-DEC-2000; 2000WO-US032919.
XX
XX 03-DEC-1999; 99US-00454684.
XX
XX 19-APR-2000; 2000US-00556877.
XX
XX 20-JUN-2000; 2000US-00598419.
XX
XX (CORI-) CORIXA CORP.
XX
XX Probst P, Bhatia A, Skeiky YAW, Fling SP, Scholler J;
XX WPI; 2001-374831/39.
XX
XX Chlamydia polypeptides and fusion proteins useful for preventing pelvic
XX inflammatory disease, trachoma, acute respiratory tract infections,
XX atherosclerosis and heart disease.
XX
XX Disclosure; Page 157; 295pp; English.
XX
XX The present peptide is provided in a specification relating to compounds
```

CC from the F2a and F2c regions of the proteins GDNF, neurturin and artemin,
 CC from humans, mice or rats. This type of protein activates the growth
 CC factor receptor alpha1-Ret protein-tyrosine kinase (GFRalpha1-RET), but
 CC does not substantially activate GFRalpha2-RET or GFRalpha3-RET. The
 CC growth factors and nucleic acids encoding them are useful for providing
 CC trophic support to a mammalian cell and/or for producing differentiation
 CC of a mammalian cell, in a patient suffering from peripheral neuropathy,
 CC amyotrophic lateral sclerosis, Alzheimer's disease, Parkinson's disease,
 CC Huntington's disease, diabetes, acquired immunodeficiency syndrome
 CC (AIDS), ischaemic stroke, acute brain injury, acute spinal cord injury,
 CC multiple sclerosis, nervous system tumours (e.g. neuroblastomas), or
 CC enteric diseases such as idiopathic constipation. The sequences are also
 CC useful for preventing or treating cellular degeneration or insufficiency
 CC in an individual, suffering from eosinopaenia, basopaenia, lymphopaenia,
 CC monocytopenia, neutropenia, anaemia, thrombocytopaenia, cardiac muscle
 CC degeneration, or congestive heart failure. The growth factors are also
 CC useful for promoting the survival of peripheral and central neuronal
 CC populations in vivo or in vitro

XX
 SQ Sequence 7 AA;

Query Match 36.5%; Score 31; DB 4; Length 7;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 YHVFVKH 11
 || :||
 DB 1 YHILRKH 7

RESULT 9
 ADB81184
 ID ADB81184 standard; peptide; 13 AA.

AC ADB81184;

DT 04-DEC-2003 (first entry)

DE Human pancreatic/heart tissue quantified by LC-MS analysis, SEQ ID No 75.
 DE quantitating relative abundance; liquid phase tandem mass spectroscopy;
 KW data set; peptide profile; toxicology analysis; classification; human.

OS Homo.

OS sapiens.

XX WO200297703-A2.

PD 05-DEC-2002.

XX 30-MAY-2002; 2002WO-CA000801.

XX 30-MAY-2001; 2001CA-02349265.

XX (EMIL/) EMILI A.
 PA (CAGN/) CAGNEY G.

PI Emili A, Cagney G;

XX WPI; 2003-175129/17.

XX Identifying and quantifying proteins/peptide sequences, comprises
 PT identifying peptides by liquid phase tandem mass spectroscopy sequencing
 PT and compiling data set/peptide profile containing collection of peptide
 PT sequences.

XX Example 3; Page 49; 84pp; English.

XX The invention relates to a novel method for identifying constituent
 CC proteins/peptide sequences or quantitating relative abundance of proteins
 CC in two samples, for a cell type, tissue or pathological sample using a
 CC database having peptide profile libraries with multiple protein/peptide
 CC sequences. The method comprises identifying peptide species by liquid

CC phase tandem mass spectroscopy sequencing and compiling a data
 CC set/peptide profile. The novel method is useful in toxicology analysis.
 CC In the method of the invention, there is no requirement for prior
 CC knowledge about the functions of the responsive peptides or parental
 CC proteins. Protein functions deduced from comparisons of profiles in a
 CC database can be derived from very subtle physiological responses. For
 CC instance, even though peptide levels may change only slightly in response
 CC to an experimental treatment, coordinate changes among many measured
 CC peptide abundances can be sufficient to characterise that phenotype. The
 CC large number of peptides measured make it unlikely that an unrelated
 CC physiological state will have an identical profile, even though this may
 CC not be apparent when using conventional experiments that measure the
 CC levels of one or a few proteins. Closely related profiles can be classed
 CC together, thus improving the understanding of the underlying biological
 CC basis of the classifications. This sequence represents a peptide
 CC sequenced and quantified from a human lung tissue lysate sample in a
 CC single liquid chromatography-mass spectrometry (LC-MS) analysis, used in
 CC the method for the measurement of protein relative abundance in complex
 CC mixtures.

XX
 SQ Sequence 13 AA;

Query Match 36.5%; Score 31; DB 7; Length 13;
 Best Local Similarity 50.0%; Pred. No. 2.4e+02;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGGVVFVKK 10
 ||| :||
 DB 4 TGGIAHLFKQ 13

RESULT 10
 AAW11603
 ID AAW11603 standard; peptide; 11 AA.

AC AAW11603;

DT 22-SEP-1997 (first entry)

DE Linear ZnF peptide.

DE Conformationally-restricted polypeptide; alpha-helical coiled coil;
 KW combinatorial library; macromolecular ligand; peptidomimetic; antibody;
 KW ion channel.

OS Synthetic.

XX Key Location/Qualifiers

FH Modified-site 1 /note= "In acetyl form"

FT Modified-site 11 /note= "In amide form"

XX WO9700267-A1.

XX 03-JAN-1997.

XX 14-JUN-1996; 96WO-CA000403.

XX 16-JUN-1995; 95US-00491527.

XX (PENC-) PENCE INC.

XX Houston ME, Hodges RS;

XX WPI; 1997-077485/07.

XX Combinatorial library of conformationally-restricted polypeptide(s) -
 PT used to screen for cpds. that react specifically with a macromolecular
 PT ligand and for developing peptidomimetics.

XX Example '6; Fig 9; 66pp; English.

CC The present sequence represents a linear ZnF peptide. This peptide was
 CC used to show that peptides with lactam bridges inhibit antibody binding
 CC more effectively than peptides without lactam bridges. The present
 CC peptide could inhibit antibody binding but not to such a high degree as
 CC lactam bridge peptides. The lactam bridge containing peptides can be used
 CC in a combinatorial library of alpha-helical polypeptides each of 15-50
 CC amino acids, stabilised by at least one lactam bridge between non-
 CC adjacent residues and with a unique variation of amino acid residues in
 CC at least 3 positions. The library can be used to identify compounds that
 CC interact specifically with a particular macromolecular ligand, e.g.
 CC antibody (or fragment), receptor, ion channel, enzyme (or substrate)
 XX

XX Sequence 11 AA;

Query Match 35.3%; Score 30; DB 2; Length 11;
 Best Local Similarity 50.0%; Pred. No. 2.9e+02;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 6 HFVKKHVVH 13
 ||: :||
 Db 2 HFLVQHTH 9

RESULT 11
 ADP83191
 ID ADP83191 standard; peptide; 12 AA.

XX
 AC ADP83191;

XX
 DT 23-SEP-2004 (first entry)

XX
 DE ICAM-5 FGFR binding motif peptide SEQ ID NO:99.

XX protein interaction modulation; cell-surface receptor;
 KW receptor binding site; neuroprotective; vulnery; antidiabetic;
 KW nephrotropic; gene therapy; fibroblast growth factor receptor; FGFR;
 KW receptor ligand; neural cell adhesion molecule; NCAM; solid tumour;
 KW neoplasia; central nervous system disorder;
 KW peripheral nervous system disorder; postoperative nerve damage;
 KW traumatic nerve damage; impaired myelination; post-ischaemic damage;
 KW stroke; Parkinson's disease; Alzheimer's disease; Huntington's disease;
 KW dementia; multiinfarct dementia; sclerosis; nerve degeneration;
 KW diabetes mellitus; schizophrenia; mood disorder; manic depression;
 KW neuro-muscular connection; organ transplantation;
 KW genetic atrophic muscle disorder; traumatic atrophic muscle disorder;
 KW degenerative condition; acute myocardial infarction; angiogenesis;
 KW wound-healing; revascularisation.

XX Synthetic.

XX WO2004056865-A2.

XX
 PN 08-JUL-2004.

XX
 PD 18-DEC-2003; 2003WO-DK000901.

XX
 PF 20-DEC-2002; 2002DK-00001982.

XX
 PR 03-MAR-2003; 2003DK-00000330.

XX (ENKA-) ENKAM PHARM AS.

XX Berezin V, Albrechtsen M, Bock E;

XX WPT; 2004-517671/49.

XX Modulating the interaction between at least two different proteins by
 FT providing a compound capable of interfering with the receptor and the
 FT polypeptide interaction and presenting the compound to the different
 PT proteins.

XX Claim 45; SEQ ID NO 99; 154pp; English.

XX The present invention describes a method for modulating the interaction

CC between at least two different proteins, where one of the proteins is
 CC represented by a functional cell-surface receptor, or its fragment or
 CC variant or by a polypeptide having a binding site to the receptor, where
 CC at least a part of the binding site comprises at least one of the
 CC sequences given in SEQ ID NO:1 to 146 (ADP83093 to ADP83238), or
 CC fragments, or variants, or homologues of the sequences, or fragments or
 CC variants of the homologues, comprising (i) providing a compound capable
 CC of interacting with the receptor and/or polypeptide to interfere with the
 CC receptor and the polypeptide interaction, and (ii) presenting the
 CC compound of step (i) to at least two different proteins. The compound has
 CC neuroprotective, vulnery, antidiabetic and nephrotropic activities, and
 CC can be used in gene therapy. The method is useful in modulating the
 CC interaction between at least two different proteins, where one of the
 CC proteins is represented by a functional cell-surface receptor, selected
 CC from the family of fibroblast growth factor receptors (FGFRs), and the
 CC other protein is the receptor ligand. A compound capable of modulating
 CC the interaction between at least two different proteins, where one of the
 CC proteins is represented by a functional cell-surface receptor, selected
 CC from the family of fibroblast growth factor receptors (FGFRs), and the
 CC other protein is the receptor ligand, can be used for treating normal,
 CC degenerated or damaged neural cell adhesion molecule (NCAM) presenting
 CC cells; solid tumour requiring neovascularisation; diseases and conditions of
 CC the central and peripheral nervous system, of the muscles or of various
 CC organs, e.g., postoperative nerve damage, traumatic nerve damage,
 CC impaired myelination of nerve fibres, post-ischaemic damage, e.g.
 CC resulting from a stroke, Parkinson's disease, Alzheimer's disease,
 CC Huntington's disease, dementias such as multiinfarct dementia, sclerosis,
 CC nerve degeneration associated with diabetes mellitus, disorders affecting
 CC the circadian clock or neuro-muscular transmission, and schizophrenia,
 CC mood disorders, such as manic depression; diseases or conditions of the
 CC muscles including conditions with impaired function of neuro-muscular
 CC connections, such as after organ transplantation, or such as genetic or
 CC traumatic atrophic muscle disorders; degenerative conditions of the
 CC gonads, of the pancreas such as diabetes mellitus type I and II, of the
 CC kidney such as nephrosis or of the heart, liver and bowel; for preventing
 CC cell death of heart muscle cells, such as after acute myocardial
 CC infarction, or after angiogenesis; for promoting wound-healing; for
 CC revascularisation; or for stimulating the ability to learn and/or the
 CC short and/or long-term memory.

XX
 SQ Sequence 12 AA;

Query Match 35.3%; Score 30; DB 8; Length 12;
 Best Local Similarity 45.5%; Pred. No. 3.2e+02;
 Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GVYHFVKKHVVH 13
 ||||:|
 Db 1 GTYHCVATNAH 11

RESULT 12

ADI32280
 ID ADI32280 standard; peptide; 13 AA.

XX
 AC ADI32280;

XX
 DT 22-APR-2004 (first entry)

XX
 DE Cosmetic agent construct peptide linker #86.

XX cosmetic; keratin; dye; hair conditioner; combability improver;
 KW surfactant; amidoamine; betaine ester; esterquats; fatty alcohol;
 KW moisturiser; vitamin; provitamin; bounce improver; betaine; sugar;
 KW UV filter; polymer; silicone polyol; chitosan.

XX Synthetic.

XX WO2004000257-A2.

XX
 PN 31-DEC-2003.

XX
 PD 14-MAY-2003; 2003WO-EP005021.